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OM protein - nucleic search, using frame_plus_p2n model

Run on: January 13, 2005, 00:43:34 ; Search time 490 Seconds
(without alignments)
3072.291 Million cell updates/sec

Perfect score: 1343

Sequence: 1 MTQVPRLSPVPAALGSA.....VRVYISLLPLGDGTLPFKI 262

Scoring table: BLOSUM62

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4300275 seqs, 2872944193 residues

Total number of hits satisfying chosen parameters: 8600550

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

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Database : Published Applications NA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result Query

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40	1343	100.0	989	15	US-10-013-909A-305	Sequence 305, App
63	1343	100.0	989	15	US-10-211-858-21	Sequence 21, Appl
69	1343	100.0	989	16	US-10-307-817-121	Sequence 121, App
70	1343	100.0	989	16	US-10-307-817-125	Sequence 125, App
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74	884	65.8	787	16	US-10-307-817-123	Sequence 123, App
c 75	707	52.6	620	16	US-10-240-425-182	Sequence 182, App
76	509	37.9	458	10	US-09-918-995-23102	Sequence 23102, A
77	509	37.9	474	10	US-09-918-995-22407	Sequence 22407, A
78	428.5	31.9	1512	18	US-10-739-930-3516	Sequence 3516, Ap
c 79	425.5	31.7	84428	16	US-10-329-1488-1	Sequence 1, Appli
80	413	30.8	849	16	US-10-425-114-25410	Sequence 25410, A
81	413	30.8	1159	16	US-10-425-114-2777	Sequence 2777, Ap
82	413	30.8	1218	15	US-10-361-460-77	Sequence 77, Appl
83	411	30.6	86941	16	US-10-461-194-2	Sequence 2, Appli
84	409.5	30.5	85692	16	US-10-461-194-1	Sequence 1, Appli
85	407	30.3	901	16	US-10-425-114-27082	Sequence 27082, A
86	407	30.3	2381	18	US-10-425-115-138013	Sequence 138013, A
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93	396	29.5	1058	9	US-09-452-239-11	Sequence 11, Appl
94	396	29.5	1060	17	US-10-437-963-62449	Sequence 62449, A
c 95	396	29.5	3759	17	US-10-437-963-23149	Sequence 23149, A
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97	392.5	29.2	962	9	US-09-452-239-23	Sequence 23, Appl
98	392.5	29.2	1023	9	US-09-452-239-25	Sequence 25, Appl
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117	386	28.7	1146	9	US-09-452-239-3	Sequence 3, Appli
118	386	28.7	1160	15	US-10-361-460-31	Sequence 31, Appl
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137	378	28.1	1066	18	US-10-425-115-179664	Sequence 179664, A	210	173.5	12.9	584	18	US-10-425-115-53810	Sequence 53810, A
138	377.5	28.1	905	17	US-10-437-963-41715	Sequence 41715, A	211	172.5	12.8	522	15	US-10-156-761-3105	Sequence 3105, App
139	377	28.1	1233	17	US-10-767-795-6335	Sequence 6335, App	212	172	12.8	2355	16	US-10-424-599-18324	Sequence 18324, A
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149	366	27.3	326	9	US-09-880-107-632	Sequence 632, App	222	164	12.2	3011208	16	US-10-398-221-2058	Sequence 8, Appl
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152	356.5	26.5	1107	18	US-10-425-115-138003	Sequence 138003, A	225	159.5	11.9	415	16	US-09-770-423-481	Sequence 481, App
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182	276.5	20.6	343	9	US-09-917-800A-298	Sequence 298, App	255	112	8.3	2086	8	US-09-935-757-5	Sequence 5, Appl
183	276.5	20.6	343	16	US-10-152-319A-298	Sequence 298, App	256	111.5	8.3	602	18	US-10-425-115-172234	Sequence 172234, A
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187	224.5	16.7	760	15	US-10-174-693-25	Sequence 25, Appl	260	110	8.2	919	16	US-10-425-114-3232	Sequence 35115, A
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194	207	15.4	528	9	US-09-452-239-33	Sequence 33, Appl	267	107.5	8.0	1327	13	US-10-087-192-1325	Sequence 642, App
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C 282	101.5	7.6	2505	15	US-10-303-110A-1	Sequence 1, Appli	355	93	6.9	5032	17	US-10-473-576-26	Sequence 26, Appli
C 283	101.5	7.6	2505	15	US-10-303-110A-4	Sequence 4, Appli	356	93	6.9	5591	15	US-10-170-385-14	Sequence 14, Appli
C 284	101	7.5	1602	17	US-10-437-963-102014	Sequence 102014,	357	93	6.9	7788	15	US-10-329-079-8	Sequence 8, Appli
C 285	101	7.5	1786	16	US-10-302-172-657	Sequence 657, App	358	93	6.9	37360	15	US-10-329-079-6	Sequence 6, Appli
C 286	100.5	7.5	1815	15	US-10-332-813-3	Sequence 3, Appli	c 359	92.5	6.9	1107	15	US-10-156-761-6131	Sequence 6131, Ap
C 287	100.5	7.5	1815	15	US-10-339-668-3	Sequence 3, Appli	c 360	92.5	6.9	2433	11	US-09-864-636A-587	Sequence 587, App
C 288	100.5	7.5	1815	17	US-10-717-049-3	Sequence 3, Appli	c 361	92.5	6.9	2433	11	US-09-864-426A-587	Sequence 587, App
C 289	100	7.4	8460	14	US-10-237-271-2	Sequence 2, Appli	c 362	92.5	6.9	2433	15	US-10-084-839-587	Sequence 587, App
C 290	100	7.4	8460	15	US-10-191-997-115	Sequence 115, App	c 363	92.5	6.9	2445	10	US-09-864-636A-571	Sequence 571, App
C 291	100	7.4	8460	16	US-10-274-085-4	Sequence 4, Appli	c 364	92.5	6.9	2445	10	US-09-864-636A-571	Sequence 571, App
C 292	100	7.4	8460	17	US-10-717-597-192	Sequence 192, App	c 365	92.5	6.9	2445	10	US-09-864-636A-579	Sequence 579, App
C 293	99	7.4	2010	16	US-10-159-563-379	Sequence 379, App	c 366	92.5	6.9	2445	10	US-09-864-636A-581	Sequence 581, App
C 294	99	7.4	2010	15	US-10-418-007-3	Sequence 3, Appli	c 367	92.5	6.9	2445	11	US-09-864-426A-571	Sequence 571, App
C 295	99	7.4	2010	18	US-10-641-325-7	Sequence 7, Appli	c 368	92.5	6.9	2445	11	US-09-864-426A-575	Sequence 575, App
C 296	99	7.4	2430	17	US-10-437-963-10627	Sequence 10627, A	c 369	92.5	6.9	2445	11	US-09-864-426A-579	Sequence 579, App
C 297	99	7.4	2685	16	US-10-401-403-147	Sequence 147, App	c 370	92.5	6.9	2445	11	US-09-864-426A-581	Sequence 581, App
C 298	99	7.4	2685	16	US-10-401-403-171	Sequence 171, App	c 371	92.5	6.9	2445	15	US-10-084-839-571	Sequence 571, App
C 299	98.5	7.3	1338	15	US-10-156-761-3240	Sequence 3240, Ap	c 372	92.5	6.9	2445	15	US-10-084-839-575	Sequence 575, App
C 300	98.5	7.3	2384	15	US-10-104-047-567	Sequence 567, App	c 373	92.5	6.9	2445	15	US-10-084-839-579	Sequence 579, App
C 301	98.5	7.3	3147	9	US-09-741-669-216	Sequence 216, App	c 374	92.5	6.9	2445	15	US-10-084-839-581	Sequence 581, App
C 302	98.5	7.3	3147	9	US-09-815-242-5965	Sequence 5965, Ap	c 375	92.5	6.9	2445	15	US-10-084-839-589	Sequence 589, App
C 303	98.5	7.3	3147	15	US-10-301-997-84	Sequence 84, Appl	c 376	92.5	6.9	2445	15	US-10-084-839-2822	Sequence 2822, Ap
C 304	98.5	7.3	3147	16	US-10-282-122A-20260	Sequence 20260, A	c 377	92.5	6.9	2445	15	US-10-084-839-2826	Sequence 2826, Ap
C 305	98.5	7.3	3147	17	US-10-818-509-84	Sequence 84, Appl	c 378	92.5	6.9	2445	15	US-10-084-839-2828	Sequence 2828, Ap
C 306	98.5	7.3	77536	10	US-09-940-316B-1	Sequence 1, Appli	c 379	92.5	6.9	2493	10	US-09-864-636A-589	Sequence 589, App
C 307	98	7.3	828	16	US-10-282-122A-31998	Sequence 31998, A	c 380	92.5	6.9	2493	11	US-09-864-426A-589	Sequence 589, App
C 308	97.5	7.3	2505	15	US-10-303-110A-2	Sequence 2, Appli	c 381	92.5	6.9	2493	15	US-10-084-839-589	Sequence 589, App
C 309	97.5	7.3	2505	15	US-10-303-110A-3	Sequence 3, Appli	c 382	92.5	6.9	2493	15	US-10-084-839-2836	Sequence 2836, Ap
C 310	97.5	7.3	2505	15	US-10-303-110A-5	Sequence 5, Appli	c 383	92.5	6.9	2499	10	US-09-864-636A-585	Sequence 585, App
C 311	97.5	7.3	2505	15	US-10-303-110A-6	Sequence 6, Appli	c 384	92.5	6.9	2499	11	US-09-864-426A-585	Sequence 585, App
C 312	97.5	7.3	2505	15	US-10-303-110A-7	Sequence 7, Appli	c 385	92.5	6.9	2499	15	US-10-084-839-585	Sequence 585, App
C 313	97.5	7.3	2505	15	US-10-303-110A-10	Sequence 10, Appl	c 386	92.5	6.9	2508	10	US-09-864-636A-401	Sequence 401, App
C 314	97.5	7.3	2508	17	US-10-437-963-69592	Sequence 69592, A	c 387	92.5	6.9	2508	10	US-09-864-636A-405	Sequence 405, App
C 315	97	7.2	421	16	US-10-424-599-1595	Sequence 1595, Ap	c 388	92.5	6.9	2508	10	US-09-864-636A-407	Sequence 407, App
C 316	97	7.2	1104	16	US-10-282-122A-33573	Sequence 33573, A	c 389	92.5	6.9	2508	10	US-09-864-636A-409	Sequence 409, App
C 317	97	7.2	2867	17	US-10-437-963-195	Sequence 195, App	c 390	92.5	6.9	2508	10	US-09-864-636A-411	Sequence 411, App
C 318	96.5	7.2	1454	18	US-10-425-115-126435	Sequence 126435,	c 391	92.5	6.9	2508	10	US-09-864-636A-415	Sequence 415, App
C 319	96.5	7.2	2227	18	US-10-425-115-3967	Sequence 3967, Ap	c 392	92.5	6.9	2508	10	US-09-864-636A-417	Sequence 417, App
C 320	96.5	7.2	5397	17	US-10-437-963-69644	Sequence 69644, A	c 393	92.5	6.9	2508	10	US-09-864-636A-419	Sequence 419, App
C 321	96	7.1	1322	14	US-10-425-115-122270	Sequence 122270,	c 394	92.5	6.9	2508	10	US-09-864-636A-423	Sequence 423, App
C 322	96	7.1	15952	18	US-10-171-311-51	Sequence 51, Appl	c 395	92.5	6.9	2508	10	US-09-864-636A-426	Sequence 426, App
C 323	95.5	7.1	348	15	US-10-424-599-30454	Sequence 30454, A	c 396	92.5	6.9	2508	10	US-09-864-636A-431	Sequence 431, App
C 324	95.5	7.1	1272	15	US-10-369-493-37699	Sequence 37699, A	c 397	92.5	6.9	2508	10	US-09-864-636A-439	Sequence 439, App
C 325	95.5	7.1	1565	18	US-10-739-930-2155	Sequence 2155, Ap	c 398	92.5	6.9	2508	11	US-09-864-426A-401	Sequence 401, App
C 326	95.5	7.1	2261	17	US-10-437-963-15102	Sequence 15102, A	c 399	92.5	6.9	2508	11	US-09-864-426A-405	Sequence 405, App
C 327	95.5	7.1	2553	9	US-09-815-242-7690	Sequence 7690, Ap	c 400	92.5	6.9	2508	11	US-09-864-426A-407	Sequence 407, App
C 328	95.5	7.1	2553	16	US-10-282-122A-29994	Sequence 29994, A	c 401	92.5	6.9	2508	11	US-09-864-426A-409	Sequence 409, App
C 329	95	7.1	553	15	US-10-264-049-1169	Sequence 1169, Ap	c 402	92.5	6.9	2508	11	US-09-864-426A-411	Sequence 411, App
C 330	95	7.1	717	15	US-10-156-761-4336	Sequence 4336, Ap	c 403	92.5	6.9	2508	11	US-09-864-426A-415	Sequence 415, App
C 331	95	7.1	1062	18	US-10-739-930-1766	Sequence 1766, Ap	c 404	92.5	6.9	2508	11	US-09-864-426A-419	Sequence 419, App
C 332	95	7.1	1948	16	US-10-282-122A-15101	Sequence 15101, A	c 405	92.5	6.9	2508	11	US-09-864-426A-423	Sequence 423, App
C 333	95	7.1	2597	15	US-10-094-749-246	Sequence 246, App	c 406	92.5	6.9	2508	11	US-09-864-426A-426	Sequence 426, App
C 334	95	7.1	4184	10	US-09-927-827-42	Sequence 42, Appl	c 407	92.5	6.9	2508	11	US-09-864-426A-426	Sequence 426, App
C 335	94.5	7.0	373	16	US-10-424-599-109508	Sequence 109508,	c 408	92.5	6.9	2508	11	US-09-864-426A-431	Sequence 431, App
C 336	94.5	7.0	1243	18	US-10-739-930-2839	Sequence 2839, Ap	c 409	92.5	6.9	2508	11	US-09-864-426A-439	Sequence 439, App
C 337	94	7.0	717	16	US-10-282-122A-31785	Sequence 31785, A	c 410	92.5	6.9	2508	15	US-10-084-839-401	Sequence 401, App
C 338	94	7.0	4618	18	US-10-723-860-4935	Sequence 4935, Ap	c 411	92.5	6.9	2508	15	US-10-084-839-405	Sequence 405, App
C 339	94	7.0	14101	16	US-10-197-824-6	Sequence 6, Appli	c 412	92.5	6.9	2508	15	US-10-084-839-407	Sequence 407, App
C 340	94	7.0	17589	15	US-10-197-824-3	Sequence 3, Appli	c 413	92.5	6.9	2508	15	US-10-084-839-409	Sequence 409, App
C 341	93.5	7.0	840	15	US-10-156-761-1969	Sequence 1969, Ap	c 414	92.5	6.9	2508	15	US-10-084-839-411	Sequence 411, App
C 342	93.5	7.0	1107	15	US-10-156-761-4441	Sequence 4441, Ap	c 415	92.5	6.9	2508	15	US-10-084-839-415	Sequence 415, App
C 343	93.5	7.0	2505	15	US-10-303-110A-8	Sequence 8, Appli	c 416	92.5	6.9	2508	15	US-10-084-839-417	Sequence 417, App
C 344	93.5	7.0	2505	15	US-10-303-110A-9	Sequence 9, Appli	c 417	92.5	6.9	2508	15	US-10-084-839-419	Sequence 419, App
C 345	93.5	7.0	2505	15	US-10-303-110A-11	Sequence 11, Appli	c 418	92.5	6.9	2508	15	US-10-084-839-423	Sequence 423, App
C 346	93.5	7.0	2505	15	US-10-303-110A-12	Sequence 12, Appli	c 419	92.5	6.9	2508	15	US-10-084-839-426	Sequence 426, App
C 347	93.5	7.0	125746	15	US-10-156-761-15102	Sequence 15102, A	c 420	92.5	6.9	2508	15	US-10-084-839-431	Sequence 431, App
C 348	93.5	7.0	154746	10	US-09-827-688-8	Sequence 8, Appli	c 421	92.5	6.9	2508	15	US-10-084-839-439	Sequence 439, App
C 349	93	6.9	1524	18	US-10-425-115-114038	Sequence 114038,	c 422	92.5	6.9	2508	15	US-10-084-839-2737	Sequence 2737, Ap
C 350	93	6.9	1908	15	US-10-369-493-33780	Sequence 33780, A	c 423	92.5	6.9	2508	15	US-10-084-839-2739	Sequence 2739, Ap
C 351	93	6.9	2176	8	US-08-808-031A-1	Sequence 1, Appli	c 424	92.5	6.9	2508	15	US-10-084-839-2741	Sequence 2741, Ap
C 352	93	6.9	3744	16	US-10-302-172-585	Sequence 585, App	c 425	92.5	6.9	2508	15	US-10-084-839-2743	Sequence 2743, Ap
C 353	93	6.9	4018	15	US-10-172-118-308	Sequence 308, App	c 426	92.5	6.9	2508	15	US-10-084-839-2745	Sequence 2745, Ap
C 354	93	6.9	4018	16	US-10-342-887-308	Sequence 308, App	c 427	92.5	6.9	2508	15	US-10-084-839-2747	Sequence 2747, Ap

C 428	92.5	6.9	2508	15	US-10-084-839-2749	Sequence 2749, Ap	C 501	92.5	6.9	2517	15	US-10-084-839-529	Sequence 529, App
C 429	92.5	6.9	2508	15	US-10-084-839-2751	Sequence 2751, Ap	C 502	92.5	6.9	2517	15	US-10-084-839-533	Sequence 533, App
C 430	92.5	6.9	2508	15	US-10-084-839-2753	Sequence 2753, Ap	C 503	92.5	6.9	2517	15	US-10-084-839-537	Sequence 537, App
C 431	92.5	6.9	2508	15	US-10-084-839-2755	Sequence 2755, Ap	C 504	92.5	6.9	2517	15	US-10-084-839-2675	Sequence 2675, Ap
C 432	92.5	6.9	2508	15	US-10-084-839-2757	Sequence 2757, Ap	C 505	92.5	6.9	2517	15	US-10-084-839-2706	Sequence 2706, Ap
C 433	92.5	6.9	2508	15	US-10-084-839-2761	Sequence 2761, Ap	C 506	92.5	6.9	2517	15	US-10-084-839-2779	Sequence 2779, Ap
C 434	92.5	6.9	2511	9	US-09-777-430A-12	Sequence 12, Appl	C 507	92.5	6.9	2517	15	US-10-084-839-2784	Sequence 2784, Ap
C 435	92.5	6.9	2511	10	US-09-940-244-258	Sequence 258, App	C 508	92.5	6.9	2517	15	US-10-084-839-2790	Sequence 2790, Ap
C 436	92.5	6.9	2511	10	US-09-864-636A-262	Sequence 262, App	C 509	92.5	6.9	2517	15	US-10-084-839-2794	Sequence 2794, Ap
C 437	92.5	6.9	2511	10	US-09-758-282-59	Sequence 59, Appl	C 510	92.5	6.9	2517	15	US-10-084-839-2796	Sequence 2796, Ap
C 438	92.5	6.9	2511	11	US-09-864-426A-262	Sequence 262, App	C 511	92.5	6.9	2517	15	US-10-084-839-2798	Sequence 2798, Ap
C 439	92.5	6.9	2511	15	US-10-084-839-2715	Sequence 2715, Ap	C 512	92.5	6.9	2517	15	US-10-084-839-2800	Sequence 2800, Ap
C 440	92.5	6.9	2511	15	US-10-084-839-2834	Sequence 2834, Ap	C 513	92.5	6.9	2517	15	US-10-084-839-2802	Sequence 2802, Ap
C 441	92.5	6.9	2511	15	US-10-084-839-2834	Sequence 2834, Ap	C 514	92.5	6.9	2517	15	US-10-084-839-2804	Sequence 2804, Ap
C 442	92.5	6.9	2511	18	US-10-309-584-258	Sequence 258, App	C 515	92.5	6.9	2517	15	US-10-084-839-2806	Sequence 2806, Ap
C 443	92.5	6.9	2514	10	US-09-864-636A-133	Sequence 133, App	C 516	92.5	6.9	2517	15	US-10-084-839-2808	Sequence 2808, Ap
C 444	92.5	6.9	2514	10	US-09-864-636A-454	Sequence 454, App	C 517	92.5	6.9	2517	15	US-10-084-839-2856	Sequence 2856, Ap
C 445	92.5	6.9	2514	10	US-09-864-636A-475	Sequence 475, App	C 518	92.5	6.9	2520	10	US-09-864-636A-222	Sequence 222, App
C 446	92.5	6.9	2514	10	US-09-864-636A-499	Sequence 499, App	C 519	92.5	6.9	2520	10	US-09-864-636A-505	Sequence 505, App
C 447	92.5	6.9	2514	10	US-09-758-282-260	Sequence 260, App	C 520	92.5	6.9	2520	10	US-09-864-636A-541	Sequence 541, App
C 448	92.5	6.9	2514	11	US-09-864-426A-133	Sequence 133, App	C 521	92.5	6.9	2520	10	US-09-864-636A-543	Sequence 543, App
C 449	92.5	6.9	2514	11	US-09-864-426A-454	Sequence 454, App	C 522	92.5	6.9	2520	10	US-09-864-636A-577	Sequence 577, App
C 450	92.5	6.9	2514	11	US-09-864-426A-475	Sequence 475, App	C 523	92.5	6.9	2520	10	US-09-864-636A-583	Sequence 583, App
C 451	92.5	6.9	2514	11	US-09-864-426A-499	Sequence 499, App	C 524	92.5	6.9	2520	10	US-09-864-636A-587	Sequence 587, App
C 452	92.5	6.9	2514	15	US-10-084-839-133	Sequence 133, App	C 525	92.5	6.9	2520	10	US-09-758-282-279	Sequence 279, App
C 453	92.5	6.9	2514	15	US-10-084-839-454	Sequence 454, App	C 526	92.5	6.9	2520	11	US-09-864-426A-222	Sequence 222, App
C 454	92.5	6.9	2514	15	US-10-084-839-475	Sequence 475, App	C 527	92.5	6.9	2520	11	US-09-864-426A-505	Sequence 505, App
C 455	92.5	6.9	2514	15	US-10-084-839-499	Sequence 499, App	C 528	92.5	6.9	2520	11	US-09-864-426A-541	Sequence 541, App
C 456	92.5	6.9	2514	15	US-10-084-839-2708	Sequence 2708, Ap	C 529	92.5	6.9	2520	11	US-09-864-426A-543	Sequence 543, App
C 457	92.5	6.9	2514	15	US-10-084-839-2764	Sequence 2764, Ap	C 530	92.5	6.9	2520	11	US-09-864-426A-577	Sequence 577, App
C 458	92.5	6.9	2514	15	US-10-084-839-2775	Sequence 2775, Ap	C 531	92.5	6.9	2520	11	US-09-864-426A-583	Sequence 583, App
C 459	92.5	6.9	2514	15	US-10-084-839-2788	Sequence 2788, Ap	C 532	92.5	6.9	2520	11	US-09-864-426A-587	Sequence 587, App
C 460	92.5	6.9	2514	15	US-10-084-839-2850	Sequence 2850, Ap	C 533	92.5	6.9	2520	15	US-10-084-839-222	Sequence 222, App
C 461	92.5	6.9	2514	15	US-10-084-839-2854	Sequence 2852, Ap	C 534	92.5	6.9	2520	15	US-10-084-839-505	Sequence 505, App
C 462	92.5	6.9	2514	15	US-10-084-839-2854	Sequence 2854, Ap	C 535	92.5	6.9	2520	15	US-10-084-839-541	Sequence 541, App
C 463	92.5	6.9	2517	10	US-09-864-636A-69	Sequence 69, Appl	C 536	92.5	6.9	2520	15	US-10-084-839-543	Sequence 543, App
C 464	92.5	6.9	2517	10	US-09-864-636A-128	Sequence 128, App	C 537	92.5	6.9	2520	15	US-10-084-839-577	Sequence 577, App
C 465	92.5	6.9	2517	10	US-09-864-636A-484	Sequence 484, App	C 538	92.5	6.9	2520	15	US-10-084-839-577	Sequence 577, App
C 466	92.5	6.9	2517	10	US-09-864-636A-495	Sequence 495, App	C 539	92.5	6.9	2520	15	US-10-084-839-583	Sequence 583, App
C 467	92.5	6.9	2517	10	US-09-864-636A-501	Sequence 501, App	C 540	92.5	6.9	2520	15	US-10-084-839-2711	Sequence 2711, Ap
C 468	92.5	6.9	2517	10	US-09-864-636A-509	Sequence 509, App	C 541	92.5	6.9	2520	15	US-10-084-839-2792	Sequence 2792, Ap
C 469	92.5	6.9	2517	10	US-09-864-636A-513	Sequence 513, App	C 542	92.5	6.9	2520	15	US-10-084-839-2792	Sequence 2792, Ap
C 470	92.5	6.9	2517	10	US-09-864-636A-517	Sequence 517, App	C 543	92.5	6.9	2520	15	US-10-084-839-2810	Sequence 2810, Ap
C 471	92.5	6.9	2517	10	US-09-864-636A-521	Sequence 521, App	C 544	92.5	6.9	2520	15	US-10-084-839-2812	Sequence 2812, Ap
C 472	92.5	6.9	2517	10	US-09-864-636A-525	Sequence 525, App	C 545	92.5	6.9	2520	15	US-10-084-839-2820	Sequence 2820, Ap
C 473	92.5	6.9	2517	10	US-09-864-636A-529	Sequence 529, App	C 546	92.5	6.9	2520	15	US-10-084-839-2824	Sequence 2824, Ap
C 474	92.5	6.9	2517	10	US-09-864-636A-533	Sequence 533, App	C 547	92.5	6.9	2520	15	US-10-084-839-2830	Sequence 2830, Ap
C 475	92.5	6.9	2517	10	US-09-864-636A-537	Sequence 537, App	C 548	92.5	6.9	2526	9	US-09-777-430A-14	Sequence 14, Appl
C 476	92.5	6.9	2517	10	US-09-758-282-74	Sequence 74, Appl	C 549	92.5	6.9	2526	9	US-09-777-430A-19	Sequence 19, Appl
C 477	92.5	6.9	2517	10	US-09-758-282-238	Sequence 238, App	C 550	92.5	6.9	2526	9	US-09-777-430A-22	Sequence 22, Appl
C 478	92.5	6.9	2517	11	US-09-864-426A-69	Sequence 69, Appl	C 551	92.5	6.9	2526	9	US-09-777-430A-25	Sequence 25, Appl
C 479	92.5	6.9	2517	11	US-09-864-426A-128	Sequence 128, App	C 552	92.5	6.9	2526	10	US-09-864-636A-103	Sequence 103, App
C 480	92.5	6.9	2517	11	US-09-864-426A-484	Sequence 484, App	C 553	92.5	6.9	2526	10	US-09-864-636A-104	Sequence 104, App
C 481	92.5	6.9	2517	11	US-09-864-426A-495	Sequence 495, App	C 554	92.5	6.9	2526	10	US-09-864-636A-117	Sequence 117, App
C 482	92.5	6.9	2517	11	US-09-864-426A-501	Sequence 501, App	C 555	92.5	6.9	2526	10	US-09-864-636A-118	Sequence 118, App
C 483	92.5	6.9	2517	11	US-09-864-426A-509	Sequence 509, App	C 556	92.5	6.9	2526	10	US-09-864-636A-119	Sequence 119, App
C 484	92.5	6.9	2517	11	US-09-864-426A-513	Sequence 513, App	C 557	92.5	6.9	2526	10	US-09-864-636A-132	Sequence 132, App
C 485	92.5	6.9	2517	11	US-09-864-426A-517	Sequence 517, App	C 558	92.5	6.9	2526	10	US-09-864-636A-137	Sequence 137, App
C 486	92.5	6.9	2517	11	US-09-864-426A-521	Sequence 521, App	C 559	92.5	6.9	2526	10	US-09-864-636A-267	Sequence 267, App
C 487	92.5	6.9	2517	11	US-09-864-426A-525	Sequence 525, App	C 560	92.5	6.9	2526	10	US-09-864-636A-349	Sequence 349, App
C 488	92.5	6.9	2517	11	US-09-864-426A-529	Sequence 529, App	C 561	92.5	6.9	2526	10	US-09-864-636A-373	Sequence 373, App
C 489	92.5	6.9	2517	11	US-09-864-426A-533	Sequence 533, App	C 562	92.5	6.9	2526	10	US-09-864-636A-375	Sequence 375, App
C 490	92.5	6.9	2517	11	US-09-864-426A-537	Sequence 537, App	C 563	92.5	6.9	2526	10	US-09-864-636A-379	Sequence 379, App
C 491	92.5	6.9	2517	15	US-10-084-839-69	Sequence 69, Appl	C 564	92.5	6.9	2526	10	US-09-864-636A-383	Sequence 383, App
C 492	92.5	6.9	2517	15	US-10-084-839-128	Sequence 128, App	C 565	92.5	6.9	2526	10	US-09-864-636A-387	Sequence 387, App
C 493	92.5	6.9	2517	15	US-10-084-839-484	Sequence 484, App	C 566	92.5	6.9	2526	10	US-09-864-636A-391	Sequence 391, App
C 494	92.5	6.9	2517	15	US-10-084-839-495	Sequence 495, App	C 567	92.5	6.9	2526	10	US-09-864-636A-395	Sequence 395, App
C 495	92.5	6.9	2517	15	US-10-084-839-501	Sequence 501, App	C 568	92.5	6.9	2526	10	US-09-864-636A-399	Sequence 399, App
C 496	92.5	6.9	2517	15	US-10-084-839-509	Sequence 509, App	C 569	92.5	6.9	2526	10	US-09-864-636A-452	Sequence 452, App
C 497	92.5	6.9	2517	15	US-10-084-839-513	Sequence 513, App	C 570	92.5	6.9	2526	10	US-09-864-636A-455	Sequence 455, App
C 498	92.5	6.9	2517	15	US-10-084-839-517	Sequence 517, App	C 571	92.5	6.9	2526	10	US-09-864-636A-459	Sequence 459, App
C 499	92.5	6.9	2517	15	US-10-084-839-521	Sequence 521, App	C 572	92.5	6.9	2526	10	US-09-864-636A-471	Sequence 471, App
C 500	92.5	6.9	2517	15	US-10-084-839-525	Sequence 525, App	C 573	92.5	6.9	2526	10	US-09-864-636A-497	Sequence 497, App
												US-09-864-636A-558	Sequence 558, App

C 574	92.5	6.9	2526	10	US-09-758-282-64	Sequence 64, Appl	C 647	92.5	6.9	2526	15	US-10-084-839-2767	Sequence 2767, Ap
C 575	92.5	6.9	2526	10	US-09-758-282-70	Sequence 70, Appl	C 648	92.5	6.9	2526	15	US-10-084-839-2773	Sequence 2773, Ap
C 576	92.5	6.9	2526	10	US-09-758-282-162	Sequence 162, Appl	C 649	92.5	6.9	2526	15	US-10-084-839-2786	Sequence 2786, Ap
C 577	92.5	6.9	2526	10	US-09-758-282-162	Sequence 162, Appl	C 650	92.5	6.9	2526	15	US-10-084-839-2832	Sequence 2832, Ap
C 578	92.5	6.9	2526	10	US-09-758-282-211	Sequence 211, Appl	C 651	92.5	6.9	2526	15	US-10-084-839-2838	Sequence 2838, Ap
C 579	92.5	6.9	2526	10	US-09-758-282-211	Sequence 211, Appl	C 652	92.5	6.9	2526	15	US-10-084-839-2840	Sequence 2840, Ap
C 580	92.5	6.9	2526	10	US-09-758-282-215	Sequence 215, Appl	C 653	92.5	6.9	2526	15	US-10-084-839-2842	Sequence 2842, Ap
C 581	92.5	6.9	2526	10	US-09-758-282-258	Sequence 258, Appl	C 654	92.5	6.9	2526	15	US-10-084-839-2844	Sequence 2844, Ap
C 582	92.5	6.9	2526	11	US-09-864-426A-103	Sequence 103, Appl	C 655	92.5	6.9	2526	15	US-10-084-839-2846	Sequence 2846, Ap
C 583	92.5	6.9	2526	11	US-09-864-426A-104	Sequence 104, Appl	C 656	92.5	6.9	2526	15	US-10-084-839-2848	Sequence 2848, Ap
C 584	92.5	6.9	2526	11	US-09-864-426A-117	Sequence 117, Appl	C 657	92.5	6.9	2532	10	US-09-864-426A-463	Sequence 463, App
C 585	92.5	6.9	2526	11	US-09-864-426A-118	Sequence 118, Appl	C 658	92.5	6.9	2532	10	US-09-864-426A-467	Sequence 467, App
C 586	92.5	6.9	2526	11	US-09-864-426A-119	Sequence 119, Appl	C 659	92.5	6.9	2532	11	US-09-864-426A-467	Sequence 467, App
C 587	92.5	6.9	2526	11	US-09-864-426A-132	Sequence 132, Appl	C 660	92.5	6.9	2532	11	US-09-864-426A-467	Sequence 467, App
C 588	92.5	6.9	2526	11	US-09-864-426A-167	Sequence 167, Appl	C 661	92.5	6.9	2532	11	US-09-864-426A-467	Sequence 467, App
C 589	92.5	6.9	2526	11	US-09-864-426A-273	Sequence 273, Appl	C 662	92.5	6.9	2532	15	US-10-084-839-467	Sequence 467, App
C 590	92.5	6.9	2526	11	US-09-864-426A-349	Sequence 349, Appl	C 663	92.5	6.9	2532	15	US-10-084-839-2769	Sequence 2769, Ap
C 591	92.5	6.9	2526	11	US-09-864-426A-373	Sequence 373, Appl	C 664	92.5	6.9	2532	15	US-10-084-839-2771	Sequence 2771, Ap
C 592	92.5	6.9	2526	11	US-09-864-426A-375	Sequence 375, Appl	C 665	92.5	6.9	2619	10	US-09-864-426A-563	Sequence 563, App
C 593	92.5	6.9	2526	11	US-09-864-426A-379	Sequence 379, Appl	C 666	92.5	6.9	2619	11	US-09-864-426A-563	Sequence 563, App
C 594	92.5	6.9	2526	11	US-09-864-426A-383	Sequence 383, Appl	C 667	92.5	6.9	2619	15	US-10-084-839-563	Sequence 563, App
C 595	92.5	6.9	2526	11	US-09-864-426A-387	Sequence 387, Appl	C 668	92.5	6.9	2619	15	US-10-084-839-2816	Sequence 2816, Ap
C 596	92.5	6.9	2526	11	US-09-864-426A-391	Sequence 391, Appl	C 669	92.5	6.9	2643	10	US-09-864-426A-559	Sequence 559, App
C 597	92.5	6.9	2526	11	US-09-864-426A-395	Sequence 395, Appl	C 670	92.5	6.9	2643	11	US-09-864-426A-559	Sequence 559, App
C 598	92.5	6.9	2526	11	US-09-864-426A-452	Sequence 452, Appl	C 671	92.5	6.9	2643	15	US-10-084-839-559	Sequence 559, App
C 599	92.5	6.9	2526	11	US-09-864-426A-455	Sequence 455, Appl	C 672	92.5	6.9	2643	15	US-10-084-839-2814	Sequence 2814, Ap
C 600	92.5	6.9	2526	11	US-09-864-426A-459	Sequence 459, Appl	C 673	92.5	6.9	3135	10	US-09-864-426A-481	Sequence 481, App
C 601	92.5	6.9	2526	11	US-09-864-426A-471	Sequence 471, Appl	C 674	92.5	6.9	3135	11	US-09-864-426A-481	Sequence 481, App
C 602	92.5	6.9	2526	11	US-09-864-426A-497	Sequence 497, Appl	C 675	92.5	6.9	3135	15	US-10-084-839-481	Sequence 481, App
C 603	92.5	6.9	2526	11	US-09-864-426A-558	Sequence 558, Appl	C 676	92.5	6.9	3135	15	US-10-084-839-2777	Sequence 2777, Ap
C 604	92.5	6.9	2526	11	US-10-084-839-104	Sequence 104, Appl	C 677	92	6.9	813	15	US-10-369-493-33103	Sequence 33103, A
C 605	92.5	6.9	2526	15	US-10-084-839-110	Sequence 110, Appl	C 678	92	6.9	942	10	US-09-942-025-8	Sequence 8, Appl
C 606	92.5	6.9	2526	15	US-10-084-839-114	Sequence 114, Appl	C 679	92	6.9	1130	16	US-10-282-122A-19437	Sequence 19437, A
C 607	92.5	6.9	2526	15	US-10-084-839-117	Sequence 117, Appl	C 680	92	6.9	1932	16	US-10-282-122A-19437	Sequence 19437, A
C 608	92.5	6.9	2526	15	US-10-084-839-118	Sequence 118, Appl	C 681	92	6.9	67311	10	US-09-942-025-1	Sequence 1, Appl
C 609	92.5	6.9	2526	15	US-10-084-839-119	Sequence 119, Appl	C 682	91.5	6.8	903	15	US-10-156-761-642	Sequence 642, App
C 610	92.5	6.9	2526	15	US-10-084-839-132	Sequence 132, Appl	C 683	91.5	6.8	1092	17	US-10-437-963-97637	Sequence 97637, A
C 611	92.5	6.9	2526	15	US-10-084-839-267	Sequence 267, Appl	C 684	91.5	6.8	1116	16	US-10-282-122A-32148	Sequence 32148, A
C 612	92.5	6.9	2526	15	US-10-084-839-273	Sequence 273, Appl	C 685	91.5	6.8	1149	15	US-10-156-761-5745	Sequence 5745, A
C 613	92.5	6.9	2526	15	US-10-084-839-349	Sequence 349, Appl	C 686	91.5	6.8	1896	15	US-10-156-761-5658	Sequence 5658, Ap
C 614	92.5	6.9	2526	15	US-10-084-839-373	Sequence 373, Appl	C 687	91.5	6.8	2253	16	US-10-282-122A-30610	Sequence 30610, A
C 615	92.5	6.9	2526	15	US-10-084-839-375	Sequence 375, Appl	C 688	91.5	6.8	2499	10	US-09-864-426A-79	Sequence 79, Appl
C 616	92.5	6.9	2526	15	US-10-084-839-379	Sequence 379, Appl	C 689	91.5	6.8	2499	10	US-09-758-282-94	Sequence 94, Appl
C 617	92.5	6.9	2526	15	US-10-084-839-383	Sequence 383, Appl	C 690	91.5	6.8	2499	11	US-09-864-426A-79	Sequence 79, Appl
C 618	92.5	6.9	2526	15	US-10-084-839-387	Sequence 387, Appl	C 691	91.5	6.8	2499	15	US-10-084-839-79	Sequence 79, Appl
C 619	92.5	6.9	2526	15	US-10-084-839-391	Sequence 391, Appl	C 692	91.5	6.8	2499	15	US-10-084-839-2682	Sequence 2682, Ap
C 620	92.5	6.9	2526	15	US-10-084-839-395	Sequence 395, Appl	C 693	91.5	6.8	2505	10	US-09-864-426A-155	Sequence 155, App
C 621	92.5	6.9	2526	15	US-10-084-839-399	Sequence 399, Appl	C 694	91.5	6.8	2505	10	US-09-758-282-266	Sequence 266, App
C 622	92.5	6.9	2526	15	US-10-084-839-452	Sequence 452, Appl	C 695	91.5	6.8	2505	11	US-09-864-426A-155	Sequence 155, App
C 623	92.5	6.9	2526	15	US-10-084-839-455	Sequence 455, Appl	C 696	91.5	6.8	2505	15	US-10-084-839-155	Sequence 155, App
C 624	92.5	6.9	2526	15	US-10-084-839-459	Sequence 459, Appl	C 697	91.5	6.8	2505	15	US-10-084-839-2709	Sequence 2709, Ap
C 625	92.5	6.9	2526	15	US-10-084-839-471	Sequence 471, Appl	C 698	91.5	6.8	2511	9	US-09-777-430A-9	Sequence 9, Appl
C 626	92.5	6.9	2526	15	US-10-084-839-497	Sequence 497, Appl	C 699	91.5	6.8	2511	10	US-09-864-426A-244	Sequence 244, App
C 627	92.5	6.9	2526	15	US-10-084-839-558	Sequence 558, Appl	C 700	91.5	6.8	2511	10	US-09-758-282-3	Sequence 3, Appl
C 628	92.5	6.9	2526	15	US-10-084-839-2701	Sequence 2701, Ap	C 701	91.5	6.8	2511	11	US-09-864-426A-244	Sequence 244, App
C 629	92.5	6.9	2526	15	US-10-084-839-2702	Sequence 2702, Ap	C 702	91.5	6.8	2511	15	US-10-084-839-244	Sequence 244, App
C 630	92.5	6.9	2526	15	US-10-084-839-2703	Sequence 2703, Ap	C 703	91.5	6.8	2511	15	US-10-084-839-2713	Sequence 2713, Ap
C 631	92.5	6.9	2526	15	US-10-084-839-2704	Sequence 2704, Ap	C 704	91.5	6.8	2653	17	US-10-469-858-1	Sequence 1, Appl
C 632	92.5	6.9	2526	15	US-10-084-839-2705	Sequence 2705, Ap	C 705	91.5	6.8	2731748	17	US-10-297-465A-1	Sequence 1, Appl
C 633	92.5	6.9	2526	15	US-10-084-839-2706	Sequence 2706, Ap	C 706	91.5	6.8	2731748	17	US-10-297-465A-1	Sequence 1, Appl
C 634	92.5	6.9	2526	15	US-10-084-839-2716	Sequence 2716, Ap	C 707	91.5	6.8	798	18	US-10-425-115-60646	Sequence 60646, A
C 635	92.5	6.9	2526	15	US-10-084-839-2717	Sequence 2717, Ap	C 708	91	6.8	846	16	US-10-282-122A-23727	Sequence 23727, A
C 636	92.5	6.9	2526	15	US-10-084-839-2718	Sequence 2718, Ap	C 709	91	6.8	1209	16	US-10-425-114-16417	Sequence 16417, A
C 637	92.5	6.9	2526	15	US-10-084-839-2720	Sequence 2720, Ap	C 710	91	6.8	1400	17	US-10-437-963-22255	Sequence 22255, A
C 638	92.5	6.9	2526	15	US-10-084-839-2721	Sequence 2721, Ap	C 711	91	6.8	1590	16	US-10-282-122A-41291	Sequence 41291, A
C 639	92.5	6.9	2526	15	US-10-084-839-2723	Sequence 2723, Ap	C 712	91	6.8	2064	15	US-10-156-761-2902	Sequence 2902, Ap
C 640	92.5	6.9	2526	15	US-10-084-839-2725	Sequence 2725, Ap	C 713	91	6.8	2259	17	US-10-466-531-49	Sequence 49, Appl
C 641	92.5	6.9	2526	15	US-10-084-839-2727	Sequence 2727, Ap	C 714	91	6.8	2454	15	US-10-156-761-2410	Sequence 2410, Ap
C 642	92.5	6.9	2526	15	US-10-084-839-2729	Sequence 2729, Ap	C 715	91	6.8	2749	14	US-09-997-428-516	Sequence 516, App
C 643	92.5	6.9	2526	15	US-10-084-839-2731	Sequence 2731, Ap	C 716	91	6.8	2749	14	US-10-140-002-385	Sequence 385, App
C 644	92.5	6.9	2526	15	US-10-084-839-2733	Sequence 2733, Ap	C 717	91	6.8	2749	14	US-10-167-749-215	Sequence 215, App
C 645	92.5	6.9	2526	15	US-10-084-839-2735	Sequence 2735, Ap	C 718	91	6.8	2749	15	US-10-223-085-59	Sequence 59, Appl
C 646	92.5	6.9	2526	15	US-10-084-839-2763	Sequence 2763, Ap	C 719	91	6.8	2749	15	US-10-223-085-59	Sequence 59, Appl
C 647	92.5	6.9	2526	15	US-10-084-839-2765	Sequence 2765, Ap	C 720	91	6.8	2749	15	US-10-223-085-59	Sequence 59, Appl

967	91	6.8	2749	15	US-10-223-088-59	Sequence 59, Appl	cl393	88.5	6.6	3289	18	US-10-723-860-6374	Sequence 6374, Ap
968	91	6.8	2749	15	US-10-223-090-59	Sequence 59, Appl	1394	88.5	6.6	3413	16	US-10-424-599-52304	Sequence 52304, A
969	91	6.8	2749	15	US-10-223-087-59	Sequence 59, Appl	1395	88.5	6.6	22459	11	US-09-973-278-883	Sequence 883, App
971	91	6.8	2749	15	US-10-223-083-59	Sequence 59, Appl	cl396	88.5	6.6	30350	17	US-10-118-328-3	Sequence 3, Appl1
972	91	6.8	2749	15	US-10-175-590-385	Sequence 385, App	cl397	88.5	6.6	30350	13	US-10-694-438-3	Sequence 3, Appl1
973	91	6.8	2749	15	US-10-223-089-59	Sequence 59, Appl	1398	88.5	6.6	37116	15	US-10-107-431-279	Sequence 279, App
1145	91	6.8	2749	15	US-10-223-081-59	Sequence 59, Appl	1399	88.5	6.6	84428	16	US-10-229-1488-1	Sequence 1, Appl1
1145	91	6.8	2749	15	US-10-223-082-59	Sequence 59, Appl	1400	88.5	6.6	84428	11	US-09-758-759-1	Sequence 1, Appl1
1145	91	6.8	2749	15	US-10-170-814-215	Sequence 215, App	cl401	88.5	6.6	160361	16	US-10-369-493-33037	Sequence 33037, A
1234	91	6.8	2749	15	US-10-160-028-215	Sequence 215, App	1402	88	6.6	813	15	US-10-369-493-33037	Sequence 34, Appl
1236	91	6.8	2749	15	US-10-162-521A-215	Sequence 215, App	1403	88	6.6	852	16	US-10-389-647-34	Sequence 2040, Ap
1236	91	6.8	2749	15	US-10-305-654-59	Sequence 59, Appl	1404	88	6.6	931	17	US-10-767-701-2040	Sequence 14306, A
1305	91	6.8	2749	16	US-10-081-056-59	Sequence 59, Appl	1405	88	6.6	1043	18	US-10-425-115-143306	Sequence 140838, A
1318	91	6.8	2749	16	US-10-081-056-59	Sequence 31552, A	1406	88	6.6	1087	15	US-10-425-115-140838	Sequence 4499, A
cl333	91	6.8	3459	15	US-10-369-493-31552	Sequence 96859, A	cl407	88	6.6	1281	15	US-10-369-493-44499	Sequence 1666, Ap
1334	90.5	6.7	1023	17	US-10-437-963-96859	Sequence 1741, Ap	1408	88	6.6	1461	15	US-10-156-761-1666	Sequence 12874, A
1335	90.5	6.7	1248	15	US-10-156-761-1741	Sequence 1534, Ap	cl409	88	6.6	1464	16	US-10-424-599-128274	Sequence 97638, A
1336	90.5	6.7	1611	16	US-10-260-238-1534	Sequence 49451, A	cl410	88	6.6	1694	17	US-10-437-963-97638	Sequence 18431, A
1337	90.5	6.7	1820	17	US-10-437-963-49451	Sequence 159, App	1411	88	6.6	2006	17	US-10-437-963-97638	Sequence 12874, A
cl338	90.5	6.7	2526	10	US-09-864-636A-102	Sequence 102, App	1412	88	6.6	2402	15	US-10-369-493-32004	Sequence 32004, A
cl339	90.5	6.7	2526	11	US-09-864-426A-102	Sequence 102, App	1413	88	6.6	2487	16	US-09-864-636A-127	Sequence 127, App
cl341	90.5	6.7	2526	15	US-10-084-839-102	Sequence 2700, Ap	cl414	88	6.6	2517	11	US-09-758-282-235	Sequence 235, App
cl342	90.5	6.7	2526	15	US-10-084-839-2700	Sequence 174346, A	cl415	88	6.6	2517	11	US-09-864-426A-127	Sequence 127, App
1343	90.5	6.7	2538	18	US-10-425-115-174346	Sequence 1, Appl1	cl416	88	6.6	2517	15	US-10-084-839-127	Sequence 81418, A
1344	90.5	6.7	135638	15	US-10-314-657-1	Sequence 1, Appl1	cl417	88	6.6	2528	17	US-10-437-963-81418	Sequence 3914, Ap
1345	90.5	6.7	3309400	9	US-09-738-626-1	Sequence 875, App	cl418	88	6.6	2565	15	US-10-156-761-3914	Sequence 5493, Ap
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SUMMARIES

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4	396	29.5	1058	4	US-09-452-239-11	Sequence 11, Appl
5	394	29.3	1078	4	US-09-452-239-41	Sequence 41, Appl
6	392.5	29.2	962	4	US-09-452-239-23	Sequence 23, Appl
7	392.5	29.2	1023	4	US-09-452-239-25	Sequence 25, Appl
8	389	29.0	997	4	US-09-452-239-13	Sequence 13, Appl
9	387	28.8	953	4	US-09-452-239-45	Sequence 45, Appl
10	386.5	28.8	967	4	US-09-453-323-5	Sequence 5, Appl
11	386	28.7	1012	4	US-09-615-192A-94	Sequence 94, Appl
12	386	28.7	1012	4	US-09-169-789-94	Sequence 94, Appl
13	386	28.7	1026	2	US-09-713-000-6	Sequence 6, Appl

14	386	28.7	1026	2	US-08-975-316-6	Sequence 6, Appl
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C 99	99	7.4	2030	5	US-07-977-434-7	Sequence 7, Appli	C 172	92.5	6.9	2526	4	US-09-577-304A-162	Sequence 162, App
C 100	99	7.4	2505	1	US-08-458-819-7	Sequence 1, Appli	C 173	92.5	6.9	2526	4	US-09-577-304A-165	Sequence 165, App
C 101	99	7.4	2505	1	PCT-US91-07035-7	Sequence 7, Appli	C 174	92.5	6.9	2526	4	US-09-577-304A-211	Sequence 211, App
C 102	99	7.4	2505	5	US-09-252-991A-9422	Sequence 9422, App	C 175	92.5	6.9	2526	4	US-09-577-304A-213	Sequence 213, App
C 103	99	7.4	8519	3	US-09-252-991A-9455	Sequence 9455, App	C 176	92.5	6.9	2526	4	US-09-577-304A-215	Sequence 215, App
C 104	99	7.4	855	4	US-08-887-534A-84	Sequence 84, Appl	C 177	92.5	6.9	2526	4	US-09-577-304A-258	Sequence 258, App
C 105	98.5	7.3	3147	4	US-09-527-431-84	Sequence 84, Appl	C 178	92.5	6.9	2526	4	US-09-777-430C-14	Sequence 14, Appl
C 106	98.5	7.3	3147	4	US-09-446-861-84	Sequence 1, Appli	C 179	92.5	6.9	2526	4	US-09-777-430C-19	Sequence 19, Appl
C 107	98.5	7.3	3147	4	US-09-410-551B-1	Sequence 1, Appli	C 180	92.5	6.9	2526	4	US-09-777-430C-22	Sequence 22, Appl
C 108	98.5	7.3	77536	4	US-09-252-991A-109	Sequence 109, App	C 181	92.5	6.9	2526	4	US-09-777-430C-94	Sequence 94, Appl
C 109	98.5	7.3	77536	4	US-09-351-150A-1	Sequence 1, Appli	C 182	92.5	6.9	2526	4	US-09-777-430C-99	Sequence 99, Appli
C 110	98.5	7.3	657	4	US-09-252-991A-12098	Sequence 12098, App	C 183	92.5	6.9	2526	4	US-09-684-938-159	Sequence 159, App
C 111	98.5	7.3	657	4	US-09-351-150A-14	Sequence 14, Appl	C 184	91.5	6.8	2505	1	US-09-308-825A-159	Sequence 159, App
C 112	97.5	7.3	1632	4	US-09-252-991A-11756	Sequence 11756, A	C 185	91.5	6.8	2505	4	US-09-758-282B-286	Sequence 286, App
C 113	97.5	7.3	2232	4	US-09-252-991A-11836	Sequence 11836, A	C 186	91.5	6.8	2505	4	US-09-758-282B-94	Sequence 94, Appl
C 114	97.5	7.3	2274	4	US-09-252-991A-11836	Sequence 1, Appli	C 187	91.5	6.8	2499	4	US-09-577-304A-94	Sequence 94, Appl
C 115	97.5	7.3	2274	4	US-09-252-991A-11836	Sequence 1, Appli	C 188	91.5	6.8	2499	4	US-09-577-304A-94	Sequence 94, Appl
C 116	97.5	7.3	2274	4	US-09-252-991A-11836	Sequence 1, Appli	C 189	91.5	6.8	2499	4	US-09-577-304A-94	Sequence 94, Appl
C 117	97.5	7.3	2274	4	US-09-252-991A-11836	Sequence 1, Appli	C 190	91.5	6.8	2499	4	US-09-577-304A-94	Sequence 94, Appl
C 118	97.5	7.3	2274	4	US-09-252-991A-11836	Sequence 1, Appli	C 191	91.5	6.8	2499	4	US-09-577-304A-94	Sequence 94, Appl
C 119	97.5	7.3	2274	4	US-09-252-991A-11836	Sequence 1, Appli	C 192	91.5	6.8	2499	4	US-09-577-304A-94	Sequence 94, Appl
C 120	97.5	7.3	2274	4	US-09-252-991A-11836	Sequence 1, Appli	C 193	91.5	6.8	2499	4	US-09-577-304A-94	Sequence 94, Appl
C 121	97	7.2	1086	4	US-09-252-991A-10259	Sequence 10259, A	C 194	91.5	6.8	2505	5	PCT-US91-07035-9	Sequence 9, Appli
C 122	97	7.2	1101	4	US-09-252-991A-10597	Sequence 10597, A	C 195	91.5	6.8	2505	5	PCT-US91-07035-9	Sequence 9, Appli
C 123	96.5	7.2	783	4	US-09-252-991A-12098	Sequence 12098, A	C 196	91.5	6.8	2505	5	PCT-US91-07035-9	Sequence 9, Appli
C 124	96.5	7.2	984	4	US-09-252-991A-12173	Sequence 12173, A	C 197	91.5	6.8	2511	4	US-09-684-938-161	Sequence 161, App
C 125	96.5	7.2	1254	4	US-09-252-991A-12420	Sequence 12420, A	C 198	91.5	6.8	2511	4	US-09-308-825A-161	Sequence 161, App
C 126	96	7.1	3135	4	US-09-252-991A-12420	Sequence 12420, A	C 199	91.5	6.8	2511	4	US-09-577-304A-3	Sequence 3, Appli
C 127	95.5	7.1	852	4	US-09-252-991A-12420	Sequence 12420, A	C 200	91.5	6.8	2511	4	US-09-577-304A-3	Sequence 3, Appli
C 128	95.5	7.1	1452	4	US-09-252-991A-12420	Sequence 12420, A	C 201	91.5	6.8	2511	4	US-09-577-304A-3	Sequence 3, Appli
C 129	95.5	7.1	1794	5	PCT-US95-14418-3	Sequence 3, Appli	C 202	91.5	6.8	2640	1	US-08-384-490-30	Sequence 30, Appl
C 130	95.5	7.1	1794	5	PCT-US95-14418-3	Sequence 3, Appli	C 203	91.5	6.8	2640	1	US-08-384-490-30	Sequence 30, Appl
C 131	95.5	7.1	3048	5	PCT-US95-14418-1	Sequence 1, Appli	C 204	91.5	6.8	2640	1	US-08-384-490-30	Sequence 30, Appl
C 132	95.5	7.1	3048	5	PCT-US95-15327-1	Sequence 1, Appli	C 205	91.5	6.8	2640	1	US-08-384-490-30	Sequence 30, Appl
C 133	95.5	7.1	4284	4	US-09-252-991A-4006	Sequence 4006, App	C 206	91	6.8	3660	4	US-09-489-039A-3080	Sequence 3080, App
C 134	94.5	7.0	2304	1	US-08-464-266-1	Sequence 1, Appli	C 207	91	6.8	966	4	US-09-252-991A-13273	Sequence 13273, A
C 135	94.5	7.0	2304	1	US-08-464-272-1	Sequence 1, Appli	C 208	91	6.8	966	4	US-09-252-991A-13273	Sequence 13273, A
C 136	94.5	7.0	2304	1	US-08-464-514-1	Sequence 1, Appli	C 209	91	6.8	1083	4	US-09-252-991A-14709	Sequence 14709, A
C 137	94.5	7.0	2304	3	US-08-464-514-1	Sequence 1, Appli	C 210	91	6.8	1200	4	US-09-252-991A-15040	Sequence 15040, A
C 138	94	7.0	1527	4	US-09-252-991A-12042	Sequence 12042, A	C 211	91	6.8	1290	4	US-09-252-991A-15040	Sequence 15040, A
C 139	94	7.0	1962	4	US-09-252-991A-12042	Sequence 12042, A	C 212	91	6.8	1290	4	US-09-252-991A-15040	Sequence 15040, A
C 140	94	7.0	2313	4	US-09-252-991A-11939	Sequence 11939, A	C 213	91	6.8	1290	4	US-09-252-991A-15040	Sequence 15040, A
C 141	93.5	7.0	1233	4	US-09-252-991A-8712	Sequence 8712, App	C 214	91	6.8	1290	4	US-09-252-991A-15040	Sequence 15040, A
C 142	93.5	7.0	1233	4	US-09-252-991A-8712	Sequence 8712, App	C 215	91	6.8	1290	4	US-09-252-991A-15040	Sequence 15040, A
C 143	93	6.9	1701	4	US-09-252-991A-19071	Sequence 19071, App	C 216	91	6.8	1290	4	US-09-252-991A-15040	Sequence 15040, A
C 144	93	6.9	1848	4	US-09-252-991A-19071	Sequence 19071, App	C 217	90.5	6.7	2496	4	US-09-252-991A-15040	Sequence 15040, A
C 145	93	6.9	2169	4	US-09-252-991A-19071	Sequence 19071, App	C 218	90.5	6.7	2496	4	US-09-252-991A-15040	Sequence 15040, A
C 146	93	6.9	2946	4	US-09-252-991A-2045	Sequence 2045, App	C 219	90.5	6.7	2496	4	US-09-252-991A-15040	Sequence 15040, A
C 147	93	6.9	3744	4	US-09-799-451-585	Sequence 585, App	C 220	90.5	6.7	2496	4	US-09-252-991A-15040	Sequence 15040, A
C 148	92.5	6.9	1200	4	US-09-252-991A-2649	Sequence 2649, App	C 221	90.5	6.7	2496	4	US-09-252-991A-15040	Sequence 15040, A
C 149	92.5	6.9	1311	4	US-09-252-991A-3649	Sequence 3649, App	C 222	90.5	6.7	2496	4	US-09-252-991A-15040	Sequence 15040, A
C 150	92.5	6.9	2511	4	US-09-684-938-163	Sequence 163, App	C 223	90	6.7	1069	4	US-09-614-912-203	Sequence 203, App
C 151	92.5	6.9	2511	4	US-09-308-825A-163	Sequence 163, App	C 224	90	6.7	1069	4	US-09-614-912-203	Sequence 203, App
C 152	92.5	6.9	2511	4	US-09-758-282B-59	Sequence 59, Appl	C 225	90	6.7	1069	4	US-09-614-912-203	Sequence 203, App
C 153	92.5	6.9	2511	4	US-09-940-244-258	Sequence 59, Appl	C 226	89.5	6.7	1947	4	US-09-252-991A-7111	Sequence 7111, App
C 154	92.5	6.9	2511	4	US-09-577-304A-59	Sequence 59, Appl	C 227	89.5	6.7	1947	4	US-09-252-991A-7111	Sequence 7111, App
C 155	92.5	6.9	2511	4	US-09-777-430C-12	Sequence 12, Appl	C 228	89.5	6.7	1947	4	US-09-252-991A-7111	Sequence 7111, App
C 156	92.5	6.9	2514	4	US-09-758-282B-260	Sequence 260, App	C 229	89.5	6.7	1947	4	US-09-252-991A-7111	Sequence 7111, App
C 157	92.5	6.9	2514	4	US-09-577-304A-260	Sequence 260, App	C 230	89.5	6.7	1947	4	US-09-252-991A-7111	Sequence 7111, App
C 158	92.5	6.9	2514	4	US-09-758-282B-74	Sequence 74, Appl	C 231	89.5	6.7	1947	4	US-09-252-991A-7111	Sequence 7111, App
C 159	92.5	6.9	2517	4	US-09-758-282B-238	Sequence 238, App	C 232	89.5	6.7	1947	4	US-09-252-991A-7111	Sequence 7111, App

C 233	89.5	6.7	1605	4	US-09-252-991A-3610	Sequence 3610, Ap	C 306	85.5	6.4	909	4	US-09-252-991A-12929	Sequence 12929, A
C 234	89.5	6.7	3270	4	US-09-252-991A-3763	Sequence 3763, Ap	C 307	85.5	6.4	1269	4	US-09-252-991A-8698	Sequence 8698, Ap
C 235	88.5	6.6	969	4	US-09-252-991A-8841	Sequence 8841, Ap	C 308	85.5	6.4	1944	4	US-09-252-991A-8981	Sequence 8981, Ap
C 236	88.5	6.6	1008	4	US-09-252-991A-8953	Sequence 8953, Ap	C 309	85.5	6.4	29598	3	US-09-341-587-6	Sequence 6, Appl
C 237	88.5	6.6	1035	4	US-09-252-991A-185	Sequence 185, Ap	C 310	85	6.3	666	4	US-09-252-991A-7202	Sequence 7202, Ap
C 238	88.5	6.6	1074	4	US-09-252-991A-162	Sequence 162, Ap	C 311	85	6.3	798	4	US-09-543-681A-2640	Sequence 2640, Ap
C 239	88.5	6.6	1293	4	US-09-252-991A-12484	Sequence 12484, A	C 312	85	6.3	53165	4	US-09-214-808-1	Sequence 1, Appl
C 240	88.5	6.6	1422	4	US-09-252-991A-12989	Sequence 12989, A	C 313	84.5	6.3	1260	4	US-09-252-991A-6317	Sequence 6317, Ap
C 241	88.5	6.6	1455	4	US-09-252-991A-151	Sequence 151, Ap	C 314	84.5	6.3	1524	4	US-09-252-991A-9472	Sequence 9472, Ap
C 242	88.5	6.6	1696	4	US-09-774-528-151	Sequence 151, Ap	C 315	84.5	6.3	2406	4	US-09-252-991A-11299	Sequence 11299, A
C 243	88.5	6.6	2403	3	US-09-367-206-2	Sequence 2, Appl	C 316	84.5	6.3	2517	4	US-09-758-282B-80	Sequence 80, Appl
C 244	88.5	6.6	2517	4	US-08-471-066B-1	Sequence 1, Appl	C 317	84.5	6.3	2517	4	US-09-577-304A-80	Sequence 80, Appl
C 245	88.5	6.6	2511	4	US-09-252-991A-9132	Sequence 9132, Ap	C 318	84.5	6.3	2526	4	US-09-758-282B-92	Sequence 92, Appl
C 246	88.5	6.6	30350	4	US-10-118-328-3	Sequence 3, Appl	C 319	84.5	6.3	2526	4	US-09-577-304A-92	Sequence 92, Appl
C 247	88	6.6	2517	4	US-09-758-282B-235	Sequence 235, Ap	C 320	84.5	6.3	3358	3	US-09-248-571-2	Sequence 2, Appl
C 248	88	6.6	2517	4	US-09-577-304A-235	Sequence 235, Ap	C 321	84.5	6.3	3358	3	US-09-553-736-2	Sequence 2, Appl
C 249	87.5	6.5	849	4	US-09-252-991A-617	Sequence 617, Ap	C 322	84.5	6.3	3358	3	US-09-103-330-35	Sequence 35, Appl
C 250	87.5	6.5	1575	4	US-09-252-991A-3100	Sequence 3100, Ap	C 323	84	6.3	34446	3	US-09-060-756-582	Sequence 582, Ap
C 251	87.5	6.5	1866	4	US-09-252-991A-16213	Sequence 16213, A	C 324	84	6.3	314	3	US-09-670-314-582	Sequence 582, Ap
C 252	87.5	6.5	1956	4	US-09-252-991A-3189	Sequence 3189, Ap	C 325	84	6.3	314	3	US-09-583-110-637	Sequence 637, Ap
C 253	87.5	6.5	2379	4	US-09-252-991A-686	Sequence 686, Ap	C 326	84	6.3	759	4	US-08-253-155A-11	Sequence 11, Appl
C 254	87.5	6.5	2499	4	US-09-252-991A-696	Sequence 696, Ap	C 327	84	6.3	1065	4	US-09-252-991A-16320	Sequence 16320, A
C 255	87.5	6.5	2526	4	US-09-758-282B-156	Sequence 156, Ap	C 328	84	6.3	1332	4	US-09-252-991A-15961	Sequence 15961, A
C 256	87.5	6.5	2526	4	US-09-577-304A-156	Sequence 156, Ap	C 329	84	6.3	1341	4	US-09-252-991A-16544	Sequence 16544, A
C 257	87	6.5	930	4	US-09-252-991A-6618	Sequence 6618, Ap	C 330	84	6.3	1405	1	US-08-035-558-3	Sequence 3, Appl
C 258	87	6.5	1074	4	US-09-351-150A-36	Sequence 36, Appl	C 331	84	6.3	1405	2	US-08-682-847-5	Sequence 5, Appl
C 259	87	6.5	1158	4	US-09-252-991A-14214	Sequence 14214, A	C 332	84	6.3	1405	3	US-09-063-676-1	Sequence 1, Appl
C 260	87	6.5	1308	4	US-09-252-991A-6649	Sequence 6649, Ap	C 333	84	6.3	1785	1	US-07-865-662B-4	Sequence 4, Appl
C 261	87	6.5	1377	4	US-09-351-150A-12	Sequence 12, Appl	C 334	84	6.3	1785	1	US-08-374-219B-4	Sequence 4, Appl
C 262	87	6.5	1535	1	US-08-910-973-10	Sequence 10, Appl	C 335	84	6.3	2055	4	US-08-252-991A-1845	Sequence 1845, Ap
C 263	87	6.5	1535	4	US-09-499-227-10	Sequence 10, Appl	C 336	84	6.3	2067	4	US-09-252-991A-1398	Sequence 1398, Ap
C 264	87	6.5	1625	4	US-09-799-451-594	Sequence 594, Ap	C 337	84	6.3	2100	4	US-09-252-991A-1209	Sequence 1209, Ap
C 265	87	6.5	1650	4	US-09-252-991A-10150	Sequence 10150, A	C 338	84	6.3	2480	4	US-09-064-199-15	Sequence 15, Appl
C 266	87	6.5	1725	4	US-09-252-991A-9926	Sequence 9926, Ap	C 339	84	6.3	3393	1	US-08-295-502-1	Sequence 1, Appl
C 267	87	6.5	2145	4	US-09-252-991A-13235	Sequence 13235, A	C 340	84	6.3	3393	5	PCT-US95-10691-1	Sequence 1, Appl
C 268	87	6.5	3390	4	US-09-489-039A-3029	Sequence 3029, Ap	C 341	84	6.3	3884	4	US-10-140-002-145	Sequence 145, Ap
C 269	87	6.5	3741	4	US-09-252-991A-6569	Sequence 6569, Ap	C 342	84	6.3	3884	4	US-09-064-199-12	Sequence 12, Appl
C 270	87	6.5	4431	4	US-09-252-991A-12856	Sequence 12856, A	C 343	84	6.3	4366	4	US-09-064-199-14	Sequence 14, Appl
C 271	87	6.5	10095	3	US-08-822-586-45	Sequence 45, Appl	C 344	84	6.3	4418	4	US-09-064-199-13	Sequence 13, Appl
C 272	87	6.5	24494	4	US-09-351-150A-1	Sequence 1, Appl	C 345	84	6.3	4431	4	US-09-064-199-8	Sequence 8, Appl
C 273	86.5	6.4	888	4	US-09-540-236-1514	Sequence 1514, Ap	C 346	84	6.3	4441	3	US-09-641-999-2	Sequence 2, Appl
C 274	86.5	6.4	1086	4	US-09-252-991A-11554	Sequence 11554, A	C 347	84	6.3	4441	3	US-09-064-199-10	Sequence 10, Appl
C 275	86.5	6.4	1251	4	US-09-252-991A-3770	Sequence 3770, Ap	C 348	84	6.3	4543	2	US-08-519-547A-5	Sequence 5, Appl
C 276	86.5	6.4	1425	4	US-09-252-991A-6019	Sequence 6019, Ap	C 349	84	6.3	4549	4	US-09-064-199-9	Sequence 9, Appl
C 277	86.5	6.4	1707	4	US-09-489-039A-2690	Sequence 2690, Ap	C 350	84	6.3	4564	4	US-09-064-199-2	Sequence 2, Appl
C 278	86.5	6.4	1989	4	US-09-252-991A-6290	Sequence 6290, Ap	C 351	84	6.3	4649	4	US-09-064-199-11	Sequence 11, Appl
C 279	86.5	6.4	2367	4	US-09-252-991A-726	Sequence 726, Ap	C 352	84	6.3	4746	4	US-09-064-199-7	Sequence 7, Appl
C 280	86.5	6.4	3825	4	US-09-252-991A-3815	Sequence 3815, Ap	C 353	84	6.3	5105	4	US-09-064-199-3	Sequence 3, Appl
C 281	86.5	6.4	4506	4	US-09-252-991A-3695	Sequence 3695, Ap	C 354	84	6.3	5463	4	US-09-064-199-1	Sequence 1, Appl
C 282	86.5	6.4	7001	1	US-08-258-261B-1	Sequence 1, Appl	C 355	83.5	6.2	1251	4	US-09-252-991A-8004	Sequence 8004, Ap
C 283	86.5	6.4	7001	1	US-08-456-837-1	Sequence 1, Appl	C 356	83.5	6.2	1308	4	US-09-252-991A-7182	Sequence 7182, Ap
C 284	86.5	6.4	7001	1	US-08-457-342-1	Sequence 1, Appl	C 357	83.5	6.2	1344	4	US-09-252-991A-6363	Sequence 6363, Ap
C 285	86.5	6.4	7001	1	US-08-457-646A-1	Sequence 1, Appl	C 358	83.5	6.2	1550	3	US-09-234-332-3	Sequence 3, Appl
C 286	86.5	6.4	7001	1	US-08-458-076A-1	Sequence 1, Appl	C 359	83.5	6.2	1671	4	US-09-252-991A-6188	Sequence 6188, Ap
C 287	86.5	6.4	7001	1	US-08-457-335A-1	Sequence 1, Appl	C 360	83.5	6.2	1767	1	US-08-399-646-1	Sequence 1, Appl
C 288	86.5	6.4	7001	1	US-08-761-258-6	Sequence 6, Appl	C 361	83.5	6.2	1767	1	US-08-607-321-1	Sequence 1, Appl
C 289	86.5	6.4	7001	1	US-08-729-214-1	Sequence 1, Appl	C 362	83.5	6.2	1767	2	US-08-961-240-1	Sequence 1, Appl
C 290	86.5	6.4	7001	2	US-08-977-306-6	Sequence 6, Appl	C 363	83.5	6.2	1767	2	US-08-605-501-1	Sequence 1, Appl
C 291	86.5	6.4	7001	3	US-09-028-934-1	Sequence 1, Appl	C 364	83.5	6.2	2161	1	US-08-399-646-11	Sequence 11, Appl
C 292	86.5	6.4	8037	4	US-09-774-528-209	Sequence 209, Ap	C 365	83.5	6.2	2161	2	US-08-607-321-11	Sequence 11, Appl
C 293	86.5	6.4	53500	4	US-09-266-965-76	Sequence 76, Appl	C 366	83.5	6.2	2161	2	US-08-961-240-11	Sequence 11, Appl
C 294	86.5	6.4	62909	4	US-09-596-002-32	Sequence 32, Appl	C 367	83.5	6.2	2161	2	US-08-605-501-11	Sequence 11, Appl
C 295	86	6.4	822	4	US-09-252-991A-6178	Sequence 6178, Ap	C 368	83.5	6.2	2484	4	US-09-252-991A-7462	Sequence 7462, Ap
C 296	86	6.4	1221	4	US-09-252-991A-7107	Sequence 7107, Ap	C 369	83.5	6.2	2499	4	US-09-758-282B-98	Sequence 98, Appl
C 297	86	6.4	1488	4	US-09-252-991A-9231	Sequence 9231, Ap	C 370	83.5	6.2	2499	4	US-09-577-304A-98	Sequence 98, Appl
C 298	86	6.4	2019	4	US-09-252-991A-8818	Sequence 8818, Ap	C 371	83.5	6.2	3251	3	US-09-085-199B-6	Sequence 6, Appl
C 299	86	6.4	2094	4	US-09-252-991A-7438	Sequence 7438, Ap	C 372	83.5	6.2	3876	4	US-09-849-602-4	Sequence 4, Appl
C 300	86	6.4	2517	4	US-09-758-282B-174	Sequence 174, Ap	C 373	83.5	6.2	11219	1	US-07-642-734C-1	Sequence 1, Appl
C 301	86	6.4	2517	4	US-09-577-304A-174	Sequence 174, Ap	C 374	83.5	6.2	11219	3	US-08-439-009A-1	Sequence 1, Appl
C 302	86	6.4	2814	4	US-09-252-991A-15765	Sequence 15765, A	C 375	83	6.2	774	4	US-09-252-991A-13331	Sequence 13331, A
C 303	86	6.4	3012	4	US-09-252-991A-7498	Sequence 7498, Ap	C 376	83	6.2	933	4	US-09-252-991A-10917	Sequence 10917, A
C 304	86	6.4	3357	4	US-09-252-991A-15868	Sequence 15868, A	C 377	83	6.2	964	4	US-09-513-999C-14934	Sequence 14934, A
C 305	86	6.4	47981	4	US-09-679-279-1	Sequence 1, Appl	C 378	83	6.2	1152	4	US-09-252-991A-5237	Sequence 5237, Ap

379	83	6.2	1617	4	US-09-265-013-2	Sequence 2, Appli	C 452	82	6.1	1068	4	US-09-252-991A-6432	Sequence 6432, Ap
380	83	6.2	1851	4	US-09-252-991A-9067	Sequence 9067, Ap	C 453	82	6.1	1737	4	US-09-252-991A-2085	Sequence 2085, Ap
381	83	6.2	2046	4	US-09-252-991A-5266	Sequence 5266, Ap	C 454	82	6.1	2517	4	US-09-758-282B-138	Sequence 138, App
382	83	6.2	2328	4	US-09-252-991A-11890	Sequence 11890, A	C 455	82	6.1	2517	4	US-09-577-304A-138	Sequence 138, App
383	83	6.2	4143	4	US-09-252-991A-9151	Sequence 9151, Ap	C 456	82	6.1	3186	4	US-09-489-039A-5569	Sequence 5569, Ap
384	83	6.2	4212	4	US-09-252-991A-8929	Sequence 8929, Ap	C 457	82	6.1	3236	4	US-08-961-527-222	Sequence 222, App
385	83	6.2	7308	3	US-09-011-745-3	Sequence 3, Appli	C 458	82	6.1	3378	4	US-09-252-991A-2158	Sequence 2158, Ap
386	83	6.2	7616	3	US-09-011-745-4	Sequence 4, Appli	C 459	82	6.1	5661	3	US-08-938-105-2	Sequence 2, Appli
387	83	6.2	8202	1	US-08-258-420-13	Sequence 13, Appli	C 460	82	6.1	7661	4	US-09-774-528-305	Sequence 305, App
388	83	6.2	8332	3	US-08-850-961-1	Sequence 1, Appli	C 461	81.5	6.1	7744	4	US-09-252-991A-15563	Sequence 15563, A
389	83	6.2	8332	3	US-09-479-776-1	Sequence 11, Appli	C 462	81.5	6.1	837	4	US-09-252-991A-5702	Sequence 5702, Ap
390	83	6.2	8332	4	US-09-309-572-11	Sequence 11, Appli	C 463	81.5	6.1	1080	4	US-09-892-188B-1	Sequence 4093, Ap
391	83	6.2	8332	4	US-09-315-127-1	Sequence 1, Appli	C 464	81.5	6.1	1161	4	US-09-252-991A-7990	Sequence 1, Appli
392	83	6.2	8332	4	US-09-265-013-1	Sequence 1, Appli	C 465	81.5	6.1	1221	4	US-09-252-991A-8268	Sequence 8268, Ap
393	83	6.2	8332	4	US-09-554-572-25	Sequence 25, Appli	C 466	81.5	6.1	1233	4	US-09-252-991A-8268	Sequence 8268, Ap
394	83	6.2	8332	4	US-09-718-096-11	Sequence 11, Appli	C 467	81.5	6.1	1302	4	US-09-252-991A-8677	Sequence 8677, Ap
395	83	6.2	8332	4	US-09-815-048-3	Sequence 3, Appli	C 468	81.5	6.1	1362	4	US-09-252-991A-8259	Sequence 8259, Ap
396	83	6.2	42450	4	US-08-804-227C-1	Sequence 1, Appli	C 470	81.5	6.1	1503	4	US-09-252-991A-13684	Sequence 13684, A
397	83	6.2	43280	2	US-09-252-991A-2095	Sequence 2095, Ap	C 471	81.5	6.1	1584	4	US-09-252-991A-625	Sequence 625, App
398	82.5	6.1	651	4	US-09-252-991A-507	Sequence 507, App	C 472	81.5	6.1	1674	4	US-09-252-991A-3990	Sequence 3990, Ap
399	82.5	6.1	816	4	US-09-252-991A-6278	Sequence 6278, Ap	C 473	81.5	6.1	1746	4	US-09-252-991A-13461	Sequence 13461, A
400	82.5	6.1	1209	4	US-09-252-991A-572	Sequence 572, App	C 474	81.5	6.1	1983	4	US-09-252-991A-15635	Sequence 15635, A
401	82.5	6.1	1245	4	US-09-252-991A-594	Sequence 594, App	C 475	81.5	6.1	2190	4	US-09-252-991A-10256	Sequence 10256, A
402	82.5	6.1	1623	4	US-09-613-303-3	Sequence 3, Appli	C 476	81.5	6.1	2211	4	US-09-252-991A-15685	Sequence 15685, A
403	82.5	6.1	1623	4	US-10-267-311-3	Sequence 3, Appli	C 477	81.5	6.1	2325	4	US-09-252-991A-8064	Sequence 8064, Ap
404	82.5	6.1	1764	4	US-09-252-991A-6133	Sequence 6133, Ap	C 478	81.5	6.1	2403	4	US-09-252-991A-7056	Sequence 7056, Ap
405	82.5	6.1	1785	4	US-09-252-991A-4278	Sequence 4278, Ap	C 479	81.5	6.1	4242	4	US-09-919-039-112	Sequence 112, App
406	82.5	6.1	1879	4	US-09-614-748A-10	Sequence 10, Appli	C 480	81.5	6.1	4346	4	US-09-252-991A-6997	Sequence 6997, Ap
407	82.5	6.1	1886	1	US-07-980-526-1	Sequence 1, Appli	C 481	81.5	6.1	10023	4	US-09-489-039A-2253	Sequence 2253, Ap
408	82.5	6.1	1920	4	US-09-613-303-16	Sequence 16, Appli	C 482	81	6.0	915	4	US-08-960-756-3	Sequence 3, Appli
409	82.5	6.1	1920	4	US-10-267-311-16	Sequence 16, Appli	C 483	81	6.0	999	2	US-09-266-965-45	Sequence 45, Appli
410	82.5	6.1	1947	4	US-09-613-303-28	Sequence 28, Appli	C 484	81	6.0	1152	4	US-08-960-022-17	Sequence 17, Appli
411	82.5	6.1	1947	4	US-10-267-311-28	Sequence 28, Appli	C 485	81	6.0	1307	2	US-09-252-991A-3389	Sequence 3389, Ap
412	82.5	6.1	1947	4	US-10-267-311-28	Sequence 28, Appli	C 486	81	6.0	1470	4	US-09-489-039A-2524	Sequence 2524, Ap
413	82.5	6.1	1956	4	US-09-252-991A-12032	Sequence 8, Appli	C 487	81	6.0	1584	4	US-09-096-399-1	Sequence 1, Appli
414	82.5	6.1	2017	4	US-09-614-748A-8	Sequence 8, Appli	C 488	81	6.0	1682	3	US-09-096-399-3	Sequence 3, Appli
415	82.5	6.1	2067	4	US-09-252-991A-527	Sequence 527, App	C 489	81	6.0	1696	3	US-09-640-958-9	Sequence 9, Appli
416	82.5	6.1	2499	4	US-09-758-282B-96	Sequence 96, Appli	C 490	81	6.0	1899	4	US-09-640-958-9	Sequence 9, Appli
417	82.5	6.1	2499	4	US-09-577-304A-96	Sequence 96, Appli	C 491	81	6.0	1904	4	US-09-252-991A-16245	Sequence 16245, A
418	82.5	6.1	2517	4	US-09-758-282B-78	Sequence 78, Appli	C 492	81	6.0	1944	4	US-09-640-958-11	Sequence 11, Appli
419	82.5	6.1	2517	4	US-09-758-282B-86	Sequence 86, Appli	C 493	81	6.0	1965	4	US-07-977-434-1	Sequence 1, Appli
420	82.5	6.1	2517	4	US-09-758-282B-102	Sequence 102, App	C 494	81	6.0	2499	1	US-08-458-819-1	Sequence 1, Appli
421	82.5	6.1	2517	4	US-09-758-282B-105	Sequence 105, App	C 495	81	6.0	2499	3	US-07-602-848E-1	Sequence 1, Appli
422	82.5	6.1	2517	4	US-09-758-282B-108	Sequence 108, App	C 496	81	6.0	2499	3	US-09-587-856-1	Sequence 1, Appli
423	82.5	6.1	2517	4	US-09-758-282B-111	Sequence 111, App	C 497	81	6.0	2499	3	US-09-777-537-1	Sequence 1, Appli
424	82.5	6.1	2517	4	US-09-758-282B-135	Sequence 135, App	C 498	81	6.0	2499	3	US-09-777-538-1	Sequence 1, Appli
425	82.5	6.1	2517	4	US-09-758-282B-135	Sequence 135, App	C 499	81	6.0	2499	3	US-09-758-282B-100	Sequence 100, App
426	82.5	6.1	2517	4	US-09-777-304A-78	Sequence 78, Appli	C 500	81	6.0	2499	4	US-09-577-304A-100	Sequence 100, App
427	82.5	6.1	2517	4	US-09-777-304A-84	Sequence 84, Appli	C 501	81	6.0	2499	5	PCT-US91-07035-1	Sequence 167, App
428	82.5	6.1	2517	4	US-09-777-304A-86	Sequence 86, Appli	C 502	81	6.0	2499	5	US-08-757-653-167	Sequence 65, Appli
429	82.5	6.1	2517	4	US-09-777-304A-102	Sequence 102, App	C 503	81	6.0	2505	2	US-08-823-516-65	Sequence 106, App
430	82.5	6.1	2517	4	US-09-777-304A-105	Sequence 105, App	C 504	81	6.0	2505	2	US-08-759-038-106	Sequence 106, App
431	82.5	6.1	2517	4	US-09-777-304A-108	Sequence 108, App	C 505	81	6.0	2505	3	US-08-758-314-106	Sequence 106, App
432	82.5	6.1	2517	4	US-09-777-304A-111	Sequence 111, App	C 506	81	6.0	2505	4	US-09-684-938-106	Sequence 106, App
433	82.5	6.1	2517	4	US-09-777-304A-135	Sequence 135, App	C 507	81	6.0	2505	4	US-09-308-825A-106	Sequence 55, Appli
434	82.5	6.1	2526	4	US-09-758-282B-90	Sequence 90, Appli	C 508	81	6.0	2505	4	US-09-758-282B-55	Sequence 55, Appli
435	82.5	6.1	2526	4	US-09-777-304A-90	Sequence 90, Appli	C 509	81	6.0	2505	4	US-09-940-244-65	Sequence 55, Appli
436	82.5	6.1	2766	4	US-09-252-991A-3756	Sequence 3756, Ap	C 510	81	6.0	2505	4	US-09-577-304A-55	Sequence 1, Appli
437	82.5	6.1	2847	4	US-09-613-303-20	Sequence 20, Appli	C 511	81	6.0	2506	1	US-08-073-384C-1	Sequence 1, Appli
438	82.5	6.1	2847	4	US-10-267-311-20	Sequence 20, Appli	C 512	81	6.0	2506	1	US-08-254-359A-1	Sequence 1, Appli
439	82.5	6.1	2874	4	US-09-252-991A-3637	Sequence 3637, Ap	C 513	81	6.0	2506	1	US-08-483-043-1	Sequence 1, Appli
440	82.5	6.1	3390	4	US-09-252-991A-11981	Sequence 11981, A	C 514	81	6.0	2506	1	US-08-483-043-1	Sequence 1, Appli
441	82.5	6.1	3390	4	US-08-955-565A-3	Sequence 3, Appli	C 515	81	6.0	2506	2	US-08-484-956-1	Sequence 1, Appli
442	82.5	6.1	28804	2	US-08-592-874-1	Sequence 2, Appli	C 516	81	6.0	2506	2	US-08-484-956-1	Sequence 1, Appli
443	82.5	6.1	28804	3	US-09-096-867-2	Sequence 2, Appli	C 517	81	6.0	2506	2	US-08-757-653-1	Sequence 1, Appli
444	82.5	6.1	28804	3	US-09-096-867-2	Sequence 2, Appli	C 518	81	6.0	2506	2	US-08-599-491-1	Sequence 1, Appli
445	82	6.1	789	1	US-08-181-335B-3	Sequence 3, Appli	C 519	81	6.0	2506	2	US-08-756-386-1	Sequence 1, Appli
446	82	6.1	789	1	US-08-181-335B-5	Sequence 5, Appli	C 520	81	6.0	2506	2	US-08-823-516-1	Sequence 1, Appli
447	82	6.1	789	1	US-08-181-335B-6	Sequence 6, Appli	C 521	81	6.0	2506	3	US-08-682-833A-1	Sequence 1, Appli
448	82	6.1	789	5	PCT-US95-00129-3	Sequence 3, Appli	C 522	81	6.0	2506	3	US-08-758-314-1	Sequence 1, Appli
449	82	6.1	789	5	PCT-US95-00129-5	Sequence 5, Appli	C 523	81	6.0	2506	3	US-08-758-314-1	Sequence 1, Appli
450	82	6.1	789	5	PCT-US95-00129-6	Sequence 6, Appli	C 524	81	6.0	2506	3	US-09-350-309-1	Sequence 1, Appli
451	82	6.1	852	4	US-09-252-991A-6125	Sequence 6125, Ap							

C 525	81	6.0	2506	3	US-08-520-946-1	Sequence 1, Appli	C 598	81	6.0	2517	4	US-09-577-304A-233	Sequence 233, App
C 526	81	6.0	2506	4	US-09-684-938-1	Sequence 1, Appli	C 599	81	6.0	2526	4	US-09-758-282B-76	Sequence 76, Appl
C 527	81	6.0	2506	4	US-09-308-822A-1	Sequence 1, Appli	C 600	81	6.0	2526	4	US-09-758-282B-240	Sequence 240, App
C 528	81	6.0	2506	4	US-09-758-282B-1	Sequence 1, Appli	C 601	81	6.0	2526	4	US-09-758-282B-362	Sequence 362, App
C 529	81	6.0	2506	4	US-09-655-378A-1	Sequence 1, Appli	C 602	81	6.0	2526	4	US-09-577-304A-76	Sequence 76, Appl
C 530	81	6.0	2506	4	US-09-940-244-1	Sequence 1, Appli	C 603	81	6.0	2526	4	US-09-577-304A-240	Sequence 240, App
C 531	81	6.0	2506	4	US-09-333-145-1	Sequence 1, Appli	C 604	81	6.0	2526	4	US-09-577-304A-262	Sequence 262, App
C 532	81	6.0	2506	4	US-09-577-304A-1	Sequence 1, Appli	C 605	81	6.0	2626	1	US-08-156-020-1	Sequence 1, Appli
C 533	81	6.0	2514	4	US-09-758-282B-164	Sequence 264, App	C 606	81	6.0	2626	1	US-08-156-020-3	Sequence 3, Appli
C 534	81	6.0	2514	4	US-09-577-304A-264	Sequence 264, App	C 607	81	6.0	2626	1	US-08-156-020-5	Sequence 5, Appli
C 535	81	6.0	2517	4	US-09-758-282B-62	Sequence 62, Appl	C 608	81	6.0	2626	1	US-08-156-020-7	Sequence 7, Appli
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C 537	81	6.0	2517	4	US-09-758-282B-82	Sequence 82, Appl	C 610	81	6.0	2626	3	US-08-978-806-1	Sequence 1, Appli
C 538	81	6.0	2517	4	US-09-758-282B-88	Sequence 88, Appl	C 611	81	6.0	2727	4	US-09-623-326-3	Sequence 3, Appli
C 539	81	6.0	2517	4	US-09-758-282B-114	Sequence 114, App	C 612	81	6.0	2727	4	US-09-623-326-4	Sequence 4, Appli
C 540	81	6.0	2517	4	US-09-758-282B-117	Sequence 117, App	C 613	81	6.0	2733	4	US-09-623-326-1	Sequence 1, Appli
C 541	81	6.0	2517	4	US-09-758-282B-120	Sequence 120, App	C 614	81	6.0	2733	4	US-09-623-326-2	Sequence 2, Appli
C 542	81	6.0	2517	4	US-09-758-282B-123	Sequence 123, App	C 615	81	6.0	2763	4	US-09-640-958-5	Sequence 5, Appli
C 543	81	6.0	2517	4	US-09-758-282B-126	Sequence 126, App	C 616	81	6.0	2850	4	US-09-623-326-5	Sequence 5, Appli
C 544	81	6.0	2517	4	US-09-758-282B-129	Sequence 129, App	C 617	81	6.0	2949	4	US-09-623-326-6	Sequence 6, Appli
C 545	81	6.0	2517	4	US-09-758-282B-132	Sequence 132, App	C 618	81	6.0	3114	4	US-09-252-991A-225	Sequence 225, App
C 546	81	6.0	2517	4	US-09-758-282B-141	Sequence 141, App	C 619	81	6.0	3261	4	US-09-252-991A-8480	Sequence 8480, Ap
C 547	81	6.0	2517	4	US-09-758-282B-147	Sequence 147, App	C 620	81	6.0	3345	4	US-09-252-991A-8394	Sequence 8394, Ap
C 548	81	6.0	2517	4	US-09-758-282B-149	Sequence 149, App	C 621	81	6.0	3402	4	US-09-252-991A-1374	Sequence 1374, Ap
C 549	81	6.0	2517	4	US-09-758-282B-152	Sequence 152, App	C 622	81	6.0	3687	4	US-09-252-991A-1193	Sequence 1193, Ap
C 550	81	6.0	2517	4	US-09-758-282B-168	Sequence 168, App	C 623	81	6.0	3864	4	US-09-252-991A-13035	Sequence 13035, A
C 551	81	6.0	2517	4	US-09-758-282B-177	Sequence 177, App	C 624	81	6.0	3876	4	US-09-252-991A-2933	Sequence 2933, Ap
C 552	81	6.0	2517	4	US-09-758-282B-180	Sequence 180, App	C 625	81	6.0	4266	4	US-09-252-991A-1234	Sequence 1234, Ap
C 553	81	6.0	2517	4	US-09-758-282B-183	Sequence 183, App	C 626	81	6.0	5849	3	US-09-134-246-6	Sequence 6, Appli
C 554	81	6.0	2517	4	US-09-758-282B-186	Sequence 186, App	C 627	81	6.0	6714	1	US-08-021-623C-5	Sequence 5, Appli
C 555	81	6.0	2517	4	US-09-758-282B-189	Sequence 189, App	C 628	81	6.0	6732	1	US-09-976-594-99	Sequence 99, Appl
C 556	81	6.0	2517	4	US-09-758-282B-199	Sequence 199, App	C 629	81	6.0	6732	1	US-09-453-702B-111	Sequence 111, App
C 557	81	6.0	2517	4	US-09-758-282B-201	Sequence 201, App	C 630	81	6.0	21119	3	US-08-311-731A-24	Sequence 24, Appl
C 558	81	6.0	2517	4	US-09-758-282B-203	Sequence 203, App	C 631	81	6.0	38494	4	US-08-311-731A-135	Sequence 135, App
C 559	81	6.0	2517	4	US-09-758-282B-205	Sequence 205, App	C 632	81	6.0	50937	3	US-09-428-517-1	Sequence 1, Appli
C 560	81	6.0	2517	4	US-09-758-282B-217	Sequence 217, App	C 633	81	6.0	53500	4	US-09-266-965-76	Sequence 76, Appl
C 561	81	6.0	2517	4	US-09-758-282B-220	Sequence 220, App	C 634	80.5	6.0	672	4	US-09-252-991A-9638	Sequence 9638, Ap
C 562	81	6.0	2517	4	US-09-758-282B-225	Sequence 225, App	C 635	80.5	6.0	936	4	US-09-489-039A-139	Sequence 139, App
C 563	81	6.0	2517	4	US-09-758-282B-227	Sequence 227, App	C 636	80.5	6.0	936	4	US-09-489-039A-2270	Sequence 2270, Ap
C 564	81	6.0	2517	4	US-09-758-282B-229	Sequence 229, App	C 637	80.5	6.0	957	4	US-09-252-991A-3959	Sequence 3959, Ap
C 565	81	6.0	2517	4	US-09-758-282B-231	Sequence 231, App	C 638	80.5	6.0	1362	4	US-09-252-991A-3943	Sequence 3943, Ap
C 566	81	6.0	2517	4	US-09-758-282B-233	Sequence 233, App	C 639	80.5	6.0	1449	4	US-09-252-991A-1976	Sequence 1976, Ap
C 567	81	6.0	2517	4	US-09-577-304A-62	Sequence 62, Appl	C 640	80.5	6.0	1524	4	US-09-807-897-3	Sequence 3, Appli
C 568	81	6.0	2517	4	US-09-577-304A-71	Sequence 71, Appl	C 641	80.5	6.0	1596	4	US-09-252-991A-10119	Sequence 10119, A
C 569	81	6.0	2517	4	US-09-577-304A-82	Sequence 82, Appl	C 642	80.5	6.0	1605	4	US-09-252-991A-10729	Sequence 10729, A
C 570	81	6.0	2517	4	US-09-577-304A-88	Sequence 88, Appl	C 643	80.5	6.0	1686	2	US-08-648-657-14	Sequence 14, Appl
C 571	81	6.0	2517	4	US-09-577-304A-114	Sequence 114, App	C 644	80.5	6.0	2155	4	US-09-620-312D-65	Sequence 65, Appl
C 572	81	6.0	2517	4	US-09-577-304A-117	Sequence 117, App	C 645	80.5	6.0	2220	2	US-08-864-224-1	Sequence 1, Appli
C 573	81	6.0	2517	4	US-09-577-304A-120	Sequence 120, App	C 646	80.5	6.0	2325	4	US-09-252-991A-218	Sequence 218, App
C 574	81	6.0	2517	4	US-09-577-304A-123	Sequence 123, App	C 647	80.5	6.0	2493	4	US-09-252-991A-5433	Sequence 5433, Ap
C 575	81	6.0	2517	4	US-09-577-304A-126	Sequence 126, App	C 648	80.5	6.0	2505	4	US-09-334-818A-1	Sequence 1, Appli
C 576	81	6.0	2517	4	US-09-577-304A-129	Sequence 129, App	C 649	80.5	6.0	2538	4	US-09-252-991A-1285	Sequence 1285, Ap
C 577	81	6.0	2517	4	US-09-577-304A-132	Sequence 132, App	C 650	80.5	6.0	2571	4	US-09-252-991A-1279	Sequence 1279, Ap
C 578	81	6.0	2517	4	US-09-577-304A-141	Sequence 141, App	C 651	80.5	6.0	2610	4	US-09-252-991A-8489	Sequence 8489, Ap
C 579	81	6.0	2517	4	US-09-577-304A-147	Sequence 147, App	C 652	80.5	6.0	2746	4	US-09-252-991A-194	Sequence 194, App
C 580	81	6.0	2517	4	US-09-577-304A-149	Sequence 149, App	C 653	80.5	6.0	2984	4	US-09-252-991A-227	Sequence 227, App
C 581	81	6.0	2517	4	US-09-577-304A-152	Sequence 152, App	C 654	80.5	6.0	4253	4	US-09-252-991A-10434	Sequence 10434, A
C 582	81	6.0	2517	4	US-09-577-304A-168	Sequence 168, App	C 655	80.5	6.0	4564	4	US-09-252-991A-4765	Sequence 4765, Ap
C 583	81	6.0	2517	4	US-09-577-304A-177	Sequence 177, App	C 656	80.5	6.0	7266	3	US-08-713-118-1	Sequence 1, Appli
C 584	81	6.0	2517	4	US-09-577-304A-180	Sequence 180, App	C 657	80.5	6.0	7266	3	US-09-452-007-1	Sequence 1, Appli
C 585	81	6.0	2517	4	US-09-577-304A-183	Sequence 183, App	C 658	80.5	6.0	11613	1	US-08-484-044-10	Sequence 10, Appl
C 586	81	6.0	2517	4	US-09-577-304A-186	Sequence 186, App	C 659	80.5	6.0	49377	1	US-08-764-233A-1	Sequence 1, Appli
C 587	81	6.0	2517	4	US-09-577-304A-189	Sequence 189, App	C 660	80.5	6.0	50341	1	US-08-247-901C-1	Sequence 1, Appli
C 588	81	6.0	2517	4	US-09-577-304A-199	Sequence 199, App	C 661	80.5	6.0	50341	2	US-09-075-904-1	Sequence 1, Appli
C 589	81	6.0	2517	4	US-09-577-304A-201	Sequence 201, App	C 662	80.5	6.0	52297	3	US-09-426-436-1	Sequence 1, Appli
C 590	81	6.0	2517	4	US-09-577-304A-203	Sequence 203, App	C 663	80.5	6.0	52297	3	US-08-705-557-1	Sequence 1, Appli
C 591	81	6.0	2517	4	US-09-577-304A-205	Sequence 205, App	C 664	80	6.0	618	4	US-09-489-039A-1035	Sequence 1035, Ap
C 592	81	6.0	2517	4	US-09-577-304A-217	Sequence 217, App	C 665	80	6.0	855	4	US-09-252-991A-9422	Sequence 9422, Ap
C 593	81	6.0	2517	4	US-09-577-304A-220	Sequence 220, App	C 666	80	6.0	1008	1	US-08-347-826A-3	Sequence 3, Appli
C 594	81	6.0	2517	4	US-09-577-304A-225	Sequence 225, App	C 667	80	6.0	1101	4	US-09-252-991A-9455	Sequence 9455, Ap
C 595	81	6.0	2517	4	US-09-577-304A-227	Sequence 227, App	C 668	80	6.0	1122	4	US-09-252-991A-8798	Sequence 8798, Ap
C 596	81	6.0	2517	4	US-09-577-304A-229	Sequence 229, App	C 669	80	6.0	1417	4	US-09-904-615-31	Sequence 31, Appl
C 597	81	6.0	2517	4	US-09-577-304A-231	Sequence 231, App	C 670	80	6.0	1524	4	US-09-489-039A-3444	Sequence 3444, Ap

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672	80	2037	4	US-09-489-039A-4049	Sequence 4049, Ap	745	79	5.9	1692	4	US-09-252-991A-7872	Sequence 7872, Ap
673	80	2083	4	US-09-774-528-344	Sequence 344, App	746	79	5.9	1800	4	US-09-252-991A-679	Sequence 679, App
674	80	2379	4	US-09-252-991A-9252	Sequence 9252, Ap	747	79	5.9	1816	1	US-07-865-662F-5	Sequence 5, Appli
675	80	3033	4	US-09-724-797-81	Sequence 81, Appl	748	79	5.9	1816	3	US-08-374-219B-5	Sequence 5, Appli
676	80	6401	4	US-09-221-017B-804	Sequence 804, App	749	79	5.9	1822	3	US-07-865-662F-6	Sequence 6, Appli
677	79.5	828	4	US-08-252-991A-11099	Sequence 11099, A	750	79	5.9	1822	3	US-08-374-219B-6	Sequence 6, Appli
678	79.5	850	1	US-08-114-461-2	Sequence 2, Appli	751	79	5.9	1938	4	US-09-543-681A-3585	Sequence 3585, Ap
679	79.5	850	1	US-08-192-156-2	Sequence 2, Appli	752	79	5.9	2244	5	US-08-476-519-10	Sequence 10, Appl
680	79.5	850	1	US-08-370-789-2	Sequence 2, Appli	753	79	5.9	2244	5	PCT-US95-09323-10	Sequence 10, Appl
681	79.5	852	4	US-09-252-991A-10276	Sequence 10276, A	754	79	5.9	2328	4	US-09-252-991A-5729	Sequence 5729, Ap
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683	79.5	1065	4	US-09-270-767-12932	Sequence 12932, A	756	79	5.9	2334	5	PCT-US95-09323-1	Sequence 1, Appli
684	79.5	1317	4	US-09-252-991A-10989	Sequence 10989, A	757	79	5.9	2618	4	US-09-252-991A-2294	Sequence 2294, Ap
685	79.5	1359	4	US-09-252-991A-2528	Sequence 2528, Ap	758	79	5.9	2610	4	US-09-252-991A-175	Sequence 175, App
686	79.5	1377	4	US-09-489-039A-6783	Sequence 6783, Ap	759	79	5.9	2817	4	US-09-252-991A-7311	Sequence 7311, Ap
687	79.5	1473	4	US-09-252-991A-2391	Sequence 2391, Ap	760	79	5.9	2880	4	US-09-252-991A-7187	Sequence 7187, Ap
688	79.5	1715	1	US-07-847-743B-24	Sequence 24, Appl	761	79	5.9	2943	4	US-09-379-530B-3	Sequence 3, Appli
689	79.5	1715	1	US-08-456-201-24	Sequence 24, Appl	762	79	5.9	3134	1	US-07-865-662F-7	Sequence 7, Appli
690	79.5	1715	5	PCT-US92-04295A-24	Sequence 24, Appl	763	79	5.9	3134	3	US-08-374-219B-7	Sequence 7, Appli
691	79.5	1715	5	US-08-456-241-24	Sequence 24, Appl	764	79	5.9	3373	1	US-08-273-411-2	Sequence 2, Appli
692	79.5	1731	4	US-09-252-991A-15928	Sequence 15928, A	765	79	5.9	3373	1	US-09-898-361-10	Sequence 10, Appl
693	79.5	1872	4	US-09-252-991A-13815	Sequence 13815, A	766	79	5.9	4230	4	US-09-252-991A-5711	Sequence 5711, Ap
694	79.5	1964	4	US-09-774-528-308	Sequence 308, App	767	79	5.9	4941	4	US-09-252-991A-5741	Sequence 5741, Ap
695	79.5	2077	4	US-09-921-039A-16	Sequence 16, Appl	768	79	5.9	5032	4	US-09-344-510B-8	Sequence 8, Appli
696	79.5	2232	4	US-09-489-039A-3902	Sequence 3902, Ap	769	79	5.9	8091	4	US-09-230-652-1	Sequence 1, Appli
697	79.5	2431	1	US-07-847-743B-25	Sequence 25, Appl	770	79	5.9	8174	1	US-09-230-652-1	Sequence 5, Appli
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700	79.5	2431	5	US-09-849-334-1	Sequence 1, Appli	773	79	5.9	8174	3	US-08-696-731-5	Sequence 5, Appli
701	79.5	2469	4	US-10-274-878-1	Sequence 1, Appli	774	79	5.9	8174	3	US-09-042-531-5	Sequence 3, Appli
702	79.5	2469	4	US-08-743-168B-35	Sequence 35, Appl	775	79	5.9	8257	4	PCT-US91-00899-3	Sequence 3, Appli
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704	79.5	2472	3	US-08-743-168B-37	Sequence 37, Appl	777	79	5.9	16080	4	US-09-724-566A-48	Sequence 48, Appl
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707	79.5	2490	1	US-08-456-201-23	Sequence 23, Appl	780	79	5.9	137000	4	US-09-557-884-1	Sequence 1, Appli
708	79.5	2490	2	US-08-456-241-23	Sequence 23, Appl	781	79	5.9	137000	4	US-09-557-884-1	Sequence 1, Appli
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711	79.5	2517	4	US-09-758-282B-144	Sequence 144, App	784	78.5	5.8	681	4	US-09-252-991A-3852	Sequence 3852, Ap
712	79.5	2517	4	US-09-577-304A-144	Sequence 144, App	785	78.5	5.8	791	3	US-08-858-207A-219	Sequence 219, App
713	79.5	2742	4	US-09-252-991A-10556	Sequence 5556, App	786	78.5	5.8	801	4	US-09-489-039A-5911	Sequence 5911, Ap
714	79.5	2742	4	US-09-252-991A-10486	Sequence 10486, A	787	78.5	5.8	831	4	US-09-489-039A-5052	Sequence 5052, Ap
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716	79.5	3321	4	US-09-252-991A-5668	Sequence 5668, Ap	789	78.5	5.8	1014	4	US-09-252-991A-195	Sequence 195, App
717	79.5	3339	4	US-09-252-991A-10685	Sequence 10685, A	790	78.5	5.8	1245	4	US-09-252-991A-5535	Sequence 5535, Ap
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719	79.5	6575	3	US-08-450-562-3	Sequence 3, Appli	792	78.5	5.8	1527	4	US-09-244-111-7	Sequence 7, Appli
720	79.5	6575	3	US-08-984-709A-3	Sequence 3, Appli	793	78.5	5.8	1546	3	US-09-383-318A-1	Sequence 1, Appli
721	79.5	6575	3	US-08-450-272-3	Sequence 3, Appli	794	78.5	5.8	1650	4	US-09-252-991A-3338	Sequence 3338, Ap
722	79.5	6575	3	US-08-450-273-3	Sequence 36, Appl	795	78.5	5.8	1695	4	US-09-252-991A-1686	Sequence 1686, Ap
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725	79.5	6725	3	US-08-984-709A-36	Sequence 36, Appl	798	78.5	5.8	1869	4	US-09-799-451-646	Sequence 646, App
726	79.5	6725	3	US-08-450-272-36	Sequence 36, Appl	799	78.5	5.8	2166	2	US-09-252-991A-3231	Sequence 3231, Ap
727	79.5	6725	3	US-08-450-273-36	Sequence 36, Appl	800	78.5	5.8	2283	4	US-09-252-991A-1654	Sequence 1654, Ap
728	79.5	15872	3	US-09-105-537-1	Sequence 1, Appli	801	78.5	5.8	2499	4	US-09-252-991A-3231	Sequence 30, Appl
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732	79.5	193303	4	US-09-497-855A-44	Sequence 44, Appl	805	78.5	5.8	2499	4	US-09-577-304A-250	Sequence 9494, Ap
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736	79	1174	5	US-09-252-991A-7454	Sequence 7454, Ap	809	78.5	5.8	2514	4	US-09-577-304A-264	Sequence 264, App
737	79	1194	4	US-09-252-991A-7020	Sequence 7020, Ap	810	78.5	5.8	2583	4	US-09-577-304A-264	Sequence 9541, Ap
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739	79	1263	4	US-09-252-991A-11762	Sequence 11762, A	812	78.5	5.8	3024	1	US-07-923-976-7	Sequence 7, Appli
740	79	1305	4	US-09-252-991A-1330	Sequence 1330, Ap	813	78.5	5.8	3264	4	US-09-252-991A-12013	Sequence 12013, A
741	79	1350	4	US-09-252-991A-197	Sequence 197, App	814	78.5	5.8	3279	4	US-09-252-991A-11905	Sequence 11905, A
742	79	1488	4	US-09-252-991A-166	Sequence 166, App	815	78.5	5.8	3625	4	US-09-023-655-1180	Sequence 1180, Ap
743	79	1560	4	US-09-252-991A-166	Sequence 166, App	816	78.5	5.8	3702	4	US-09-252-991A-6666	Sequence 6666, Ap

968	76.5	5.7	1215	4	US-09-252-991A-2595	Sequence 2595, Ap	1046	76.5	5.7	22108	3	US-09-085-761A-3	Sequence 3, Appli
969	76.5	5.7	1227	4	US-09-252-991A-9232	Sequence 9232, Ap	c1047	76.5	5.7	44453	3	US-09-146-053-5	Sequence 5, Appli
c 970	76.5	5.7	1239	4	US-09-252-991A-13781	Sequence 13781, A	1048	76	5.7	398	4	US-09-513-999C-2203	Sequence 2203, Ap
971	76.5	5.7	1245	4	US-09-252-991A-4611	Sequence 4611, Ap	c1049	76	5.7	720	4	US-09-252-991A-12414	Sequence 12414, A
972	76.5	5.7	1251	4	US-09-252-991A-16089	Sequence 16089, A	c1050	76	5.7	990	4	US-09-252-991A-1849	Sequence 1849, Ap
973	76.5	5.7	1443	4	US-09-252-991A-10295	Sequence 10295, A	1051	76	5.7	1002	4	US-09-252-991A-58	Sequence 58, Appl
974	76.5	5.7	1503	3	US-09-463-702A-33	Sequence 33, Appl	1052	76	5.7	1011	4	US-09-252-991A-12242	Sequence 12242, A
975	76.5	5.7	1503	4	US-09-699-135-33	Sequence 33, Appl	1053	76	5.7	1101	3	US-08-987-904A-1	Sequence 1, Appli
976	76.5	5.7	1527	4	US-09-252-991A-16194	Sequence 16194, A	1054	76	5.7	1101	4	US-09-438-623A-1	Sequence 1, Appli
977	76.5	5.7	1557	1	US-08-481-130-26	Sequence 26, Appl	1055	76	5.7	1118	4	US-09-489-039A-2636	Sequence 2636, Ap
978	76.5	5.7	1557	1	US-08-656-984A-26	Sequence 26, Appl	c1056	76	5.7	1146	4	US-09-252-991A-56	Sequence 56, Appl
979	76.5	5.7	1557	1	US-08-485-604-26	Sequence 26, Appl	1057	76	5.7	1188	4	US-09-252-991A-1940	Sequence 1940, Ap
980	76.5	5.7	1557	2	US-08-487-595-26	Sequence 26, Appl	c1058	76	5.7	1311	4	US-09-252-991A-3685	Sequence 3685, Ap
981	76.5	5.7	1566	4	US-09-252-991A-14361	Sequence 14361, A	c1059	76	5.7	1311	4	US-09-252-991A-12317	Sequence 12317, A
982	76.5	5.7	1569	4	US-09-252-991A-15857	Sequence 15857, A	1060	76	5.7	1371	4	US-09-489-039A-3192	Sequence 3192, Ap
c 983	76.5	5.7	1662	4	US-09-252-991A-16399	Sequence 16399, A	1061	76	5.7	1387	6	5270178-1	Patent No. 5270178
984	76.5	5.7	1686	4	US-09-252-991A-10406	Sequence 10406, A	c1062	76	5.7	1461	4	US-09-894-844-84	Sequence 84, Appl
985	76.5	5.7	1824	4	US-09-252-991A-4025	Sequence 4025, Ap	c1068	76	5.7	1662	4	US-09-252-991A-1413	Sequence 1413, Ap
986	76.5	5.7	1854	4	US-09-252-991A-4542	Sequence 4542, Ap	c1069	76	5.7	1785	2	US-08-910-856-1	Sequence 1, Appli
c 992	76.5	5.7	1875	4	US-09-252-991A-3919	Sequence 3919, Ap	c1070	76	5.7	1869	4	US-09-252-991A-3694	Sequence 3694, Ap
c 993	76.5	5.7	1875	4	US-09-252-991A-8812	Sequence 8812, Ap	c1071	76	5.7	1896	4	US-09-252-991A-3492	Sequence 3492, Ap
994	76.5	5.7	1928	3	US-09-352-159-43	Sequence 43, Appl	1072	76	5.7	2019	4	US-09-252-991A-2359	Sequence 2359, Ap
995	76.5	5.7	1928	4	US-09-771-045B-43	Sequence 43, Appl	1073	76	5.7	2052	4	US-09-252-991A-12103	Sequence 12103, A
996	76.5	5.7	2028	4	US-09-252-991A-12590	Sequence 12590, A	1074	76	5.7	2061	4	US-09-252-991A-3398	Sequence 3398, Ap
c 997	76.5	5.7	2040	4	US-09-252-991A-10540	Sequence 10540, A	1075	76	5.7	2077	4	US-09-221-017B-821	Sequence 821, App
c 998	76.5	5.7	2046	4	US-09-490-291-3	Sequence 3, Appli	c1076	76	5.7	2141	4	US-09-774-528-373	Sequence 373, Appl
c 999	76.5	5.7	2076	4	US-09-490-291-5	Sequence 5, Appli	1077	76	5.7	2163	1	US-07-731-157A-1	Sequence 1, Appli
1000	76.5	5.7	2116	4	US-09-023-655-1256	Sequence 1256, Ap	1078	76	5.7	2163	2	US-08-541-780-1	Sequence 1, Appli
1001	76.5	5.7	2176	6	5320958-1	Patent No. 5320958	1079	76	5.7	2196	4	US-09-252-991A-2198	Sequence 2198, Ap
1002	76.5	5.7	2196	4	US-09-252-991A-9319	Sequence 9319, Ap	1080	76	5.7	2316	4	US-09-252-991A-3884	Sequence 3884, Ap
1003	76.5	5.7	2217	4	US-09-252-991A-9238	Sequence 9238, Ap	c1081	76	5.7	2328	4	US-09-252-991A-3955	Sequence 3955, Ap
1004	76.5	5.7	2241	4	US-09-252-991A-7209	Sequence 7209, Ap	1082	76	5.7	2406	4	US-09-634-955B-3	Sequence 3, Appli
c1005	76.5	5.7	2266	1	US-08-156-020-9	Sequence 9, Appli	1083	76	5.7	2406	4	US-09-816-760-3	Sequence 3, Appli
c1006	76.5	5.7	2715	4	US-09-252-991A-8715	Sequence 8715, Ap	1084	76	5.7	2406	4	US-09-838-561-3	Sequence 3, Appli
c1007	76.5	5.7	2715	1	US-08-481-130-25	Sequence 25, Appl	c1085	76	5.7	2493	1	US-07-977-434-5	Sequence 5, Appli
1008	76.5	5.7	2775	1	US-08-656-984A-25	Sequence 25, Appl	c1086	76	5.7	2493	5	US-08-458-819-5	Sequence 5, Appli
1009	76.5	5.7	2775	1	US-08-485-604-25	Sequence 25, Appl	c1087	76	5.7	2493	5	PCT-US91-07035-5	Sequence 5, Appli
1010	76.5	5.7	2775	2	US-08-487-595-25	Sequence 25, Appl	1088	76	5.7	2660	4	US-09-634-955B-1	Sequence 1, Appli
c1011	76.5	5.7	2850	2	US-08-224-482-7	Sequence 7, Appli	1089	76	5.7	2660	4	US-09-816-760-1	Sequence 1, Appli
c1012	76.5	5.7	2896	4	US-09-266-228D-9	Sequence 9, Appli	1090	76	5.7	2660	4	US-09-838-561-1	Sequence 1, Appli
1013	76.5	5.7	2927	1	US-08-481-130-27	Sequence 27, Appl	1091	76	5.7	2754	4	US-09-252-991A-1147	Sequence 1147, Ap
1014	76.5	5.7	2927	1	US-08-656-984A-27	Sequence 27, Appl	1092	76	5.7	2754	4	US-07-928-464-1	Sequence 1, Appli
1015	76.5	5.7	2927	1	US-08-485-604-27	Sequence 27, Appl	1093	76	5.7	2890	5	PCT-US93-07347-1	Sequence 1, Appli
1016	76.5	5.7	2927	2	US-08-487-595-27	Sequence 27, Appl	1094	76	5.7	3033	1	US-08-003-311B-1	Sequence 1, Appli
c1017	76.5	5.7	3000	3	US-08-460-269C-5	Sequence 5, Appli	1095	76	5.7	3033	2	US-08-261-430-1	Sequence 3, Appli
c1018	76.5	5.7	3059	4	US-09-620-312D-213	Sequence 213, App	c1096	76	5.7	3107	2	US-08-813-942-3	Sequence 3, Appli
1019	76.5	5.7	3068	4	US-09-620-312D-214	Sequence 214, App	c1097	76	5.7	3187	2	US-08-910-856-9	Sequence 9, Appli
1020	76.5	5.7	3099	4	US-09-252-991A-7487	Sequence 7487, Ap	c1098	76	5.7	3187	2	US-08-910-856-10	Sequence 10, Appl
1021	76.5	5.7	3134	4	US-09-620-312D-212	Sequence 212, App	c1099	76	5.7	3187	4	US-09-672-749-16	Sequence 16, Appl
1022	76.5	5.7	3175	4	US-09-799-451-793	Sequence 793, Ap	1100	76	5.7	3518	4	US-10-044-882-3	Sequence 3, Appli
c1023	76.5	5.7	3196	2	US-09-096-982-4	Sequence 4, Appli	1101	76	5.7	3525	4	US-09-252-991A-12708	Sequence 12708, A
c1024	76.5	5.7	3196	2	US-08-653-650A-4	Sequence 4, Appli	c1102	76	5.7	3525	4	US-09-252-991A-1324	Sequence 1324, Ap
1025	76.5	5.7	3199	4	US-09-023-655-947	Sequence 947, App	1103	76	5.7	3651	2	US-08-790-374-1	Sequence 1, Appli
1026	76.5	5.7	3223	2	US-08-620-694A-9	Sequence 9, Appli	c1104	76	5.7	3906	4	US-09-252-991A-13251	Sequence 1, Appli
1027	76.5	5.7	3223	3	US-09-022-255-9	Sequence 9, Appli	1105	76	5.7	15894	1	US-08-348-931A-1	Sequence 1, Appli
1028	76.5	5.7	3223	3	US-09-022-696-9	Sequence 9, Appli	1106	76	5.7	15894	1	US-08-905-817-1	Sequence 1, Appli
1029	76.5	5.7	3223	3	US-08-978-773-3	Sequence 3, Appli	c1107	76	5.7	34094	4	US-09-292-034-1	Sequence 1, Appli
1030	76.5	5.7	3223	3	US-09-022-253-9	Sequence 9, Appli	1108	76	5.7	41684	4	US-09-536-059-1	Sequence 1, Appli
1031	76.5	5.7	3223	3	US-09-022-260-9	Sequence 9, Appli	c1109	76	5.7	70559	4	US-09-409-800B-1	Sequence 1, Appli
1032	76.5	5.7	3223	3	US-09-022-259-9	Sequence 9, Appli	c1110	75.5	5.6	699	4	US-09-252-991A-7077	Sequence 7077, Ap
1033	76.5	5.7	3223	3	US-09-022-257-9	Sequence 9, Appli	1111	75.5	5.6	858	4	US-09-252-991A-10979	Sequence 10979, A
1034	76.5	5.7	3223	4	US-09-549-679-9	Sequence 9, Appli	1112	75.5	5.6	867	4	US-09-252-991A-4037	Sequence 4037, Ap
1035	76.5	5.7	3540	4	US-09-252-991A-1324	Sequence 1324, Ap	1113	75.5	5.6	951	4	US-09-252-991A-14310	Sequence 14310, A
1036	76.5	5.7	3627	4	US-09-792-594-3	Sequence 3, Appli	1114	75.5	5.6	1035	4	US-09-252-991A-14547	Sequence 14547, A
1037	76.5	5.7	3850	3	US-09-463-702A-1	Sequence 1, Appli	1115	75.5	5.6	1116	3	US-09-252-991A-15677	Sequence 15677, A
1038	76.5	5.7	3850	4	US-09-699-135-1	Sequence 1, Appli	1116	75.5	5.6	1149	3	US-08-660-645A-8	Sequence 8, Appli
1039	76.5	5.7	3981	4	US-09-252-991A-1361	Sequence 1361, Ap	1117	75.5	5.6	1149	3	US-09-298-718-8	Sequence 8, Appli
c1040	76.5	5.7	4179	4	US-09-252-991A-1244	Sequence 1244, Ap	1118	75.5	5.6	1149	3	US-09-548-969-8	Sequence 8, Appli
c1041	76.5	5.7	4408	4	US-09-321-017B-830	Sequence 830, App	c1119	75.5	5.6	1149	4	US-09-252-991A-9883	Sequence 8, Appli
c1042	76.5	5.7	5215	4	US-09-231-899-71	Sequence 71, Appl	1120	75.5	5.6	1173	4	US-09-547-267-8	Sequence 8, Appli
1043	76.5	5.7	5581	4	US-09-023-655-966	Sequence 966, App	c1121	75.5	5.6	1173	4	US-09-252-991A-9487	Sequence 9487, Ap
1044	76.5	5.7	6200	4	US-09-795-061-3	Sequence 3, Appli	1122	75.5	5.6	1197	4	US-09-252-991A-14720	Sequence 14720, A
1045	76.5	5.7	22108	3	US-09-053-197A-3	Sequence 3, Appli	1123	75.5	5.6	1197	4	US-09-774-528-421	Sequence 421, App

c1124	75.5	5.6	1209	4	US-09-252-991A-9346	Sequence 9346, Ap	c1197	75.5	5.6	3425	4	US-09-800-971-1	Sequence 1, Appli
c1125	75.5	5.6	1212	4	US-09-252-991A-807	Sequence 807, App	c1198	75.5	5.6	3456	4	US-09-854-845-9	Sequence 9, Appli
c1126	75.5	5.6	1215	4	US-09-252-991A-847	Sequence 847, App	c1199	75.5	5.6	3685	4	US-09-919-039-239	Sequence 239, App
c1127	75.5	5.6	1236	4	US-09-252-991A-3079	Sequence 3079, Ap	1200	75.5	5.6	3801	4	US-09-252-991A-14280	Sequence 14280, A
c1128	75.5	5.6	1234	4	US-09-252-991A-415	Sequence 415, App	c1201	75.5	5.6	3883	4	US-09-620-312D-780	Sequence 780, App
c1129	75.5	5.6	1293	4	US-09-252-991A-14817	Sequence 14817, A	c1202	75.5	5.6	4074	4	US-09-854-845-17	Sequence 17, Appl
c1130	75.5	5.6	1309	4	US-09-544-618-5	Sequence 5, Appli	c1203	75.5	5.6	4389	4	US-09-023-655-991	Sequence 991, App
c1131	75.5	5.6	1344	4	US-09-252-991A-6450	Sequence 6450, Ap	1204	75.5	5.6	6039	1	US-08-324-977-11	Sequence 11, Appl
c1132	75.5	5.6	1401	2	US-08-812-412-1	Sequence 4, Appli	1205	75.5	5.6	6039	2	US-08-384-616-11	Sequence 11, Appl
c1133	75.5	5.6	1401	3	US-09-180-271-4	Sequence 1, Appli	1206	75.5	5.6	6039	2	US-08-904-686A-11	Sequence 11, Appl
c1134	75.5	5.6	1446	4	US-09-252-991A-6746	Sequence 6746, Ap	1207	75.5	5.6	6039	3	US-09-315-850-11	Sequence 11, Appl
c1135	75.5	5.6	1500	4	US-09-489-039A-2856	Sequence 2856, Ap	1208	75.5	5.6	7863	1	US-08-324-977-35	Sequence 35, Appl
c1136	75.5	5.6	1506	4	US-09-252-991A-6098	Sequence 6098, Ap	1209	75.5	5.6	7863	2	US-08-384-616-35	Sequence 35, Appl
c1137	75.5	5.6	1506	4	US-09-252-991A-10637	Sequence 10637, A	1210	75.5	5.6	7863	2	US-08-904-686A-35	Sequence 35, Appl
c1138	75.5	5.6	1521	4	US-09-252-991A-6686	Sequence 6686, Ap	1211	75.5	5.6	7863	3	US-09-315-850-35	Sequence 35, Appl
c1139	75.5	5.6	1569	4	US-09-252-991A-423	Sequence 423, App	1212	75.5	5.6	7917	1	US-08-324-977-31	Sequence 31, Appl
c1140	75.5	5.6	1590	4	US-09-252-991A-14397	Sequence 14397, A	1213	75.5	5.6	7917	2	US-08-384-616-31	Sequence 31, Appl
c1141	75.5	5.6	1617	4	US-09-252-991A-381	Sequence 381, App	1214	75.5	5.6	7917	2	US-08-904-686A-31	Sequence 31, Appl
c1142	75.5	5.6	1629	4	US-09-252-991A-2042	Sequence 2042, Ap	1215	75.5	5.6	7917	3	US-09-315-850-31	Sequence 31, Appl
c1143	75.5	5.6	1818	4	US-09-252-991A-2891	Sequence 2891, Ap	1216	75.5	5.6	8625	3	US-08-980-832-1	Sequence 1, Appli
c1144	75.5	5.6	1827	4	US-09-252-991A-1375	Sequence 1375, Ap	c1217	75.5	5.6	8625	4	US-09-920-923B-1	Sequence 1, Appli
c1145	75.5	5.6	1839	4	US-09-489-039A-2969	Sequence 2969, Ap	1218	75.5	5.6	9030	1	US-08-324-977-13	Sequence 13, Appl
c1146	75.5	5.6	1866	4	US-09-252-991A-11804	Sequence 11804, A	1219	75.5	5.6	9030	2	US-08-384-616-13	Sequence 13, Appl
c1147	75.5	5.6	1908	4	US-09-252-991A-1914	Sequence 1914, Ap	1220	75.5	5.6	9030	2	US-08-904-686A-13	Sequence 13, Appl
c1148	75.5	5.6	1908	4	US-09-252-991A-15513	Sequence 15513, A	1221	75.5	5.6	9030	3	US-09-315-850-13	Sequence 13, Appl
c1149	75.5	5.6	1941	4	US-09-252-991A-11635	Sequence 11635, A	1222	75.5	5.6	9416	1	US-08-324-977-1	Sequence 1, Appli
c1150	75.5	5.6	1986	4	US-09-107-532A-23	Sequence 23, Appl	1223	75.5	5.6	9416	2	US-08-384-616-1	Sequence 1, Appli
c1151	75.5	5.6	2103	4	US-09-252-991A-2813	Sequence 2813, Ap	1224	75.5	5.6	9416	2	US-08-904-686A-1	Sequence 1, Appli
c1152	75.5	5.6	2169	4	US-09-252-991A-10268	Sequence 10268, A	1225	75.5	5.6	9416	3	US-09-315-850-1	Sequence 1, Appli
c1153	75.5	5.6	2181	4	US-09-252-991A-14909	Sequence 14909, A	1226	75.5	5.6	9416	4	US-08-823-895A-27	Sequence 27, Appl
c1154	75.5	5.6	2211	4	US-09-800-971-3	Sequence 3, Appli	1227	75.5	5.6	11220	4	US-09-105-537-2	Sequence 27, Appl
c1155	75.5	5.6	2262	4	US-09-252-991A-1416	Sequence 1416, Ap	c1228	75.5	5.6	11233	3	US-08-980-832-27	Sequence 27, Appl
c1156	75.5	5.6	2316	4	US-09-252-991A-13835	Sequence 13835, A	c1229	75.5	5.6	11233	4	US-09-920-923B-27	Sequence 27, Appl
c1157	75.5	5.6	2363	3	US-09-721-383-1	Sequence 1, Appli	c1230	75.5	5.6	11558	5	PCT-US93-06251-23	Sequence 23, Appl
c1158	75.5	5.6	2363	3	US-09-721-137-1	Sequence 1, Appli	1231	75.5	5.6	33529	3	US-09-144-085-3	Sequence 3, Appli
c1159	75.5	5.6	2363	4	US-09-721-251-1	Sequence 1, Appli	c1232	75.5	5.6	35524	3	US-08-923-137-1	Sequence 1, Appli
c1160	75.5	5.6	2363	4	US-10-114-764-1	Sequence 1, Appli	1233	75.5	5.6	36778	3	US-09-105-537-5	Sequence 5, Appli
c1161	75.5	5.6	2391	4	US-09-252-991A-1192	Sequence 1192, Ap	1234	75.5	5.6	38506	3	US-09-320-878-19	Sequence 19, Appl
c1162	75.5	5.6	2433	4	US-09-489-039A-2577	Sequence 2577, Ap	1235	75.5	5.6	38506	4	US-09-141-908-1	Sequence 1, Appli
c1163	75.5	5.6	2504	1	US-08-073-384C-3	Sequence 3, Appli	1236	75.5	5.6	38506	4	US-09-657-440-19	Sequence 19, Appl
c1164	75.5	5.6	2504	1	US-08-254-359A-3	Sequence 3, Appli	1237	75.5	5.6	70000	4	US-09-851-896-3	Sequence 3, Appli
c1165	75.5	5.6	2504	1	US-08-483-043-3	Sequence 3, Appli	1238	75.5	5.6	536165	4	US-09-214-808-1	Sequence 1, Appli
c1166	75.5	5.6	2504	1	US-08-481-238-3	Sequence 3, Appli	c1239	75.5	5.6	344	4	US-09-621-976-638	Sequence 638, App
c1167	75.5	5.6	2504	2	US-08-471-066B-3	Sequence 3, Appli	1240	75.5	5.6	591	4	US-09-583-110-31	Sequence 31, Appl
c1168	75.5	5.6	2504	2	US-08-484-956-3	Sequence 3, Appli	1241	75.5	5.6	603	4	US-09-252-991A-3222	Sequence 3222, Ap
c1169	75.5	5.6	2504	2	US-08-757-653-3	Sequence 3, Appli	c1242	75.5	5.6	603	4	US-09-252-991A-7177	Sequence 7177, Ap
c1170	75.5	5.6	2504	2	US-08-599-491-3	Sequence 3, Appli	1243	75.5	5.6	828	4	US-09-266-965-35	Sequence 35, Appl
c1171	75.5	5.6	2504	2	US-08-756-386-3	Sequence 3, Appli	1244	75.5	5.6	846	4	US-09-252-991A-3287	Sequence 3287, Ap
c1172	75.5	5.6	2504	2	US-08-823-516-3	Sequence 3, Appli	c1245	75.5	5.6	879	4	US-09-252-991A-12575	Sequence 12575, A
c1173	75.5	5.6	2504	3	US-08-682-853A-3	Sequence 3, Appli	c1246	75.5	5.6	885	4	US-09-252-991A-12721	Sequence 12721, A
c1174	75.5	5.6	2504	3	US-08-759-038-3	Sequence 3, Appli	c1247	75.5	5.6	897	4	US-09-252-991A-14531	Sequence 14531, A
c1175	75.5	5.6	2504	3	US-08-758-314-3	Sequence 3, Appli	c1248	75.5	5.6	915	4	US-09-252-991A-7455	Sequence 7455, Ap
c1176	75.5	5.6	2504	3	US-09-350-309-3	Sequence 3, Appli	c1249	75.5	5.6	954	4	US-09-252-991A-15575	Sequence 15575, A
c1177	75.5	5.6	2504	3	US-08-520-946-3	Sequence 3, Appli	1250	75.5	5.6	1014	4	US-09-252-991A-13650	Sequence 13650, A
c1178	75.5	5.6	2504	4	US-09-684-938-3	Sequence 3, Appli	1251	75.5	5.6	1290	4	US-09-489-039A-5088	Sequence 5088, Ap
c1179	75.5	5.6	2504	4	US-09-308-825A-3	Sequence 3, Appli	1252	75.5	5.6	1335	4	US-09-252-991A-3925	Sequence 3925, Ap
c1180	75.5	5.6	2504	4	US-09-655-378A-3	Sequence 3, Appli	c1253	75.5	5.6	1341	4	US-09-252-991A-8747	Sequence 8747, Ap
c1181	75.5	5.6	2504	4	US-09-940-244-3	Sequence 3, Appli	1254	75.5	5.6	1344	4	US-09-252-991A-11184	Sequence 11184, A
c1182	75.5	5.6	2504	4	US-09-333-145-3	Sequence 3, Appli	1255	75.5	5.6	1352	1	US-08-552-142A-10	Sequence 10, Appl
c1183	75.5	5.6	2811	4	US-09-252-991A-13619	Sequence 13619, A	c1256	75.5	5.6	1374	4	US-09-252-991A-11074	Sequence 11074, A
c1184	75.5	5.6	3105	4	US-09-854-845-5	Sequence 5, Appli	1257	75.5	5.6	1386	4	US-10-182-263-8	Sequence 8, Appli
c1185	75.5	5.6	3150	4	US-09-252-991A-11487	Sequence 11487, A	c1258	75.5	5.6	1404	4	US-09-252-991A-12291	Sequence 12291, A
c1186	75.5	5.6	3150	4	US-09-854-845-1	Sequence 1, Appli	c1259	75.5	5.6	1407	3	US-09-193-377B-2	Sequence 2, Appli
c1187	75.5	5.6	3153	4	US-09-922-501-13	Sequence 13, Appl	c1260	75.5	5.6	1407	4	US-09-252-991A-11004	Sequence 11004, A
c1188	75.5	5.6	3237	4	US-09-854-845-7	Sequence 7, Appli	c1261	75.5	5.6	1428	3	US-09-193-377B-1	Sequence 1, Appli
c1189	75.5	5.6	3264	2	US-08-708-541A-31	Sequence 31, Appl	c1262	75.5	5.6	1446	4	US-09-252-991A-7984	Sequence 7984, Ap
c1190	75.5	5.6	3264	2	US-08-708-541A-33	Sequence 33, Appl	1263	75.5	5.6	1476	4	US-09-252-991A-7653	Sequence 7653, Ap
c1191	75.5	5.6	3264	4	US-09-147-771-31	Sequence 31, Appl	1264	75.5	5.6	1485	4	US-09-252-991A-7738	Sequence 7738, Ap
c1192	75.5	5.6	3264	4	US-09-147-771-33	Sequence 33, Appl	c1265	75.5	5.6	1500	3	US-09-193-377B-3	Sequence 3, Appli
c1193	75.5	5.6	3282	4	US-09-854-845-3	Sequence 3, Appli	c1266	75.5	5.6	1536	4	US-09-252-991A-12037	Sequence 12037, A
c1194	75.5	5.6	3372	4	US-09-252-991A-11405	Sequence 11405, A	1267	75.5	5.6	1584	4	US-09-252-991A-5109	Sequence 5109, Ap
c1195	75.5	5.6	3387	4	US-09-252-991A-14461	Sequence 14461, A	1268	75.5	5.6	1605	4	US-09-252-991A-3897	Sequence 3897, Ap
c1196	75.5	5.6	3411	4	US-09-854-845-11	Sequence 11, Appl	c1269	75.5	5.6	1680	3	US-09-603-185-1	Sequence 1, Appli

1270	75	5.6	1686	4	US-09-252-991A-5746	Sequence 5746, Ap	1343	74.5	5.5	1602	4	US-09-252-991A-6382	Sequence 6382, Ap
1271	75	5.6	1716	4	US-09-252-991A-11978	Sequence 11978, A	1344	74.5	5.5	1638	4	US-09-252-991A-14339	Sequence 14339, A
1272	75	5.6	1728	4	US-09-252-991A-13641	Sequence 13641, A	1345	74.5	5.5	1662	4	US-09-252-991A-1413	Sequence 1413, Ap
1273	75	5.6	1755	6	5225537-1	Patent No. 5225537	1346	74.5	5.5	1680	4	US-09-252-991A-9536	Sequence 9536, Ap
1274	75	5.6	1761	4	US-09-252-991A-5762	Sequence 5762, Ap	1347	74.5	5.5	1728	4	US-09-252-991A-12870	Sequence 12870, A
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OM protein - nucleic search, using frame_plus_p2n model

Run on: January 12, 2005, 21:39:08 ; Search time 3347 Seconds

(without alignments)
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Maximum Match 100%

Listing first 1500 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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105	382.5	28.5	929	6	AR236703	Sequence	178	335	24.9	1464	8	AY279015	Zea mays
106	381	28.4	1049	6	AR236715	Sequence	179	335	24.9	1464	8	AY279006	Zea mays
107	379.5	28.3	1258	6	AR225248	Sequence	180	333	24.8	1172	8	AY279007	Zea mays
108	379.5	28.3	1258	6	A22706	Caffeoyl-Co	181	333	24.8	1172	8	AY279007	Zea mays
109	379	28.2	1112	6	AX660732	Sequence	182	333	24.8	1442	8	AY279017	Zea mays
110	377.5	28.1	959	8	AK108479	Oryza sat	183	333	24.8	1442	8	AY279018	Zea mays
111	377	28.1	1018	8	AB158406	Triticum	184	333	24.8	1442	8	AY279019	Zea mays
112	377	28.1	1018	8	BT009093	Triticum	185	333	24.8	1445	8	AY279018	Zea mays
113	376	28.0	923	6	BT013139	Lycopersi	186	333	24.8	1445	8	AY279022	Zea mays
114	376	28.0	923	6	AR236697	Sequence	187	333	24.8	1445	8	AY279022	Zea mays
115	373.5	27.8	816	8	AF022775	Sequence	188	332.5	24.8	1438	8	AY279021	Zea mays
116	373.5	27.8	870	6	AR225246	Sequence	189	332.5	24.8	1451	8	AY279020	Zea mays
117	373.5	27.8	890	8	NTU38612	Nicotiana t	190	331	24.6	908	8	AY500159	Corchorus
118	373.5	27.8	955	8	NTU62736	Nicotiana t	191	331	24.6	1298	8	AY323255	Zea mays
119	373.5	27.8	1003	8	NTU62735	Nicotiana t	192	331	24.6	1298	8	AY323258	Zea mays
120	373.5	27.8	1014	8	NTU62734	Nicotiana t	193	331	24.6	1298	8	AY323259	Zea mays
121	372.5	27.7	811	6	AR225247	Sequence	194	331	24.6	1298	8	AY323261	Zea mays
122	372.5	27.7	1104	8	AF053553	Mesembrya	195	331	24.6	1298	8	AY323261	Zea mays
123	372.5	27.7	1258	6	AR122016	Sequence	196	331	24.6	1298	8	AY323263	Zea mays
124	372.5	27.7	1258	6	I92681	Sequence 1	197	331	24.6	1298	8	AY323265	Zea mays
125	369	27.5	730	8	AY056313	Arabidops	198	331	24.6	1536	8	AY323241	Zea mays
126	369	27.5	956	8	AF360317	Arabidops	199	331	24.6	1536	8	AY323241	Zea mays
127	369	27.5	1098	8	AY128822	Arabidops	200	331	24.6	1536	8	AY323243	Zea mays
128	369	27.5	1185	8	AY087981	Arabidops	201	331	24.6	1536	8	AY323245	Zea mays
129	369	27.5	1201	8	AY093172	Arabidops	202	331	24.6	1536	8	AY323247	Zea mays
130	368.5	27.4	744	8	AF327458	Populus a	203	331	24.6	1536	8	AY323248	Zea mays
131	368.5	27.4	1013	8	AF168780	Eucalyptu	204	331	24.6	1536	8	AY323250	Zea mays
132	368.5	27.4	1018	6	AR236711	Sequence	205	331	24.6	1537	8	AY323251	Zea mays
133	367.5	27.4	835	6	AX660084	Sequence	206	330.5	24.6	772	8	FVAJ1447	Fragaria
134	366	27.3	326	6	AX407985	Sequence	207	329.5	24.5	1153	8	AY279010	Zea mays
135	365	27.2	1232	3	AC116551	Dictyoste	208	327.5	24.4	1314	8	AY323253	Zea mays
136	365	27.2	153751	3	ZEUI13151	Pinus tae	209	327.5	24.4	1314	8	AY323258	Zea mays
137	364.5	27.1	1158	8	AY644637	Oryza sat	210	327	24.3	105815	8	AP002536	Oryza sat
138	364.5	27.1	137354	8	AF000364	Oryza sat	211	327	24.3	156054	8	AB023482	Oryza sat
139	364.5	27.1	137354	8	AF000364	Oryza sat	212	327	24.3	156054	8	AB023482	Oryza sat
140	363.5	27.1	1116	8	AY087244	Arabidops	213	326	24.3	1311	8	AY323252	Zea mays
141	362	27.0	917	8	AY087244	Arabidops	214	326	24.3	1311	8	AY323257	Zea mays
142	360.5	26.8	730	8	AF060180	Nicotiana	215	326	24.3	1311	8	AY323264	Zea mays
143	360	26.8	729	6	AX507705	Sequence	216	326	24.3	1311	8	AY323267	Zea mays
144	354	26.4	912	6	AR236707	Sequence	217	326	24.3	1549	8	AY323249	Zea mays
145	353.5	26.3	1136	8	AY279011	Zea mays	218	324	24.1	833	8	AY088274	Arabidops
146	353.5	26.3	1152	8	AY279023	Zea mays	219	323	24.1	60090	1	U30252	Synechococ
147	353.5	26.3	1180	6	AX798857	Sequence	220	320.5	23.9	1320	8	AY323271	Zea mays
148	353	26.3	148	6	AX065515	Oryza sat	221	318.5	23.7	1309	8	AY323239	Zea mays
149	351.5	26.1	1466	8	AX279034	Zea mays	222	318.5	23.7	1309	8	AY323256	Zea mays
150	350.5	26.1	1136	8	AX279034	Zea mays	223	318.5	23.7	1309	8	AY323266	Zea mays

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370	168.5	12.5	302325	1	AE017236	Mycobacte	443	121.5	9.0	11309	6	CQ789017	Sequence
C 371	168	12.5	2233	6	AX416554	Sequence	444	121.5	9.0	11309	6	AR218876	Sequence
C 372	168	12.5	290507	1	AE017327	Listeria	445	121.5	9.0	11309	6	BD003788	Polynucle
C 373	166	12.4	4560	1	L1LVSPFEP	X99710 L.lactis OR	446	121.5	9.0	11552	1	AE008462	Streptoco
C 374	164.5	12.2	296750	1	AE003191	AE003191 Clostridi	447	121.5	9.0	113378	1	AE007401	Streptoco
C 375	164	12.2	399	6	BD224469	Materials	448	121.5	9.0	111135	2	SPNEU1906	Sequence
C 376	164	12.2	399	6	BD224469	Sequence	449	121.5	9.0	349980	6	AX571762	Sequence
C 377	164	12.2	330350	1	AL596168	Listeria	450	121	9.0	518	6	CQ720861	Sequence
C 378	164	12.2	349980	6	AX4113017	Sequence	C 451	120	8.9	301550	1	SC093134	Staphyloc
C 379	164	12.2	349980	6	AX4117044	Sequence	C 452	120	8.9	303450	1	SC093130	Streptomy
C 380	164	12.2	349980	6	AX4117045	Sequence	C 453	120	8.9	346300	1	AP003362	Staphyloc
C 381	162.5	12.1	702	6	AR320113	Sequence	C 454	119.5	8.9	298050	1	EX321861	Nitrosomo
C 382	162.5	12.1	12898	1	AE006403	Lactococc	C 455	119	8.9	12014	1	AE010732	Methanosa
C 383	162	12.1	13325	1	AE005016	Halobacte	C 456	118.5	8.8	1262	10	BC010402	Mus muscu
C 384	161.5	12.0	348450	1	MLPRTN4	AE005016 Halobacte	C 457	118	8.8	507	6	AX207630	Sequence
C 385	159.5	11.9	299550	1	AP001511	AE005016 Halobacte	C 458	118	8.8	37768	3	U40414	Caenorhabd
C 386	158	11.8	38675	1	MLU15180	AE005016 Halobacte	C 459	118	8.8	288404	1	AE017272	Bacillus
C 387	158	11.8	38675	6	AR345367	AE005016 Halobacte	C 460	116.5	8.7	10763	1	AE010544	Fusobacte
C 388	158	11.8	110000	1	AE016822_09	Continuation (10 o	C 461	115	8.6	639	6	AX121324	Sequence
C 389	157	11.7	801	6	AR394036	AE016822_09	C 462	115	8.6	639	6	BD163441	Novel pol
C 390	157	11.7	301278	1	AE015939	AE015939 Clostridi	C 463	115	8.6	769	6	AX771879	Sequence
C 391	157	11.7	302132	1	AE016955	AE016955 Enterococ	C 464	115	8.6	33150	1	AP005277	Corynebac
C 392	156	11.6	19024	6	BD193585	BD193585 Enterococ	C 465	115	8.6	349459	1	EX927151	Corynebac
C 393	154	11.5	8367	1	AF400582	AF400582 Acinetoba	C 466	115	8.6	349980	6	AX127146	Sequence
C 394	154	11.5	110000	1	CR543861_14	Continuation (15 o	C 467	114.5	8.5	2868	1	AB049411	Oryza sat
C 395	150.5	11.2	81866	8	NC64C2	Continuation (15 o	C 468	114.5	8.5	143109	8	OSUN00224	Oryza sat
C 396	149.5	11.1	508	6	AR236701	Sequence	C 469	114.5	8.5	300750	1	AP005217	Corynebac
C 397	147	10.9	1433	8	AF168779	AF168779 Eucalyptu	C 470	114	8.5	636	6	AX617408	Sequence
C 398	147	10.9	199173	1	BSUB0014	Z99117 Bacillus su	C 471	114	8.5	1255	10	AF076156	Mus muscu
C 399	146.5	10.9	110000	1	AE017180_05	Continuation (6 of	C 472	114	8.5	1605	8	PAN245505	Podospora
C 400	145	10.8	1504	8	AY267760	AY267760 Fusarium	C 473	114	8.5	110000	1	AE000516_19	Continuation (20 o
C 401	144	10.7	300050	1	AP004599	AP004599 Oceanobac	C 474	114	8.5	110000	1	EX571857_16	Continuation (17 o
C 402	141	10.5	957	5	EX930132	EX930132 Gallus ga	C 475	114	8.5	291050	1	BD248340	Mycobacte
C 403	139	10.3	51454	1	AE014157	AE014157 Streptoco	C 476	114	8.5	333750	1	AP004827	Staphyloc
C 404	139	10.3	310950	1	AP005143	AP005143 Streptoco	C 477	114	8.5	347496	1	EX842577	Mycobacte
C 405	137	10.2	115339	8	AP003940	AP003940 Oryza sat	C 478	113.5	8.5	5514	6	CQ587772	Sequence
C 406	137	10.2	174478	8	AP005467	AP005467 Oryza sat	C 479	112	8.3	2066	6	AX394673	Sequence
C 407	136	10.1	705	6	CQ649680	CQ649680 Sequence	C 480	112	8.3	7912	10	RNCATOMET	Z12651 R.norvegicu
C 408	136	10.1	10844	1	AE010080	AE010080 Sequence	C 481	112	8.3	110000	1	EX571856_17	Continuation (18 o
C 409	136	10.1	11615	1	AE010060	AE010060 Streptoco	C 482	112	8.3	300052	1	AE017232	Mycobacte
C 410	136	10.1	110000	1	CP000003_10	CP000003_10	C 483	112	8.3	300115	1	AP005076	Vibrio pa
C 411	136	10.1	110000	1	CP000003_11	CP000003_11	C 484	112	8.3	300115	1	AP005217	Corynebac
C 412	134	10.0	324050	1	EX251410_11	EX251410 Tropherym	C 485	111	8.3	300750	1	AP005217	Corynebac
C 413	134	10.0	324227	1	AE016852	AE016852 Tropherym	C 486	111	8.3	495	6	AR485101	Sequence
C 414	131	9.8	304282	1	AE017005	AE017005 Bacillus	C 487	111	8.3	3715	6	AR354077	Sequence
C 415	130.5	9.7	12012	1	AE011847	AE011847 Xanthomon	C 488	111	8.3	38494	6	AR354077	Sequence
C 416	130	9.7	10398	1	AE011847	AE011847 Xanthomon	C 489	111	8.3	38503	1	MSGB1912CS	leprae g
C 417	128	9.5	2316	6	AX207632	AX207632 Sequence	C 490	110.5	8.2	301443	1	AE017239	Mycobacte
C 418	127.5	9.5	10069	1	AE007678	AE007678 Clostridi	C 491	110	8.2	236	6	BD224451	Materials
C 419	126.5	9.4	534	6	AX433853	AX433853 Sequence	C 492	110	8.2	236	6	AR216501	Sequence
C 420	126	9.4	777	6	AX377804	AX377804 Sequence	C 493	110	8.2	236	6	AR432903	Sequence
C 421	126	9.4	777	6	AX377804	AX377804 Sequence	C 494	110	8.2	236	6	AR432903	Sequence
C 422	125.5	9.3	705	6	CQ649678	CQ649678 Sequence	C 495	110	8.2	247910	11	EX784390	Pinus pin
C 423	125.5	9.3	20639	1	AE014228	AE014228 Streptoco	C 496	109.5	8.2	348411	1	AE017307	Thermus t
C 424	125.5	9.3	349980	6	CQ650069	CQ650069 Sequence	C 497	109	8.1	11847	1	AP003007	Mesorhizo
C 425	125.5	9.3	349980	6	AX954529	AX954529 Sequence	C 498	109	8.1	11847	1	AE0031918	Deinococc
C 426	124.5	9.3	708	6	AX607661	AX607661 Sequence	C 499	108.5	8.1	213732	1	AE001862	Deinococc
C 427	124.5	9.3	6641	6	AX602145	AX602145 Sequence	C 500	108.5	8.1	1107	6	CQ812330	Sequence
C 428	124.5	9.3	167050	1	SAG766847	SAG766847 Streptoco	C 501	108.5	8.1	1107	9	HUMCOMTA	M65212 Homo sapi
C 429	124.5	9.3	292200	1	SC0939129	SC0939129 Streptomy	C 502	108	8.0	920	4	BC011935	Homo sapi
C 430	124	9.2	1605	1	AF016233	AF016233 Enterococ	C 503	108	8.0	10288	9	BC011935	Canis fam
C 431	124	9.2	110000	1	AE017225_22	Continuation (23 o	C 504	108	8.0	120528	9	AE001862	Chlorobiu
C 432	124	9.2	110000	1	AE017334_22	Continuation (23 o	C 505	108	8.0	132544	1	AF521085	Homo sapi
C 433	124	9.2	110000	1	AE017355_23	Continuation (24 o	C 506	108	8.0	155892	2	AF521085	Streptomy
C 434	124	9.2	293264	1	AE017031	AE017031 Bacillus	C 507	107.5	8.0	1206	6	AX774876	Sequence
C 435	123	9.2	498	6	AR347999	AR347999 Sequence	C 508	107.5	8.0	1206	6	AX774876	Sequence
C 436	123	9.2	3673	6	AF269748	AF269748 Streptoco	C 509	107.5	8.0	1291	9	CQ716680	Sequence
C 437	123	9.2	3673	6	AR485702	AR485702 Staphyloc	C 510	107.5	8.0	139628	2	AC150112	Gallus ga
C 438	123	9.2	3673	6	AX145066	AX145066 Sequence	C 511	107.5	8.0	166863	2	AC150112	Gallus ga
C 439	123	9.2	30029	1	AE016748	AE016748 Staphyloc	C 512	107.5	8.0	250950	1	AP005335	Vibrio vu
C 440	122	9.1	201	11	BV202015	BV202015 sqgm20798	C 513	107.5	8.0	302174	1	AE017241	Mycobacte
C 441	121.5	9.0	714	6	AX568724	AX568724 Sequence	C 514	107.5	8.0	304490	1	AE016806	Vibrio vu
C 442	121.5	9.0	714	6	AX481634	AX481634 Sequence	C 515	107	8.0	12397	1	AE010715	Methanosa

516	106.5	7.9	10113	1	AE011156	AE011156 Methanosa	c 589	100.5	7.5	1979	6	E11456	E11456 cDNA encodi
517	105.5	7.9	816	9	CR456997	CR456997 Homo sapi	c 590	100.5	7.5	1987	6	AR448000	AR448000 Sequence
518	105.5	7.9	873	9	CR456422	CR456422 Homo sapi	c 591	100.5	7.5	2014	6	BC047750	BC047750 Homo sapi
519	105.5	7.9	9463	1	SCRT05CLUS	X95596 S.grubeus c	c 592	100.5	7.5	2070	9	BC074500	BC074500 Homo sapi
520	105.5	7.9	11464	1	SCRT05CLUS	AE005915 Caulobact	c 593	100.5	7.5	247151	2	AC126662	AC126662 Rattus no
521	105.5	7.9	347625	1	BX248356	BX248356 Corynebac	c 594	100	7.4	2734	8	AK067366	AK067366 Oryza sat
522	105.5	7.9	349354	1	BX640416	BX640416 Bordetell	c 595	100	7.4	6806	1	SMWTN4556	M29297 S.fradiae c
523	105	7.8	457	6	AX394671	AX394671 Sequence	c 596	100	7.4	8460	6	I64893	I64893 Sequence 9
524	105	7.8	110000	2	AP006502_14	Continuation (15 o	c 597	100	7.4	8460	6	HSU29344	U29344 Human bres
525	105	7.8	308050	1	SC0939124	AL939124 Streptomy	c 598	100	7.4	10677	1	AE005967	AE005967 Caulobact
526	104.5	7.8	1895	8	AK108846	AK108846 Oryza sat	c 599	100	7.4	8460	6	HSU29344	Continuation (2 of
527	104.5	7.8	10878	1	AF272737	AF272737 Streptomy	c 600	100	7.4	110000	1	AY316747_1	AY316747_1
528	104.5	7.8	148762	8	AP002843	AP002843 Oryza sat	c 601	100	7.4	145911	1	AP003014	AP003014 Mesorhizo
529	104.5	7.8	278289	1	AE017306	AE017306 Thermus t	c 602	100	7.4	164628	2	AC073646	AC073646 Homo sapi
530	104	7.7	1628	10	AE010089S1	AE010089 Mus muscu	c 603	100	7.4	179937	2	AF546190	AF546190 Zea mays
531	104	7.7	158344	10	AL133401	AL133401 Mouse DNA	c 604	100	7.4	230146	2	AC134057	AC134057 Rattus no
532	104	7.7	180000	1	AF322012S1	AF322012 Bradyrhiz	c 605	100	7.4	299991	1	AE016776	AE016776 Pseudomon
533	104	7.7	299600	1	AP005941	AP005941 Bradyrhiz	c 606	100	7.4	300450	1	AP005960	AP005960 Bradyrhiz
534	104	7.7	299600	1	AP005941	AP005941 Bradyrhiz	c 607	99.5	7.4	3079	1	PDEMXXYZ	M2421 Paracoccus
535	104	7.7	299850	1	AP005949	AP005949 Bradyrhiz	c 608	99.5	7.4	3949	1	AB015725	AB015725 Aeromonas
536	103.5	7.7	1491	10	RATCATAA	M60753 R.norvegicu	c 609	99.5	7.4	9088	5	AF327372	AF327372 Gallus ga
537	103.5	7.7	1540	10	RATCATAB	M60754 R.norvegicu	c 610	99.5	7.4	295500	1	AP005954	AP005954 Bradyrhiz
538	103.5	7.7	2138	1	STWSIGMA	L11648 Streptomyce	c 611	99.5	7.4	300350	1	AP006574	AP006574 Gloebact
539	103.5	7.7	66669	1	AME16952	Y16952 Amycolatops	c 612	99.5	7.4	339681	1	AP003009	AP003009 Mesorhizo
540	103.5	7.7	110000	2	IMFLCHR32_17	Continuation (18 o	c 613	99.5	7.4	348171	1	EX640412	EX640412 Bordetell
541	103.5	7.7	233050	1	AL627271	AL627271 Salmonell	c 614	99	7.4	2010	6	CQ785960	CQ785960 Sequence
542	103.5	7.7	30247	1	AE016837	AE016837 Salmonell	c 615	99	7.4	2010	9	HSU07132	U07132 Human stero
543	103	7.7	3307	8	AK110307	AK110307 Oryza sat	c 616	99	7.4	2030	6	I70211	I70211 Sequence 1
544	103	7.7	10732	1	AE0113407	AE0113407 Methanosa	c 617	99	7.4	2030	6	I70211	Sequence 1
545	103	7.7	11877	1	AE011683	AE011683 Xanthomon	c 618	99	7.4	2505	6	AE023937	AE023937 Sequence 7
546	103	7.7	64492	1	AB086653	AB086653 Streptomy	c 619	99	7.4	2505	6	I15438	Sequence 7
547	103	7.7	109192	8	CNS08CCR	AL954153 Oryza sat	c 620	99	7.4	2685	6	AX924362	AX924362 Sequence
548	102.5	7.6	1525	8	TAU669951	U62584 Thermus aqu	c 621	99	7.4	2685	6	AX924386	AX924386 Sequence
549	102.5	7.6	2760	1	TAU62584	U62584 Thermus aqu	c 622	99	7.4	7528	6	CQ729217	CQ729217 Sequence
550	102.5	7.6	3003	6	CQ845922	CQ845922 Sequence	c 623	99	7.4	7536	9	AY451392	AY451392 Homo sapi
551	102.5	7.6	3003	9	AK131436	AK131436 Homo sapi	c 624	99	7.4	8461	6	CQ785963	CQ785963 Sequence
552	102.5	7.6	2978	6	CQ735548	CQ735548 Sequence	c 625	99	7.4	8472	9	BC063242	BC063242 Homo sapi
553	102.5	7.6	5502	9	HSM08450	BX648302 Homo sapi	c 626	99	7.4	10029	1	AE010416	AE010416 Methanopy
554	102.5	7.6	10245	1	AE004569	AE004569 Pseudomon	c 627	99	7.4	10202	1	AE004483	AE004483 Pseudomon
555	102.5	7.6	119115	8	AP003568	AP003568 Oryza sat	c 628	99	7.4	18843	9	AY148100	AY148100 Homo sapi
556	102.5	7.6	298550	1	AP005961	AP005961 Bradyrhiz	c 629	99	7.4	110000	2	AP006484	AP006484 Cyanidios
557	102.5	7.6	300129	1	AE017309	AE017309 Desulfovi	c 630	99	7.4	138939	9	AC119675	AC119675 Homo sapi
558	102.5	7.6	300531	1	AE016932	AE016932 Bacteroid	c 631	99	7.4	163978	10	AC140411	AC140411 Mus muscu
559	102	7.6	1746	9	HSU14534	U14534 Human orpha	c 632	99	7.4	193057	10	AL663067	AL663067 Mouse DNA
560	102	7.6	1898	6	I46765	I46765 Sequence 1	c 633	99	7.4	299450	1	AP005938	AP005938 Bradyrhiz
561	102	7.6	2084	11	BV177077	BV177077 sqm92606	c 634	99	7.4	300181	1	AE017318	AE017318 Desulfovi
562	102	7.6	14138	1	AE004766	AE004766 Pseudomon	c 635	99	7.4	346294	1	AP002999	AP002999 Mesorhizo
563	102	7.6	14469	1	AE011498	AE011498 Leptospir	c 636	98.5	7.3	1217	9	BC000419	BC000419 Homo sapi
564	102	7.6	21394	2	ACL15937	ACL15937 Mus muscu	c 637	98.5	7.3	1217	9	BC005867	BC005867 Homo sapi
565	102	7.6	301250	1	AP000590	AP000590 Bradyrhiz	c 638	98.5	7.3	1695	8	AK072292	AK072292 Oryza sat
566	102	7.6	303550	1	SC0939118	AL939118 Streptomy	c 639	98.5	7.3	2384	6	AX747042	AX747042 Sequence
567	102	7.6	305541	1	AE017290	AE017290 Leptospir	c 640	98.5	7.3	2384	9	AK091535	AK091535 Homo sapi
568	102	7.6	348068	1	BX572604	BX572604 Rhodopaeu	c 641	98.5	7.3	3147	6	AR232445	AR232445 Sequence
569	101.5	7.6	601	11	BV167609	BV167609 sqm6022	c 642	98.5	7.3	3147	6	AR256497	AR256497 Sequence
570	101.5	7.6	2039	9	AK130031	AK130031 Homo sapi	c 643	98.5	7.3	3147	6	AX189015	AX189015 Sequence
571	101.5	7.6	2084	11	BV177509	BV177509 sqm95100	c 644	98.5	7.3	3147	6	BD132995	BD132995 Anti-bact
572	101.5	7.6	2084	11	BV179316	BV179316 sqm10484	c 645	98.5	7.3	4355	1	ECORARJ	M4787 E.coli sbcc
573	101.5	7.6	153875	9	AC003682	AC003682 Homo sapi	c 646	98.5	7.3	5125	1	ECSCBC	U15981 E. coli sbc
574	101.5	7.6	188324	2	BX530094	BX530094 Homo sapi	c 647	98.5	7.3	8008	1	PAU93274	PAU93274 Pseudomonas
575	101.5	7.6	189326	9	AC018462	AC018462 Homo sapi	c 648	98.5	7.3	11015	1	AE004736	AE004736 Pseudomon
576	101	7.5	1543	8	AK120652	AK120652 Oryza sat	c 649	98.5	7.3	16675	1	AE011814	AE011814 Xanthomon
577	101	7.5	1820	9	BC035516	BC035516 Homo sapi	c 650	98.5	7.3	177534	1	AF233504	AF233504 Streptomy
578	101	7.5	129778	8	AC091123	AC091123 Oryza sat	c 651	98.5	7.3	77536	6	BD235937	BD235937 Polyketid
579	101	7.5	154620	2	BX323047	BX323047 Danio rer	c 652	98.5	7.3	77536	6	AR271638	AR271638 Sequence
580	101	7.5	163962	9	BS000233	BS000233 Pan trogl	c 653	98.5	7.3	110000	1	U00096	Continuation (5 of
581	101	7.5	178158	8	AC084320	AC084320 Oryza sat	c 654	98.5	7.3	128824	1	ECU73857	U73857 Escherichia
582	101	7.5	349771	1	BX572594	BX572594 Rhodopseu	c 655	98.5	7.3	19439	2	AC104882	AC104882 Mus muscu
583	100.5	7.5	1447	5	BC049292	BC049292 Xenopus 1	c 656	98.5	7.3	20200	1	AP000058	AP000058 Streptomy
584	100.5	7.5	1688	6	AR035537	AR035537 Sequence	c 657	98.5	7.3	296300	1	AP005035	AP005035 Streptomy
585	100.5	7.5	1688	6	E11457	E11457 cDNA encodi	c 658	98.5	7.3	300271	8	AE016901	AE016901 Eremothec
586	100.5	7.5	1815	6	AB477499	AB477499 Sequence	c 659	98.5	7.3	302300	1	AP005034	AP005034 Streptomy
587	100.5	7.5	1934	9	BC007790	BC007790 Homo sapi	c 660	98.5	7.3	302550	1	AP006581	AP006581 Gloebact
588	100.5	7.5	1979	6	AR035536	AR035536 Sequence	c 661	98	7.3	1782	6	AX879871	AX879871 Sequence

C 662	98	7.3	1782	6	BD158070	BD158070 Primer fo	C 735	95.5	7.1	300810	8	AE016896	AE016896 Eremothec
C 663	98	7.3	1782	9	AK022862	AK022862 Homo sapi	736	95.5	7.1	300861	1	AE016777	AE016777 Pseudomon
C 664	98	7.3	12772	1	AE004727	AE004727 Pseudomon	737	95.5	7.1	303550	1	SC0939131	SC0939131 Streptomy
C 665	98	7.3	75196	1	AY354515	AY354515 Streptomy	C 738	95.5	7.1	349572	1	BX640419	BX640419 Bordetell
C 666	98	7.3	174363	9	AC135506	AC135506 Homo sapi	739	95.5	7.1	349726	1	BX640421	BX640421 Bordetell
C 667	98	7.3	185146	2	AC104311	AC104311 Homo sapi	C 740	95	7.1	1416	6	BX876143	BX876143 Sequence
C 668	98	7.3	215342	9	AC109322	AC109322 Homo sapi	C 741	95	7.1	1416	6	BD155975	BD155975 Primer fo
C 669	98	7.3	279912	2	AC126572	AC126572 Rattus no	C 742	95	7.1	1416	6	BD155975	BD155975 Primer fo
C 670	98	7.3	310581	1	AE016863	AE016863 Pseudomon	C 743	95	7.1	2597	9	AK001168	AK001168 Homo sapi
C 671	98	7.3	348971	1	AY572594	AY572594 Rhodospheu	C 744	95	7.1	2597	9	AK001168	AK001168 Homo sapi
C 672	97.5	7.3	861	12	AY658649	AY658649 Synthetic	C 745	95	7.1	3009	9	HSN800570	HSN800570
C 673	97.5	7.3	1632	6	AK301781	AK301781 Sequence	C 746	95	7.1	3346	1	PS081032	PS081032
C 674	97.5	7.3	10130	1	AE002085	AE002085 Deinococc	C 747	95	7.1	4941	6	CQ730770	CQ730770
C 675	97.5	7.3	20235	1	SRER0YAB	SRER0YAB S. erythraea	C 748	95	7.1	4962	9	BC035577	BC035577 Homo sapi
C 676	97.5	7.3	20235	6	AR049368	AR049368 Sequence	C 749	95	7.1	4962	9	BC035577	BC035577 Homo sapi
C 677	97.5	7.3	20235	6	AR095529	AR095529 Sequence	C 750	95	7.1	4962	9	BC035577	BC035577 Homo sapi
C 678	97.5	7.3	20444	6	AE016863	AE016863 S. erythraea	C 751	95	7.1	4962	9	BC035577	BC035577 Homo sapi
C 679	97.5	7.3	24494	6	AK301774	AK301774 Sequence	C 752	95	7.1	4962	9	BC035577	BC035577 Homo sapi
C 680	97.5	7.3	42805	9	AC004421	AC004421 Homo sapi	C 753	95	7.1	4962	9	BC035577	BC035577 Homo sapi
C 681	97.5	7.3	188108	2	AC118207	AC118207 Mus muscu	C 754	95	7.1	4962	9	BC035577	BC035577 Homo sapi
C 682	97.5	7.3	302650	1	AP005958	AP005958 Bradyrhiz	C 755	95	7.1	4962	9	BC035577	BC035577 Homo sapi
C 683	97.5	7.3	310550	1	SC0939113	SC0939113 Streptomy	C 756	95	7.1	4962	9	BC035577	BC035577 Homo sapi
C 684	97	7.2	1192	5	BX932533	BX932533 Gallus ga	C 757	95	7.1	4962	9	BC035577	BC035577 Homo sapi
C 685	97	7.2	2585	1	CEICEX	CEICEX Cellulomona	C 758	95	7.1	4962	9	BC035577	BC035577 Homo sapi
C 686	97	7.2	12541	1	AE001956	AE001956 Deinococc	C 759	95	7.1	4962	9	BC035577	BC035577 Homo sapi
C 687	97	7.2	13026	1	AE002510	AE002510 Neisseria	C 760	95	7.1	4962	9	BC035577	BC035577 Homo sapi
C 688	97	7.2	25184	1	AE008779	AE008779 Salmonell	C 761	95	7.1	4962	9	BC035577	BC035577 Homo sapi
C 689	97	7.2	241178	2	AC130508	AC130508 Rattus no	C 762	95	7.1	4962	9	BC035577	BC035577 Homo sapi
C 690	97	7.2	280558	1	AE017301	AE017301 Thermus t	C 763	95	7.1	4962	9	BC035577	BC035577 Homo sapi
C 691	97	7.2	296282	2	AC111857	AC111857 Rattus no	C 764	95	7.1	4962	9	BC035577	BC035577 Homo sapi
C 692	97	7.2	299175	1	AP005023	AP005023 Streptomy	C 765	95	7.1	4962	9	BC035577	BC035577 Homo sapi
C 693	97	7.2	300704	1	AE017316	AE017316 Desulfovi	C 766	95	7.1	4962	9	BC035577	BC035577 Homo sapi
C 694	97	7.2	310029	1	AE016868	AE016868 Pseudomon	C 767	95	7.1	4962	9	BC035577	BC035577 Homo sapi
C 695	97	7.2	348074	1	BX640449	BX640449 Bordetell	C 768	95	7.1	4962	9	BC035577	BC035577 Homo sapi
C 696	97	7.2	349980	6	AK044033	AK044033 Sequence	C 769	95	7.1	4962	9	BC035577	BC035577 Homo sapi
C 697	96.5	7.2	11426	1	AE004590	AE004590 Pseudomon	C 770	95	7.1	4962	9	BC035577	BC035577 Homo sapi
C 698	96.5	7.2	22233	1	SPDBFB	SPDBFB Spingomona	C 771	95	7.1	4962	9	BC035577	BC035577 Homo sapi
C 699	96.5	7.2	106707	2	AC019314	AC019314 Homo sapi	C 772	95	7.1	4962	9	BC035577	BC035577 Homo sapi
C 700	96.5	7.2	128342	9	AL627313	AL627313 Human DNA	C 773	95	7.1	4962	9	BC035577	BC035577 Homo sapi
C 701	96.5	7.2	128342	9	AL627313	AL627313 Human DNA	C 774	95	7.1	4962	9	BC035577	BC035577 Homo sapi
C 702	96.5	7.2	152523	2	AC131998	AC131998 Mus muscu	C 775	95	7.1	4962	9	BC035577	BC035577 Homo sapi
C 703	96.5	7.2	171525	2	AC145473	AC145473 Rattus no	C 776	95	7.1	4962	9	BC035577	BC035577 Homo sapi
C 704	96.5	7.2	182061	10	AF107869	AF107869 Mus muscu	C 777	95	7.1	4962	9	BC035577	BC035577 Homo sapi
C 705	96.5	7.2	195859	14	AF281817	AF281817 Tupiaia he	C 778	95	7.1	4962	9	BC035577	BC035577 Homo sapi
C 706	96.5	7.2	219252	2	AC026760	AC026760 Mus muscu	C 779	95	7.1	4962	9	BC035577	BC035577 Homo sapi
C 707	96.5	7.2	242203	2	AC037860	AC037860 Rattus no	C 780	95	7.1	4962	9	BC035577	BC035577 Homo sapi
C 708	96.5	7.2	258888	2	AC109677	AC109677 Rattus no	C 781	95	7.1	4962	9	BC035577	BC035577 Homo sapi
C 709	96.5	7.2	272101	1	AE017302	AE017302 Thermus t	C 782	95	7.1	4962	9	BC035577	BC035577 Homo sapi
C 710	96.5	7.2	299750	1	AP005964	AP005964 Bradyrhiz	C 783	95	7.1	4962	9	BC035577	BC035577 Homo sapi
C 711	96	7.1	1657	9	AK098658	AK098658 Homo sapi	C 784	95	7.1	4962	9	BC035577	BC035577 Homo sapi
C 712	96	7.1	2004	6	BD180143	BD180143 Highly th	C 785	95	7.1	4962	9	BC035577	BC035577 Homo sapi
C 713	96	7.1	2588	1	CEICEX	CEICEX Cellulomona	C 786	95	7.1	4962	9	BC035577	BC035577 Homo sapi
C 714	96	7.1	10066	14	BHV12US	BHV12US Bovine herp	C 787	95	7.1	4962	9	BC035577	BC035577 Homo sapi
C 715	96	7.1	15534	6	CQ776613	CQ776613 Sequence	C 788	95	7.1	4962	9	BC035577	BC035577 Homo sapi
C 716	96	7.1	15534	9	AB051895	AB051895 Homo sapi	C 789	95	7.1	4962	9	BC035577	BC035577 Homo sapi
C 717	96	7.1	110000	2	AP006497	AP006497 (3 of	C 790	95	7.1	4962	9	BC035577	BC035577 Homo sapi
C 718	96	7.1	160714	2	AC150149	AC150149 Gallus ga	C 791	95	7.1	4962	9	BC035577	BC035577 Homo sapi
C 719	96	7.1	202432	2	AC143119	AC143119 Macaca mu	C 792	95	7.1	4962	9	BC035577	BC035577 Homo sapi
C 720	96	7.1	210472	9	AC035139	AC035139 Homo sapi	C 793	95	7.1	4962	9	BC035577	BC035577 Homo sapi
C 721	96	7.1	233568	2	AC150275	AC150275 Mus muscu	C 794	95	7.1	4962	9	BC035577	BC035577 Homo sapi
C 722	96	7.1	301191	1	AE017152	AE017152 Haemophil	C 795	95	7.1	4962	9	BC035577	BC035577 Homo sapi
C 723	96	7.1	302134	8	AE016906	AE016906 Eremothec	C 796	95	7.1	4962	9	BC035577	BC035577 Homo sapi
C 724	96	7.1	308151	1	AE016783	AE016783 Pseudomon	C 797	95	7.1	4962	9	BC035577	BC035577 Homo sapi
C 725	95.5	7.1	666	12	AY657499	AY657499 Synthetic	C 798	95	7.1	4962	9	BC035577	BC035577 Homo sapi
C 726	95.5	7.1	2696	8	AK121206	AK121206 Oryza sat	C 799	95	7.1	4962	9	BC035577	BC035577 Homo sapi
C 727	95.5	7.1	2926	1	AY667481	AY667481 Lysobacte	C 800	95	7.1	4962	9	BC035577	BC035577 Homo sapi
C 728	95.5	7.1	3173	6	E05949	E05949 DNA encodin	C 801	95	7.1	4962	9	BC035577	BC035577 Homo sapi
C 729	95.5	7.1	159119	1	AP006583	AP006583 Gloebact	C 802	95	7.1	4962	9	BC035577	BC035577 Homo sapi
C 730	95.5	7.1	192202	2	AC134315	AC134315 Lemur cat	C 803	95	7.1	4962	9	BC035577	BC035577 Homo sapi
C 731	95.5	7.1	277000	1	SC0939109	SC0939109 Streptomy	C 804	95	7.1	4962	9	BC035577	BC035577 Homo sapi
C 732	95.5	7.1	298550	1	AP005029	AP005029 Streptomy	C 805	95	7.1	4962	9	BC035577	BC035577 Homo sapi
C 733	95.5	7.1	290550	1	SC0939104	SC0939104 Streptomy	C 806	95	7.1	4962	9	BC035577	BC035577 Homo sapi
C 734	95.5	7.1	300350	1	AP006574	AP006574 Gloebact	C 807	95	7.1	4962	9	BC035577	BC035577 Homo sapi

C 808	94	7.0	123402	2	AC148071	AC148071 Dasyptus n	C 881	93	6.9	10765	1	AE004555	AE004555 Pseudomon
C 809	94	7.0	154605	2	AC046161	AC046161 Homo sapi	C 882	93	6.9	10829	1	AE004655	AE004655 Pseudomon
C 810	94	7.0	156677	2	AC092550	AC092550 Homo sapi	C 883	93	6.9	12891	1	AE004192	AE004192 Vibrio ch
C 811	94	7.0	166050	1	AL646085	AL646085 Ralstonia	C 884	93	6.9	13750	1	AY260903	AY260903 Rhodospir
C 812	94	7.0	169247	9	AL666970	AL666970 Human DNA	C 885	93	6.9	37360	6	AX803722	AX803722 Sequence
C 813	94	7.0	180097	9	AC123978	AC123978 Papio anu	C 886	93	6.9	62070	8	NC2E4	AL451022 Neurospor
C 814	94	7.0	184495	2	AC146295	AC146295 Mus muscu	C 887	93	6.9	67523	1	SCU24241	U24241 Sorangium c
C 815	94	7.0	193015	2	AC150074	AC150074 Gallus ga	C 888	93	6.9	110000	1	AE000516_04	Continuation (5 of
C 816	94	7.0	199942	2	AC150038	AC150038 Gallus ga	C 889	93	6.9	110000	2	AE000516_05	Continuation (6 of
C 817	94	7.0	220851	2	AC097956	AC097956 Rattus no	C 890	93	6.9	110000	2	AP06495_1	Continuation (2 of
C 818	94	7.0	230278	14	MCU68299	U68299 Mouse cytom	C 891	93	6.9	110000	8	BX255276_07	Continuation (8 of
C 819	94	7.0	230993	2	AC150072	AC150072 Gallus ga	C 892	93	6.9	110000	8	CB382130_23	Continuation (24 o
C 820	94	7.0	231367	2	AC150501	AC150501 Bos tauru	C 893	93	6.9	139999	9	AC018727	AC018727 Oryza sat
C 821	94	7.0	233829	2	AC125936	AC125936 Rattus no	C 894	93	6.9	148179	9	AP001631	AP001631 Homo sapi
C 822	94	7.0	233345	2	AC150066	AC150066 Gallus ga	C 895	93	6.9	188585	10	AC114404	AC114404 Mus muscu
C 823	94	7.0	239850	1	AP005949	AP005949 Bradyrhiz	C 896	93	6.9	189050	1	AL646077	AL646077 Ralstonia
C 824	94	7.0	300200	1	AP005962	AP005962 Bradyrhiz	C 897	93	6.9	206389	2	AC110327	AC110327 Rattus no
C 825	94	7.0	300242	1	AE016790	AE016790 Pseudomon	C 898	93	6.9	213050	1	AL646067	AL646067 Ralstonia
C 826	94	7.0	300450	1	AP005960	AP005960 Bradyrhiz	C 899	93	6.9	222932	2	AC145345	AC145345 Mus muscu
C 827	94	7.0	301332	1	AE017237	AE017237 Mycobacte	C 900	93	6.9	225838	2	AC109061	AC109061 Rattus no
C 828	94	7.0	302614	1	AE016778	AE016778 Pseudomon	C 901	93	6.9	290850	1	SCO939127	AL939127 Streptomy
C 829	94	7.0	303450	1	SCO939130	AL939130 Streptomy	C 902	93	6.9	298750	1	AP005375	AP005375 Thermosyn
C 830	94	7.0	303050	1	SCO939117	AL939117 Streptomy	C 903	93	6.9	300029	8	AE017122	AE017122 Oryza sat
C 831	94	7.0	332635	1	AP003005	AP003005 Mesorhizo	C 904	93	6.9	302835	1	AE012555	AE012555 Xylella f
C 832	94	7.0	343504	2	AL158031	AL158031 Homo sapi	C 905	93	6.9	318136	1	BX572101	BX572101 Prochloro
C 833	94	7.0	349652	1	BX569690	BX569690 Synchoco	C 906	93	6.9	340000	9	AP001748	AP001748 Homo sapi
C 834	94	7.0	349970	1	BX571659	BX571659 Wolinella	C 907	93	6.9	342416	1	BX842573	BX842573 Mycobacte
C 835	93.5	7.0	801	5	BX933718	BX933718 Gallus ga	C 908	93	6.9	349142	1	BX572599	BX572599 Rhodopseu
C 836	93.5	7.0	1422	6	BD179676	BD179676 Highly th	C 909	92.5	6.9	2178	8	NCMOM72	X53735 N. crassa M
C 837	93.5	7.0	1469	8	CRE577849	AJ577849 Chlamydom	C 910	92.5	6.9	2433	6	AX317584	AX317584 Sequence
C 838	93.5	7.0	2999	8	AK111159	AK111159 Oryza sat	C 911	92.5	6.9	2445	6	AX317568	AX317568 Sequence
C 839	93.5	7.0	5998	1	AB032524	AB032524 Streptomy	C 912	92.5	6.9	2445	6	AX317572	AX317572 Sequence
C 840	93.5	7.0	10294	1	AE005909	AE005909 Caulobact	C 913	92.5	6.9	2445	6	AX317576	AX317576 Sequence
C 841	93.5	7.0	10556	1	AE011660	AE011660 Xanthomon	C 914	92.5	6.9	2445	6	AX317578	AX317578 Sequence
C 842	93.5	7.0	11134	1	AE012473	AE012473 Xanthomon	C 915	92.5	6.9	2493	6	AX317586	AX317586 Sequence
C 843	93.5	7.0	11819	1	AE011801	AE011801 Xanthomon	C 916	92.5	6.9	2493	6	AX317582	AX317582 Sequence
C 844	93.5	7.0	31800	2	AC015554	AC015554 Leishmani	C 917	92.5	6.9	2508	6	AX317398	AX317398 Sequence
C 845	93.5	7.0	41282	2	AC148873	AC148873 Chlamydom	C 918	92.5	6.9	2508	6	AX317402	AX317402 Sequence
C 846	93.5	7.0	41987	1	AY498874	AY498874 Streptomy	C 919	92.5	6.9	2508	6	AX317404	AX317404 Sequence
C 847	93.5	7.0	82232	1	AY458648	AY458648 Uncultu	C 920	92.5	6.9	2508	6	AX317406	AX317406 Sequence
C 848	93.5	7.0	154746	14	HSV2HG52	Z86099 Herpes simp	C 921	92.5	6.9	2508	6	AX317408	AX317408 Sequence
C 849	93.5	7.0	165358	9	AL353782	AL353782 Human DNA	C 922	92.5	6.9	2508	6	AX317412	AX317412 Sequence
C 850	93.5	7.0	166050	1	AL646085	AL646085 Ralstonia	C 923	92.5	6.9	2508	6	AX317414	AX317414 Sequence
C 851	93.5	7.0	230161	2	AC128213	AC128213 Rattus no	C 924	92.5	6.9	2508	6	AX317416	AX317416 Sequence
C 852	93.5	7.0	298900	1	AP005937	AP005937 Bradyrhiz	C 925	92.5	6.9	2508	6	AX317420	AX317420 Sequence
C 853	93.5	7.0	299925	1	AP005039	AP005039 Streptomy	C 926	92.5	6.9	2508	6	AX317423	AX317423 Sequence
C 854	93.5	7.0	302675	1	AP005024	AP005024 Streptomy	C 927	92.5	6.9	2508	6	AX317428	AX317428 Sequence
C 855	93.5	7.0	308550	1	BX248342	BX248342 Mycobacte	C 928	92.5	6.9	2508	6	AX317436	AX317436 Sequence
C 856	93.5	7.0	308147	1	AE016915	AE016915 Chromobac	C 929	92.5	6.9	2511	6	AX309013	AX309013 Sequence
C 857	93.5	7.0	329709	1	AP002997	AP002997 Mesorhizo	C 930	92.5	6.9	2511	6	AX317144	AX317144 Sequence
C 858	93.5	7.0	346287	1	BX640450	BX640450 Bordetell	C 931	92.5	6.9	2511	6	AR410409	AR410409 Sequence
C 859	93.5	7.0	349260	1	BX572595	BX572595 Rhodopseu	C 932	92.5	6.9	2511	6	AR474890	AR474890 Sequence
C 860	93.5	7.0	349981	1	BX572602	BX572602 Rhodopseu	C 933	92.5	6.9	2511	6	AX317259	AX317259 Sequence
C 861	93	6.9	331	11	BX546298	BX546298 Arabidops	C 934	92.5	6.9	2511	6	AX555663	AX555663 Sequence
C 862	93	6.9	1410	6	E07846	E07846 DNA sequenc	C 935	92.5	6.9	2511	6	AX698681	AX698681 Sequence
C 863	93	6.9	1462	5	SSA416953	AJ416953 Salmo sal	C 936	92.5	6.9	2511	6	BD095937	BD095937 PEN-1 end
C 864	93	6.9	1468	8	AK107128	AK107128 Oryza sat	C 937	92.5	6.9	2514	6	AR410541	AR410541 Sequence
C 865	93	6.9	1533	6	BD180585	BD180585 Highly th	C 938	92.5	6.9	2514	6	AX317130	AX317130 Sequence
C 866	93	6.9	1613	8	AK071802	AK071802 Oryza sat	C 939	92.5	6.9	2514	6	AX317451	AX317451 Sequence
C 867	93	6.9	1898	6	A31676	A31676 Sequence 1	C 940	92.5	6.9	2514	6	AX317472	AX317472 Sequence
C 868	93	6.9	1898	10	AF050165	AF050165 Mus muscu	C 941	92.5	6.9	2514	6	AX317496	AX317496 Sequence
C 869	93	6.9	1988	6	A31678	A31678 Sequence 3	C 942	92.5	6.9	2514	6	AX317472	AX317472 Sequence
C 870	93	6.9	2182	8	AK119822	AK119822 Oryza sat	C 943	92.5	6.9	2517	6	AR410420	AR410420 Sequence
C 871	93	6.9	3051	6	C0725223	C0725223 Sequence	C 944	92.5	6.9	2517	6	AX317066	AX317066 Sequence
C 872	93	6.9	3470	9	AK126854	AK126854 Homo sapi	C 945	92.5	6.9	2517	6	AX317125	AX317125 Sequence
C 873	93	6.9	4018	9	HSM801489	AL133622 Homo sapi	C 946	92.5	6.9	2517	6	AX317481	AX317481 Sequence
C 874	93	6.9	5591	6	AX511491	AX511491 Sequence	C 947	92.5	6.9	2517	6	AX317492	AX317492 Sequence
C 875	93	6.9	5595	9	AB020683	AB020683 Homo sapi	C 948	92.5	6.9	2517	6	AX317498	AX317498 Sequence
C 876	93	6.9	5828	14	MLMPROCG	J02266 Moloney mur	C 949	92.5	6.9	2517	6	AX317506	AX317506 Sequence
C 877	93	6.9	5833	14	AF033813	AF033813 Moloney m	C 950	92.5	6.9	2517	6	AX317510	AX317510 Sequence
C 878	93	6.9	5833	14	REMSVX	V01185 Genome of m	C 951	92.5	6.9	2517	6	AX317514	AX317514 Sequence
C 879	93	6.9	7788	6	AX803724	AX803724 Sequence	C 952	92.5	6.9	2517	6	AX317518	AX317518 Sequence
C 880	93	6.9	8213	1	TSE007744	AJ007744 Thauera s	C 953	92.5	6.9	2517	6	AX317522	AX317522 Sequence

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C 954	92.5	6.9	2517	6	AX317526	Sequence	AX317526	Sequence	1027	92.5	6.9	301700	1	AP005948	Bradyrhiz
C 955	92.5	6.9	2517	6	AX317530	Sequence	AX317530	Sequence	1028	92.5	6.9	301708	1	AP016792	Pseudomon
C 956	92.5	6.9	2517	6	AX317534	Sequence	AX317534	Sequence	1029	92.5	6.9	304500	1	AP005953	Bradyrhiz
C 957	92.5	6.9	2520	6	AX410555	Sequence	AX410555	Sequence	1030	92.5	6.9	305584	1	AP016920	Chromobac
C 958	92.5	6.9	2520	6	AX317219	Sequence	AX317219	Sequence	1031	92.5	6.9	338579	1	AP003004	Mesorhizo
C 959	92.5	6.9	2520	6	AX317502	Sequence	AX317502	Sequence	1032	92.5	6.9	349061	1	NMA222491	Neisseria
C 960	92.5	6.9	2520	6	AX317538	Sequence	AX317538	Sequence	1033	92	6.9	1035	6	AX079056	Sequence
C 961	92.5	6.9	2520	6	AX317540	Sequence	AX317540	Sequence	1034	92	6.9	1987	1	PASSSDAPP	X78478 Pseudomonas
C 962	92.5	6.9	2520	6	AX317570	Sequence	AX317570	Sequence	1035	92	6.9	2396	6	CQ581775	Sequence
C 963	92.5	6.9	2520	6	AX317574	Sequence	AX317574	Sequence	1036	92	6.9	2590	6	CQ59964	Sequence
C 964	92.5	6.9	2526	6	AX410413	Sequence	AX410413	Sequence	1037	92	6.9	2675	9	BC023554	Sequence
C 965	92.5	6.9	2526	6	AX410418	Sequence	AX410418	Sequence	1038	92	6.9	2682	9	BC017210	Homo sapi
C 966	92.5	6.9	2526	6	AX410473	Sequence	AX410473	Sequence	1039	92	6.9	2720	9	BC023551	Homo sapi
C 967	92.5	6.9	2526	6	AX410475	Sequence	AX410475	Sequence	1040	92	6.9	2894	6	CQ599979	Sequence
C 968	92.5	6.9	2526	6	AX410508	Sequence	AX410508	Sequence	1041	92	6.9	2955	8	AK100088	Oryza sat
C 969	92.5	6.9	2526	6	AX410509	Sequence	AX410509	Sequence	1042	92	6.9	4256	3	AY122255	Drosophil
C 970	92.5	6.9	2526	6	AX410510	Sequence	AX410510	Sequence	1043	92	6.9	5008	9	AY122255	Drosophil
C 971	92.5	6.9	2526	6	AX410540	Sequence	AX410540	Sequence	1044	92	6.9	5286	1	AE005059	Halobacte
C 972	92.5	6.9	2526	6	AX410540	Sequence	AX410540	Sequence	1045	92	6.9	10369	1	AE004503	Pseudomon
C 973	92.5	6.9	2526	6	AX317100	Sequence	AX317100	Sequence	1046	92	6.9	13197	1	AE004532	Pseudomon
C 974	92.5	6.9	2526	6	AX317101	Sequence	AX317101	Sequence	1047	92	6.9	14423	1	AE004532	Pseudomon
C 975	92.5	6.9	2526	6	AX317114	Sequence	AX317114	Sequence	1048	92	6.9	15280	9	AB107036	Homo sapi
C 976	92.5	6.9	2526	6	AX317116	Sequence	AX317116	Sequence	1049	92	6.9	24123	1	AF086815	Acidovor
C 977	92.5	6.9	2526	6	AX317129	Sequence	AX317129	Sequence	1050	92	6.9	10242	2	AF086815	Acidovor
C 978	92.5	6.9	2526	6	AX317264	Sequence	AX317264	Sequence	1051	92	6.9	106332	14	AC150097	Gallus ga
C 979	92.5	6.9	2526	6	AX317270	Sequence	AX317270	Sequence	1052	92	6.9	106332	14	AX150217	Ambystoma
C 980	92.5	6.9	2526	6	AX317346	Sequence	AX317346	Sequence	1053	92	6.9	110000	1	AE016822_15	Continuation (16 o
C 981	92.5	6.9	2526	6	AX317346	Sequence	AX317346	Sequence	1054	92	6.9	110000	1	AY16747_2	Continuation (3 of
C 982	92.5	6.9	2526	6	AX317372	Sequence	AX317372	Sequence	1055	92	6.9	110000	2	LMFLCHR12_00	Continuation (2 of
C 983	92.5	6.9	2526	6	AX317376	Sequence	AX317376	Sequence	1056	92	6.9	110000	2	LMFLCHR12_01	Continuation (17 o
C 984	92.5	6.9	2526	6	AX317384	Sequence	AX317384	Sequence	1057	92	6.9	166421	8	AP003106	Oryza sat
C 985	92.5	6.9	2526	6	AX317388	Sequence	AX317388	Sequence	1058	92	6.9	244273	2	AC106167	Rattus no
C 986	92.5	6.9	2526	6	AX317392	Sequence	AX317392	Sequence	1059	92	6.9	252109	2	AC098630	Rattus no
C 987	92.5	6.9	2526	6	AX317396	Sequence	AX317396	Sequence	1060	92	6.9	252109	2	AC150047	Gallus ga
C 988	92.5	6.9	2526	6	AX317449	Sequence	AX317449	Sequence	1061	92	6.9	269985	2	AC127669	Rattus no
C 989	92.5	6.9	2526	6	AX317452	Sequence	AX317452	Sequence	1062	92	6.9	269985	2	AC127669	Rattus no
C 990	92.5	6.9	2526	6	AX317456	Sequence	AX317456	Sequence	1063	92	6.9	293350	1	AP005025	Sirenotomy
C 991	92.5	6.9	2526	6	AX317468	Sequence	AX317468	Sequence	1064	92	6.9	300029	1	SMES91786	Al591786 Sirenotomy
C 992	92.5	6.9	2526	6	AX317494	Sequence	AX317494	Sequence	1065	92	6.9	300029	1	AE016787	Pseudomon
C 993	92.5	6.9	2526	6	AX317555	Sequence	AX317555	Sequence	1066	92	6.9	300950	1	AP005940	Bradyrhiz
C 994	92.5	6.9	2526	6	AX698683	Sequence	AX698683	Sequence	1067	91.5	6.8	1707	3	AP012276	Toxoplas
C 995	92.5	6.9	2526	6	AX698688	Sequence	AX698688	Sequence	1068	91.5	6.8	1787	9	HSPG5UT	Z14129 H.sapiens p
C 996	92.5	6.9	2526	6	AX698691	Sequence	AX698691	Sequence	1069	91.5	6.8	2004	9	AY619993	AY619993 Homo sapi
C 997	92.5	6.9	2526	6	AX698694	Sequence	AX698694	Sequence	1070	91.5	6.8	2004	9	AY619994	AY619994 Homo sapi
C 998	92.5	6.9	2526	6	AX317460	Sequence	AX317460	Sequence	1071	91.5	6.8	2499	6	AR410430	Sequence
C 999	92.5	6.9	2526	6	AX317464	Sequence	AX317464	Sequence	1072	91.5	6.8	2499	6	AX317076	Sequence
C1000	92.5	6.9	2532	6	AX317464	Sequence	AX317464	Sequence	1073	91.5	6.8	2505	6	AR023938	Sequence
C1001	92.5	6.9	2532	6	AX317556	Sequence	AX317556	Sequence	1074	91.5	6.8	2505	6	AR023938	Sequence
C1002	92.5	6.9	2643	6	AX317478	Sequence	AX317478	Sequence	1075	91.5	6.8	2505	6	AR023938	Sequence
C1003	92.5	6.9	3135	6	AX317478	Sequence	AX317478	Sequence	1076	91.5	6.8	2505	6	AR023938	Sequence
C1004	92.5	6.9	3135	6	AX317478	Sequence	AX317478	Sequence	1077	91.5	6.8	2505	6	AR023938	Sequence
C1005	92.5	6.9	4373	10	AX317478	Sequence	AX317478	Sequence	1078	91.5	6.8	2505	6	AR023938	Sequence
C1006	92.5	6.9	5956	9	AB058752	Sequence	AB058752	Sequence	1079	91.5	6.8	2505	6	AR023938	Sequence
C1007	92.5	6.9	6245	1	AF202779	Sequence	AF202779	Sequence	1080	91.5	6.8	2511	6	AR023938	Sequence
C1008	92.5	6.9	7282	1	AF548455	Sequence	AF548455	Sequence	1081	91.5	6.8	2511	6	AR023938	Sequence
C1009	92.5	6.9	11159	1	AE012066	Sequence	AE012066	Sequence	1082	91.5	6.8	2511	6	AR023938	Sequence
C1010	92.5	6.9	11267	1	AE004919	Sequence	AE004919	Sequence	1083	91.5	6.8	2511	6	AR023938	Sequence
C1011	92.5	6.9	11791	1	AE004763	Sequence	AE004763	Sequence	1084	91.5	6.8	2511	6	AR023938	Sequence
C1012	92.5	6.9	14253	1	AE015066	Sequence	AE015066	Sequence	1085	91.5	6.8	2511	6	AR023938	Sequence
C1013	92.5	6.9	3263	9	AY281354	Sequence	AY281354	Sequence	1086	91.5	6.8	2511	6	AR023938	Sequence
C1014	92.5	6.9	54184	9	AL713889	Sequence	AL713889	Sequence	1087	91.5	6.8	2511	6	AR023938	Sequence
C1015	92.5	6.9	110000	1	AE016822_12	Sequence	AE016822_12	Sequence	1088	91.5	6.8	2511	6	AR023938	Sequence
C1016	92.5	6.9	150372	2	AC150103	Sequence	AC150103	Sequence	1089	91.5	6.8	2511	6	AR023938	Sequence
C1017	92.5	6.9	189505	9	AC092138	Sequence	AC092138	Sequence	1090	91.5	6.8	2511	6	AR023938	Sequence
C1018	92.5	6.9	203050	1	AX470161	Sequence	AX470161	Sequence	1091	91.5	6.8	2511	6	AR023938	Sequence
C1019	92.5	6.9	241270	2	AC118119	Sequence	AC118119	Sequence	1092	91.5	6.8	2511	6	AR023938	Sequence
C1020	92.5	6.9	250891	2	AC111916	Sequence	AC111916	Sequence	1093	91.5	6.8	2511	6	AR023938	Sequence
C1021	92.5	6.9	262530	2	AC111916	Sequence	AC111916	Sequence	1094	91.5	6.8	2511	6	AR023938	Sequence
C1022	92.5	6.9	265693	2	AC111916	Sequence	AC111916	Sequence	1095	91.5	6.8	2511	6	AR023938	Sequence
C1023	92.5	6.9	292309	1	AE016979	Sequence	AE016979	Sequence	1096	91.5	6.8	2511	6	AR023938	Sequence
C1024	92.5	6.9	299450	1	AP006580	Sequence	AP006580	Sequence	1097	91.5	6.8	2511	6	AR023938	Sequence
C1025	92.5	6.9	299450	1	AP006580	Sequence	AP006580	Sequence	1098	91.5	6.8	2511	6	AR023938	Sequence
C1026	92.5	6.9	299450	1	AP006580	Sequence	AP006580	Sequence	1099	91.5	6.8	2511	6	AR023938	Sequence

c1100	91.5	6.8	10029	1	AE012523	AE012523 Xanthomon	1173	91	6.8	110000	1	AE000516_32	Continuation (33 o
c1101	91.5	6.8	10087	1	AE004058	AE004058 Xylella f	1174	91	6.8	110000	1	AE016822_00	AE016822 Xylella f
c1102	91.5	6.8	10189	1	AE004715	AE004715 Pseudomon	c1175	91	6.8	110000	2	AP006494_7	Continuation (8 of
c1103	91.5	6.8	10426	1	AE004699	AE004699 Pseudomon	1176	91	6.8	110000	2	AP006501_07	Continuation (8 of
c1104	91.5	6.8	11160	1	AE0009150	AE0009150 Agrobacte	1177	91	6.8	110000	2	LMFLCHR31_08	Continuation (9 of
c1105	91.5	6.8	11252	1	AE0005760	AE0005760 Caulobact	c1178	91	6.8	138203	1	AV310323	Streptomy
c1106	91.5	6.8	11258	1	AE011803	AE011803 Xanthomon	1179	91	6.8	152881	10	AC124353	Mus muscu
c1107	91.5	6.8	11665	1	AE0008115	AE0008115 Agrobacte	1180	91	6.8	168916	10	AC124373	Mus muscu
c1108	91.5	6.8	11786	1	AE0004927	AE0004927 Pseudomon	1181	91	6.8	174139	2	AC116700	Mus muscu
c1109	91.5	6.8	12675	1	AE011822	AE011822 Xanthomon	1182	91	6.8	178376	2	AC125512	AC125512 Papio anu
c1110	91.5	6.8	20021	1	AE004730	AE004730 Pseudomon	1183	91	6.8	193798	2	AC145535	AC145535 Lemur cat
c1111	91.5	6.8	35335	3	AC016161	AC016161 Leishmani	c1184	91	6.8	196216	9	AC099343	AC099343 Homo sapi
c1112	91.5	6.8	61450	8	AP006556	AP006556 Oryza sat	1185	91	6.8	202555	9	AC034159	AC034159 Homo sapi
c1113	91.5	6.8	76196	1	AX354515	AX354515 Streptomy	c1186	91	6.8	255809	2	AC108312	AC108312 Rattus no
c1114	91.5	6.8	101385	5	CNS0958W	BX629356 Tetraodon	1187	91	6.8	272101	1	AE017302	AE017302 Thermus t
c1115	91.5	6.8	140933	8	AP005063	AP005063 Oryza sat	c1188	91	6.8	299425	1	AP005037	AP005037 Streptomy
c1116	91.5	6.8	141166	10	AC122423	AC122423 Mus muscu	c1189	91	6.8	299425	1	AP005049	AP005049 Streptomy
c1117	91.5	6.8	156840	2	AC146810	AC146810 Zea mays	c1190	91	6.8	29986	1	AE017240	AE017240 Mycobacte
c1118	91.5	6.8	158749	8	AX360394	AX360394 Oryza sat	c1191	91	6.8	300550	1	AP005030	AP005030 Streptomy
c1119	91.5	6.8	160541	8	AP004458	AP004458 Oryza sat	c1192	91	6.8	300590	1	AP005939	AP005939 Bradyrhiz
c1120	91.5	6.8	160681	2	AC118586	AC118586 Pan trogl	c1193	91	6.8	301482	1	AE016916	AE016916 Chromobac
c1121	91.5	6.8	163194	3	LMFP214	AL449144 Leishmani	1194	91	6.8	301495	1	AE016779	AE016779 Pseudomon
c1122	91.5	6.8	164901	8	AX360393	AX360393 Oryza sat	c1195	91	6.8	303226	1	AE016774	AE016774 Pseudomon
c1123	91.5	6.8	174714	9	AC025280	AC025280 Homo sapi	1196	91	6.8	307050	1	BX294140	BX294140 Pirellula
c1124	91.5	6.8	180623	9	AC092341	AC092341 Homo sapi	c1197	91	6.8	325000	3	TBBCHR1A3	AL329605 Trypanoso
c1125	91.5	6.8	181161	2	AC092347	AC092347 Homo sapi	c1198	91	6.8	346362	1	BX640439	BX640439 Bordetell
c1126	91.5	6.8	196204	9	AC073957	AC073957 Homo sapi	c1199	91	6.8	346510	1	AP003011	AP003011 Mesorhizo
c1127	91.5	6.8	224650	2	AC114157	AC114157 Rattus no	1200	91	6.8	347894	1	BX640431	BX640431 Bordetell
c1128	91.5	6.8	247592	9	US2111	US2111 Homo sapien	1201	91	6.8	348411	1	AP003007	AP003007 Mesorhizo
c1129	91.5	6.8	263875	2	AC094237	AC094237 Rattus no	1202	91	6.8	348642	1	BX640446	BX640446 Bordetell
c1130	91.5	6.8	270418	1	AE017303	AE017303 Thermus t	1203	91	6.8	348676	1	BX842581	BX842581 Mycobacte
c1131	91.5	6.8	299925	1	AP005043	AP005043 Streptomy	1204	90.5	6.7	906	6	BD179555	BD179555 Highly th
c1132	91.5	6.8	300425	1	AP005044	AP005044 Streptomy	1205	90.5	6.7	909	1	AE085185	AE085185 Thermus t
c1133	91.5	6.8	300817	1	AE016756	AE016756 Escherich	1206	90.5	6.7	1668	8	AX104988	AX104988 Oryza sat
c1134	91.5	6.8	313800	1	SC0939114	AL939114 Streptomy	1207	90.5	6.7	1755	6	BD180277	BD180277 Highly th
c1135	91.5	6.8	314100	1	SC0939106	AP005106 Streptomy	c1208	90.5	6.7	2377	1	AE108682	AE108682 Streptomy
c1136	91.5	6.8	325483	1	AP005050	AP005050 Streptomy	c1209	90.5	6.7	2526	6	AR410471	AR410471 Sequence
c1137	91.5	6.8	333500	1	AP003590	AP003590 Nostoc sp	c1210	90.5	6.7	2526	6	AX317099	AX317099 Sequence
c1138	91	6.8	906	6	AR386351	AR386351 Sequence	c1211	90.5	6.7	3034	10	AK123327	AK123327 Mus muscu
c1139	91	6.8	1092	12	AY659078	AY659078 Synthetic	c1212	90.5	6.7	3065	9	BC0626278	BC0626278 Homo sapi
c1140	91	6.8	1125	12	AY659078	AY659078 Synthetic	c1213	90.5	6.7	3077	9	BC0626278	BC0626278 Homo sapi
c1141	91	6.8	1500	6	BD180484	BD180484 Highly th	c1214	90.5	6.7	3306	10	AB017609	AB017609 Mus muscu
c1142	91	6.8	1509	6	AX751797	AX751797 Sequence	c1215	90.5	6.7	3337	6	E30802	E30802 Novel prote
c1143	91	6.8	1906	6	E01303	E01303 cDNA encodi	c1216	90.5	6.7	3660	10	AB017608	AB017608 Mus muscu
c1144	91	6.8	2016	4	BOVMIS	M13151 Bovine Mue	c1217	90.5	6.7	3674	6	E30801	E30801 Novel prote
c1145	91	6.8	2085	6	AX078521	AX078521 Sequence	c1218	90.5	6.7	3680	10	BC017126	BC017126 Mus muscu
c1146	91	6.8	2299	6	AX664177	AX664177 Sequence	1219	90.5	6.7	4449	10	CGU29946	U29946 Cricetus
c1147	91	6.8	2749	6	CQ767748	CQ767748 Sequence	c1220	90.5	6.7	5054	1	AF042276	AF042276 Pseudomon
c1148	91	6.8	2749	6	AR252737	AR252737 Sequence	c1221	90.5	6.7	5054	6	AX105316	AX105316 Sequence
c1149	91	6.8	2749	6	AX403629	AX403629 Sequence	c1222	90.5	6.7	8775	3	AY061650	AY061650 Toxoplas
c1150	91	6.8	2749	6	AX454474	AX454474 Sequence	1223	90.5	6.7	10029	1	AE012488	AE012488 Xanthomon
c1151	91	6.8	2749	6	AX464252	AX464252 Sequence	1224	90.5	6.7	10312	1	AE009781	AE009781 Pyrobacul
c1152	91	6.8	2749	6	AX490952	AX490952 Sequence	c1225	90.5	6.7	10419	1	AE001865	AE001865 Deinococ
c1153	91	6.8	2749	9	AX358364	AX358364 Homo sapi	c1226	90.5	6.7	10506	1	AE004806	AE004806 Pseudomon
c1154	91	6.8	2873	1	SHU41627	U41627 Streptomyce	1227	90.5	6.7	10761	1	AE014547	AE014547 Brucella
c1155	91	6.8	3456	1	RSP543650	AF543650 Rhodobact	c1228	90.5	6.7	10963	1	AE011744	AE011744 Xanthomon
c1156	91	6.8	6175	1	AF064527	AF064527 Rhodocist	c1229	90.5	6.7	11243	1	AE012067	AE012067 Xanthomon
c1157	91	6.8	7312	9	HUMCACL1G	L29536 Homo sapien	1230	90.5	6.7	12423	1	AE005155	AE005155 Halobacte
c1158	91	6.8	7417	9	HUMCACL1E	L29534 Homo sapien	c1231	90.5	6.7	12985	1	AE009710	AE009710 Brucella
c1159	91	6.8	7499	9	HUMCACL1E	L29529 Homo sapien	1232	90.5	6.7	13341	1	AE003964	AE003964 Xylella f
c1160	91	6.8	8940	9	HUMLVDCB	L04569 Homo sapien	c1233	90.5	6.7	14618	10	AF260753	AF260753 Cricetulu
c1161	91	6.8	10057	1	AE004871	AE004871 Pseudomon	c1234	90.5	6.7	43514	9	AC005545	AC005545 Homo sapi
c1162	91	6.8	10061	1	AE004314	AE004314 Vibrio ch	1235	90.5	6.7	110000	2	LMFLCHR32	Continuation (9 of
c1163	91	6.8	10429	1	AE0004875	AE0004875 Pseudomon	c1236	90.5	6.7	127952	8	OSJN00063_08	OSJN00063_08
c1164	91	6.8	10518	1	AE0012117	AE0012117 Xanthomon	1237	90.5	6.7	135638	1	AF484556	AF484556 Oryza sat
c1165	91	6.8	10895	1	AE004521	AE004521 Pseudomon	c1238	90.5	6.7	156002	8	OSJN00050	OSJN00050
c1166	91	6.8	10950	1	AE0012119	AE0012119 Xanthomon	c1239	90.5	6.7	158170	9	AC016757	AC016757 Rattus no
c1167	91	6.8	10978	1	AE0004940	AE0004940 Pseudomon	c1240	90.5	6.7	184631	2	AC141913	AC141913 Rattus no
c1168	91	6.8	11031	1	AE004648	AE004648 Pseudomon	c1241	90.5	6.7	191762	10	AC107770	AC107770 Mus muscu
c1169	91	6.8	12201	1	AE012255	AE012255 Xanthomon	c1242	90.5	6.7	204050	1	AL646073	AL646073 Ralstonia
c1170	91	6.8	11338	1	AE012166	AE012166 Xanthomon	c1243	90.5	6.7	210010	2	AC146135	AC146135 Pan trogl
c1171	91	6.8	13446	1	AE000710	AE000710 Aquifex a	1244	90.5	6.7	210614	1	AB088224	AB088224 Streptomy
c1172	91	6.8	110000	1	AE000516_31	Continuation (32 o	c1245	90.5	6.7	220622	2	AC118570	AC118570 Lemur cat

1246	90.5	6.7	299800	1	AP005028	AP005028 Streptomy	cl1319	90	6.7	225646	10	AC024915	AC024915 Mus muscu
1247	90.5	6.7	299800	1	AP005028	AP005028 Streptomy	1320	90	6.7	227773	10	AC034109	AC034109 Mus muscu
1248	90.5	6.7	308050	1	SC0939124	AL939124 Streptomy	1321	90	6.7	230918	2	AC114190	AC114190 Rattus no
1249	90.5	6.7	340000	1	AP005274	AP005274 Coryneb	1322	90	6.7	243808	10	AC024069	AC024069 Mus muscu
1250	90.5	6.7	346274	1	EX640443	EX640443 Bordetell	cl1323	90	6.7	249910	1	AE017307	AE017307 Thersmus t
1251	90.5	6.7	346301	1	EX640432	EX640432 Bordetell	cl1324	90	6.7	260860	2	AC125982	AC125982 Rattus no
1252	90.5	6.7	348014	1	EX640430	EX640430 Bordetell	cl1325	90	6.7	273785	1	SME591793	AL591793 Sinorhizo
1253	90.5	6.7	348071	1	EX927148	EX927148 Coryneb	1326	90	6.7	298550	1	AP005047	AP005047 Streptomy
1254	90.5	6.7	348676	1	EX842581	EX842581 Mycobacte	cl1327	90	6.7	300349	1	SC0939118	AE017319 Desulfovi
1255	90.5	6.7	349876	1	EX640442	EX640442 Bordetell	cl1328	90	6.7	303550	1	AE016915	AL939118 Streptomy
1256	90.5	6.7	349980	6	AL186970	AL186970 Geothermo	cl1329	90	6.7	308147	1	AE016915	AE016915 Chromobac
1257	90	6.7	934	1	AL186970	AL186970 Geothermo	cl1330	90	6.7	308147	1	AE016915	AL591792 Sinorhizo
1258	90	6.7	1069	6	BT009567	BT009567 Triticum	1331	90	6.7	333800	1	SME591792	AE016915
1259	90	6.7	1069	6	BT009567	BT009567 Triticum	1332	90	6.7	347365	1	AP000060	AP000060 Mycopycum
1260	90	6.7	1176	1	AB014153	AB014153 Micromono	cl1333	90	6.7	347800	1	AP000060	AP000060 Mycopycum
1261	90	6.7	1194	1	AB014153	AB014153 Micromono	1334	90	6.7	348247	1	EX842579	EX842579 Mycobacte
1262	90	6.7	2016	6	AX653225	AX653225 Sequence	1335	90	6.7	348706	1	EX640445	EX640445 Bordetell
1263	90	6.7	2427	8	AF110494	AF110494 Neurospor	1336	90	6.7	348764	1	EX659689	EX659689 Streptomy
1264	90	6.7	2451	8	AX640447	AX640447 Oryza sat	cl1337	90	6.7	348764	1	EX640426	EX640426 Bordetell
1265	90	6.7	2826	8	AK100795	AK100795 Oryza sat	1338	90	6.7	348764	1	EX640426	EX640426 Bordetell
1266	90	6.7	3115	1	AF225972	AF225972 Ralstonia	cl1339	90	6.7	348764	1	EX640426	EX640426 Bordetell
1267	90	6.7	3676	10	BC055076	BC055076 Mus muscu	1340	90	6.7	348764	1	EX640426	EX640426 Bordetell
1268	90	6.7	6676	1	AF031590	AF031590 Streptomy	1341	90	6.7	348764	1	EX640426	EX640426 Bordetell
1269	90	6.7	8551	1	AE011711	AE011711 Xanthomon	1342	90	6.7	348764	1	EX640426	EX640426 Bordetell
1270	90	6.7	9427	1	SC0001205	SC0001205 Streptomy	1343	90	6.7	348764	1	EX640426	EX640426 Bordetell
1271	90	6.7	9589	1	AE005729	AE005729 Caulobact	1344	90	6.7	348764	1	EX640426	EX640426 Bordetell
1272	90	6.7	10592	1	AE012469	AE012469 Xanthomon	1345	90	6.7	348764	1	EX640426	EX640426 Bordetell
1273	90	6.7	10901	1	AE013561	AE013561 Methanosa	1346	90	6.7	348764	1	EX640426	EX640426 Bordetell
1274	90	6.7	11928	1	AF187159	AF187159 Streptomy	1347	90	6.7	348764	1	EX640426	EX640426 Bordetell
1275	90	6.7	12198	1	AE004632	AE004632 Pseudomon	1348	90	6.7	348764	1	EX640426	EX640426 Bordetell
1276	90	6.7	12249	1	AE004670	AE004670 Pseudomon	1349	90	6.7	348764	1	EX640426	EX640426 Bordetell
1277	90	6.7	12372	1	AE0091692	AE0091692 Sphingomo	1350	90	6.7	348764	1	EX640426	EX640426 Bordetell
1278	90	6.7	15816	1	AX149472	AX149472 Acinetoba	1351	90	6.7	348764	1	EX640426	EX640426 Bordetell
1279	90	6.7	21931	1	AX149472	AX149472 Acinetoba	1352	90	6.7	348764	1	EX640426	EX640426 Bordetell
1280	90	6.7	49959	6	AX15917	AX15917 Sequence	cl1353	90	6.7	348764	1	EX640426	EX640426 Bordetell
1281	90	6.7	79370	1	UNK431260	UNK431260 Uncultu	1354	90	6.7	348764	1	EX640426	EX640426 Bordetell
1282	90	6.7	79506	9	AL137247	AL137247 Human DNA	1355	90	6.7	348764	1	EX640426	EX640426 Bordetell
1283	90	6.7	87688	1	AX365053	AX365053 Wautersia	1356	90	6.7	348764	1	EX640426	EX640426 Bordetell
1284	90	6.7	95437	3	AC139742	AC139742 Leishmani	cl1357	90	6.7	348764	1	EX640426	EX640426 Bordetell
1285	90	6.7	110000	1	AE017180_34	AE017180_34 Continuation (35 o	1358	90	6.7	348764	1	EX640426	EX640426 Bordetell
1286	90	6.7	110000	1	AE016822_17	AE016822_17 Continuation (38 o	cl1360	90	6.7	348764	1	EX640426	EX640426 Bordetell
1287	90	6.7	110000	8	CR382132_37	CR382132_37 Continuation (4 of	cl1361	90	6.7	348764	1	EX640426	EX640426 Bordetell
1288	90	6.7	110000	8	CR382135_03	CR382135_03 Continuation (4 of	cl1362	90	6.7	348764	1	EX640426	EX640426 Bordetell
1289	90	6.7	126928	2	AC096673	AC096673 Trypanoso	cl1363	90	6.7	348764	1	EX640426	EX640426 Bordetell
1290	90	6.7	127403	2	AC098842	AC098842 Magnapor	cl1364	90	6.7	348764	1	EX640426	EX640426 Bordetell
1291	90	6.7	134431	14	AY386265	AY386265 Bovine pa	1365	90	6.7	348764	1	EX640426	EX640426 Bordetell
1292	90	6.7	138929	8	AP000616	AP000616 Oryza sat	cl1366	90	6.7	348764	1	EX640426	EX640426 Bordetell
1293	90	6.7	139226	8	OSJRU00274	OSJRU00274 Oryza sat	1367	90	6.7	348764	1	EX640426	EX640426 Bordetell
1294	90	6.7	143113	8	AP000559	AP000559 Oryza sat	1368	90	6.7	348764	1	EX640426	EX640426 Bordetell
1295	90	6.7	146366	2	AC091846	AC091846 Homo sapi	1369	90	6.7	348764	1	EX640426	EX640426 Bordetell
1296	90	6.7	149270	9	AC091912	AC091912 Homo sapi	1370	90	6.7	348764	1	EX640426	EX640426 Bordetell
1297	90	6.7	153551	9	AC092675	AC092675 Homo sapi	cl1371	90	6.7	348764	1	EX640426	EX640426 Bordetell
1298	90	6.7	155525	2	AP007206	AP007206 Oryza sat	cl1372	90	6.7	348764	1	EX640426	EX640426 Bordetell
1299	90	6.7	156677	9	AC021087	AC021087 Homo sapi	1373	90	6.7	348764	1	EX640426	EX640426 Bordetell
1300	90	6.7	161844	2	AC147451	AC147451 Oryza sat	cl1374	90	6.7	348764	1	EX640426	EX640426 Bordetell
1301	90	6.7	163039	8	OSJRU00156	OSJRU00156 Oryza sat	1375	90	6.7	348764	1	EX640426	EX640426 Bordetell
1302	90	6.7	164104	2	AC084049	AC084049 Homo sapi	1376	90	6.7	348764	1	EX640426	EX640426 Bordetell
1303	90	6.7	169550	2	AC084049	AC084049 Homo sapi	cl1377	90	6.7	348764	1	EX640426	EX640426 Bordetell
1304	90	6.7	171280	2	AC024186	AC024186 Homo sapi	1378	90	6.7	348764	1	EX640426	EX640426 Bordetell
1305	90	6.7	171384	2	AC136212	AC136212 Gallus ga	1379	90	6.7	348764	1	EX640426	EX640426 Bordetell
1306	90	6.7	174839	9	AL157395	AL157395 Human DNA	cl1380	90	6.7	348764	1	EX640426	EX640426 Bordetell
1307	90	6.7	175231	10	AC034108	AC034108 Mus muscu	1381	90	6.7	348764	1	EX640426	EX640426 Bordetell
1308	90	6.7	178000	1	SC0530463	SC0530463 Streptomy	1382	90	6.7	348764	1	EX640426	EX640426 Bordetell
1309	90	6.7	181105	2	AP002394	AP002394 Homo sapi	1383	90	6.7	348764	1	EX640426	EX640426 Bordetell
1310	90	6.7	183349	2	AP027501	AP027501 Homo sapi	cl1384	90	6.7	348764	1	EX640426	EX640426 Bordetell
1311	90	6.7	191996	9	AC092275	AC092275 Homo sapi	1385	90	6.7	348764	1	EX640426	EX640426 Bordetell
1312	90	6.7	192366	10	AC068906	AC068906 Mus muscu	cl1386	90	6.7	348764	1	EX640426	EX640426 Bordetell
1313	90	6.7	195791	1	AC018997	AC018997 Homo sapi	1387	90	6.7	348764	1	EX640426	EX640426 Bordetell
1314	90	6.7	197635	2	AC019079	AC019079 Homo sapi	1388	90	6.7	348764	1	EX640426	EX640426 Bordetell
1315	90	6.7	197701	9	AC091941	AC091941 Homo sapi	cl1389	90	6.7	348764	1	EX640426	EX640426 Bordetell
1316	90	6.7	201050	1	AE016925	AE016925 Chromobac	1390	90	6.7	348764	1	EX640426	EX640426 Bordetell
1317	90	6.7	208524	1	AE016925	AE016925 Chromobac	1391	90	6.7	348764	1	EX640426	EX640426 Bordetell
1318	90	6.7	210301	9	AF307337	AF307337 Homo sapi	1392	90	6.7	348764	1	EX640426	EX640426 Bordetell

c1392	89.5	6.7	207365	2	AC093653	AC093653 Homo sapi	c1465	89	6.6	180663	10	AC129079	AC129079 Mus muscu
c1393	89.5	6.7	212221	2	AC136126	AC136126 Rattus no	1466	89	6.6	188440	8	AP004771	AP004771 Oryza sat
c1394	89.5	6.7	225936	2	AC137401	AC137401 Rattus no	c1467	89	6.6	194856	8	AC146936	AC146936 Oryza sat
c1395	89.5	6.7	235036	2	AC098076	AC098076 Rattus no	c1468	89	6.6	222429	2	AC148419	AC148419 Meleagris
c1396	89.5	6.7	238123	2	AC136571	AC136571 Rattus no	c1469	89	6.6	225829	10	AC129609	AC129609 Mus muscu
c1397	89.5	6.7	241957	2	AC119587	AC119587 Rattus no	1470	89	6.6	238226	2	AC120467	AC120467 Rattus no
c1398	89.5	6.7	242806	2	AC133426	AC133426 Rattus no	1471	89	6.6	272592	2	AC121734	AC121734 Rattus no
c1399	89.5	6.7	250318	2	AC109983	AC109983 Rattus no	1472	89	6.6	291050	1	EX248340	EX248340 Mycobacte
c1400	89.5	6.7	252427	2	AC111287	AC111287 Rattus no	1473	89	6.6	299750	1	AP006575	AP006575 Gloeobact
c1401	89.5	6.7	255767	2	AC099281	AC099281 Rattus no	c1474	89	6.6	299991	1	AE016776	AE016776 Pseudomon
c1402	89.5	6.7	265197	2	AC093338	AC093338 Rattus no	1475	89	6.6	300400	1	AP005943	AP005943 Bradyrhiz
c1403	89.5	6.7	277000	1	SC0933109	SC0933109 Streptomy	c1476	89	6.6	300861	1	AE016777	AE016777 Pseudomon
c1404	89.5	6.7	295741	1	AP002551	AP002551 Escherich	1477	89	6.6	301675	1	AP005027	AP005027 Streptomy
c1405	89.5	6.7	297050	1	AP006569	AP006569 Gloeobact	c1478	89	6.6	301846	1	AE016913	AE016913 Chromobac
c1406	89.5	6.7	300217	1	AE016922	AE016922 Chromobac	c1479	89	6.6	303220	1	AP005081	AP005081 Vibrio pa
c1407	89.5	6.7	300950	1	AP005940	AP005940 Bradyrhiz	c1480	89	6.6	304517	1	AE016789	AE016789 Pseudomon
c1408	89.5	6.7	309942	2	AC137366	AC137366 Rattus no	c1481	89	6.6	305520	1	AE016780	AE016780 Pseudomon
c1409	89.5	6.7	329100	1	SME591787	AL591787 Sinorhizo	c1482	89	6.6	307435	1	AE016914	AE016914 Chromobac
c1410	89.5	6.7	333800	1	SME591792	AL591792 Sinorhizo	c1483	89	6.6	308750	1	AP005216	AP005216 Corynebac
c1411	89.5	6.7	339650	1	SC0933108	AL339108 Streptomy	c1484	89	6.6	323450	1	SME591790	AL591790 Sinorhizo
c1412	89.5	6.7	344615	1	BX569695	BX569695 Synechoco	c1485	89	6.6	347496	1	BX842577	BX842577 Mycobacte
c1413	89.5	6.7	344805	1	BX640434	BX640434 Bordetell	c1486	89	6.6	348873	3	AE003790	AE003790 Drosophil
c1414	89.5	6.7	345783	1	AP003001	AP003001 Mesorhizo	1487	88.5	6.6	936	1	AY262284	AY262284 Streptomy
c1415	89.5	6.7	347071	1	BX640415	BX640415 Bordetell	1488	88.5	6.6	1501	8	AF053340	AF053340 Schizosac
c1416	89.5	6.7	349859	1	BX571662	BX571662 Wolinella	1489	88.5	6.6	1814	3	AY069732	AY069732 Drosophil
c1417	89.5	6.7	349980	6	AX044034	AX044034 Sequence	c1490	88.5	6.6	2169	8	AK100262	AK100262 Oryza sat
c1418	89	6.6	522	1	AY324523	AY324523 Unculture	c1491	88.5	6.6	2212	8	AK066513	AK066513 Oryza sat
c1419	89	6.6	837	8	AK110606	AK110606 Oryza sat	1492	88.5	6.6	2313	9	BC006281	BC006281 Homo sapi
c1420	89	6.6	1096	1	AF137366	AF137366 Rhodother	1493	88.5	6.6	2325	6	C0720687	C0720687 Homo sapi
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c1424	89	6.6	1610	10	CP062318	AJ006218 Cavie por	c1497	88.5	6.6	2337	9	BC041418	BC041418 Homo sapi
c1425	89	6.6	1722	6	C0732593	C0732593 Oryza sat	c1498	88.5	6.6	2351	10	RN0536020	AJ536020 Rattus no
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c1427	89	6.6	2000	8	AK072215	AK072215 Oryza sat	1500	88.5	6.6	2413	6	BD222047	BD222047 SH2 domai
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c1432	89	6.6	3231	6	C0724644	C0724644 Sequence							
c1433	89	6.6	4706	6	C0610019	C0610019 Sequence							
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DEFINITION	CQ721501	Sequence	7435 from Patent WO02068579		
ACCESSION	CQ721501				
VERSION	CQ721501.1	GI:42282358			
KEYWORDS					
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	1	Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.			
AUTHORS		Kits, such as nucleic acid arrays, comprising a majority of			
TITLE		humanexons or transcripts, for detecting expression and other uses			
JOURNAL		thereof			
FEATURES		Patent: WO 02068579-A 7435 06-SEP-2002;			
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US-10-017-407A-306 (1-262) x CQ721501 (1-789)		JOURNAL Patent: WO 0183719-A 3 08-NOV-2001; Millennium Pharmaceuticals, Inc. (US)	
QY	1	MetThrGlnProValProArgLeuSerValProAlaAlaLeuAlaLeuGlySerAlaAla 20	
DB	1	ATGACCCAGCCGCTGCCCCGGCTCTCCGTGCCCGCCGCTGCGCTGGGCTCAGCGCA 60	
QY	21	LeuGlyAlaAlaPheAlaThrGlyLeuPheLeuGlyArgCysProProTrpArgGly 40	
DB	61	CTGGGCGCCGCTTCGCCACTGGCTCTCTCTGGGGAGGGGTGCCCCCATGGCGAGGC 120	
QY	41	ArgArgGluGlnCysLeuLeuProGluAspSerArgLeuTrpGlnTyrLeuLeuSer 60	
DB	121	CGCGGAGAGCAGTGCCTTCTCCCGCCGAGACAGCCGCTGTGGCAGATATCTTCTGAGC 180	
QY	61	ArgSerMetArgGluHisProAlaLeuArgSerLeuArgLeuLeuThrLeuGluGlnPro 80	
DB	181	CGCTCCATGGGGAGGACCCCGCGCGCTGCGAAGCTCTGAGGCTGTGACCTGGAGCAGCG 240	
QY	81	GlnGlyAspSerMetThrCysGluGlnAlaGlnLeuAlaGlnLeuAlaArgLeu 100	
DB	241	CAGGGGATTTCTATGATGACCTTGGAGCAGCCGCTTGGCAACCTGGCGGCGCTC 300	
QY	101	IleGlnAlaLysLysAlaLeuAspLeuGlyThrPheThrGlyTyrSerAlaLeuAlaLeu 120	
DB	301	ATCCAGGCCAAGAGGGCGCTGGACCTGGGCACTTACGGGCTACTCCGCCCTGGCCCTG 360	
QY	121	AlaLeuAlaLeuProAlaAspGlyValValThrCysGluValAlaAspAlaGlnProPro 140	
DB	361	GCCCTGGCGCTGCCCCGCGACCGCGCTGTGACCTGGAGGTGGAGCGCGCCCGC 420	
QY	141	GluLeuGlyArgProLeuTrpArgGlnAlaGluAlaGluHisLysIleAspLeuArgLeu 160	
DB	421	GAGCTGGAGCGGCCCTGTGGAGGCGAGCCCGAGGCGGAGCAACAGATCGACCTCCGGCTG 480	
QY	161	LysProAlaLeuGluThrLeuAspGluLeuAlaAlaGlyGluAlaGlyThrPheAsp 180	
DB	481	AAGCCCGCTTGGAGACCTTGGACGAGCTGTGGCGGGGCGGAGGCCGCGACCTTCGAC 540	
QY	181	ValAlaValValAspAlaAspLysGluAsnCysSerAlaTyrTyrGluArgCysLeuGln 200	
DB	541	GTGGCGCTGTGGATGCGGACCAAGAGAACTGCTCCGCTACTACGAGCGCTGCTCGAG 600	
QY	201	LeuLeuArgProGlyGlyIleLeuAlaValLeuArgValLeuTrpArgGlyLysValLeu 220	
DB	601	CTGTGCGAGCCCGGAGGCATCTCTCCGCTCTCAGAGTCTTGTGGCGGGAGGTGCTG 660	
QY	221	GlnProProLysGlyAspValAlaAlaGluCysValArgAsnLeuAsnGluArgIleArg 240	
DB	661	CAACCTCCGAAGGGGACGTGGCGCGAGTGTGTGCGAAACCTAAACGAGCATCCGG 720	
QY	241	ArgAspValArgValTyrIleSerLeuLeuProLeuGlyAspGlyThrLeuAlaPhe 260	
DB	721	CGGAGCTCAGGCTTACATCAGCTCTCTGCCCTCTGGCGATGGACTCACCTTGGCTTC 780	
QY	261	LysIle 262	
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RESULT 2		789 bp DNA linear PAT 09-JAN-2002	
AX338456		Sequence 3 from Patent WO0183719.	
LOCUS		AX338456	
DEFINITION		AX338456	
ACCESSION		AX338456.1 GI:18128895	
VERSION			
KEYWORDS		Homo sapiens (human)	
SOURCE		Homo sapiens	
ORGANISM		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
		Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
REFERENCE		1	
AUTHORS		Meyers, R.A. and Williamson, M.	
TITLE		25692, a novel human O-methyltransferase family member and uses thereof	

US-10-017-407A-306 (1-262) x AX338456 (1-789)		JOURNAL Patent: WO 0183719-A 3 08-NOV-2001; Millennium Pharmaceuticals, Inc. (US)	
QY	1	MetThrGlnProValProArgLeuSerValProAlaAlaLeuAlaLeuGlySerAlaAla 20	
DB	1	ATGACCCAGCCGCTGCCCCGGCTCTCCGTGCCCGCCGCTGCGCTGGGCTCAGCGCA 60	
QY	21	LeuGlyAlaAlaPheAlaThrGlyLeuPheLeuGlyArgCysProProTrpArgGly 40	
DB	61	CTGGGCGCCGCTTCGCCACTGGCTCTCTCTGGGGAGGGGTGCCCCCATGGCGAGGC 120	
QY	41	ArgArgGluGlnCysLeuLeuProGluAspSerArgLeuTrpGlnTyrLeuLeuSer 60	
DB	121	CGCGGAGAGCAGTGCCTTCTCCCGCCGAGACAGCCGCTGTGGCAGATATCTTCTGAGC 180	
QY	61	ArgSerMetArgGluHisProAlaLeuArgSerLeuArgLeuLeuThrLeuGluGlnPro 80	
DB	181	CGCTCCATGGGGAGGACCCCGCGCGCTGCGAAGCTCTGAGGCTGTGACCTGGAGCAGCG 240	
QY	81	GlnGlyAspSerMetThrCysGluGlnAlaGlnLeuAlaGlnLeuAlaArgLeu 100	
DB	241	CAGGGGATTTCTATGATGACCTTGGAGCAGCCGCTTGGCAACCTGGCGGCGCTC 300	
QY	101	IleGlnAlaLysLysAlaLeuAspLeuGlyThrPheThrGlyTyrSerAlaLeuAlaLeu 120	
DB	301	ATCCAGGCCAAGAGGGCGCTGGACCTGGGCACTTACGGGCTACTCCGCCCTGGCCCTG 360	
QY	121	AlaLeuAlaLeuProAlaAspGlyValValThrCysGluValAlaAspAlaGlnProPro 140	
DB	361	GCCCTGGCGCTGCCCCGCGACCGCGCTGTGACCTGGAGGTGGAGCGCGCCCGC 420	
QY	141	GluLeuGlyArgProLeuTrpArgGlnAlaGluAlaGluHisLysIleAspLeuArgLeu 160	
DB	421	GAGCTGGAGCGGCCCTGTGGAGGCGAGCCCGAGGCGGAGCAACAGATCGACCTCCGGCTG 480	
QY	161	LysProAlaLeuGluThrLeuAspGluLeuAlaAlaGlyGluAlaGlyThrPheAsp 180	
DB	481	AAGCCCGCTTGGAGACCTTGGACGAGCTGTGGCGGGGCGGAGGCCGCGACCTTCGAC 540	
QY	181	ValAlaValValAspAlaAspLysGluAsnCysSerAlaTyrTyrGluArgCysLeuGln 200	
DB	541	GTGGCGCTGTGGATGCGGACCAAGAGAACTGCTCCGCTACTACGAGCGCTGCTCGAG 600	
QY	201	LeuLeuArgProGlyGlyIleLeuAlaValLeuArgValLeuTrpArgGlyLysValLeu 220	
DB	601	CTGTGCGAGCCCGGAGGCATCTCTCCGCTCTCAGAGTCTTGTGGCGGGAGGTGCTG 660	
QY	221	GlnProProLysGlyAspValAlaAlaGluCysValArgAsnLeuAsnGluArgIleArg 240	
DB	661	CAACCTCCGAAGGGGACGTGGCGCGAGTGTGTGCGAAACCTAAACGAGCATCCGG 720	
QY	241	ArgAspValArgValTyrIleSerLeuLeuProLeuGlyAspGlyThrLeuAlaPhe 260	
DB	721	CGGAGCTCAGGCTTACATCAGCTCTCTGCCCTCTGGCGATGGACTCACCTTGGCTTC 780	
QY	261	LysIle 262	

US-10-017-407A-306 (1-262) x AX338456 (1-789)		JOURNAL Patent: WO 0183719-A 3 08-NOV-2001; Millennium Pharmaceuticals, Inc. (US)	
FEATURES	source	Location/Qualifiers	
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Pred. No.:	1343.00	Matches:	262
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	6	Gaps:	0

TITLE Compositions and methods for the treatment of tumour
JOURNAL Patent: WO 0153486-A 21 26-JUL-2001;
Genentech, Inc. (US)

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source
Location/Qualifiers
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ORIGIN

Alignment Scores:
Pred. No.: 6.4e-95 Length: 989
Score: 1343.00 Matches: 262
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

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Qy 21 LeuGlyAlaAlaPheAlaThrClyLeuPheLeuGlyArgArgCysProTirPargly 40
Db 144 CTGGCGCGCGCTTCCGACCTGCTCTCTCTGGGAGCGGTGCCCTTGGCGAGGC 203
Qy 41 ArgArgGluGlnCysLeuLeuProGluAspSerArgLeuTirParglyLeuSer 60
Db 204 CGCGAGAGCAGTGTCTCTTCCCCCGAGGACGCGCTGTGGCAGTATCTTCTGAGC 263
Qy 61 ArgSerMetArgGluHisProAlaLeuArgSerLeuArgLeuLeuGluGlnPro 80
Db 264 CGCTCCATGGCGGACACCGCGCTCGGAGCCTGAGCTGTGACCTTGGAGCAGCG 323
Qy 81 GlnGlyAspSerMetThrCysGluGlnAlaGlnLeuLeuAlaAsnLeuAlaPhe 100
Db 324 CAGGGGATTTATGATGACCTGCGAGCGGCCAGCTTGGCCAACTTGGCGGGCTC 383
Qy 101 IleGlnAlaLeuAlaLeuAspLeuGlyThrPheThrGlyTyrSerAlaLeuAlaLeu 120
Db 384 ATCCAGGCGCAGAGCGCTGACCTGGGACCTTACGGGCTACTCCGGCTTGGCGCTG 443
Qy 121 AlaLeuAlaLeuProAlaAspGlyArgValThrCysGluValAlaAlaGlnPro 140
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Qy 141 GluLeuGlyArgProLeuTirPargGlnAlaGluAlaGluHisLysIleAspLeuArgLeu 160
Db 504 GAGCTGGGACGCGCTCTGGAGGCGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGG 563
Qy 161 LysProAlaLeuGluThrLeuAspGluLeuAlaGlyGluAlaGlyThrPheAsp 180
Db 564 AAGCCCGCTTGGAGACCTTGGACGAGTGTCTGGCGGCGGCGGAGGCGGAGGCGG 623
Qy 181 ValAlaValAlaAspLysGluAsnCysSerAlaTyrTyrGluArgCysLeuGln 200
Db 624 GTGGCGGTGTGGTGTGGAGCAGAGGAGTGTCTCGGCTACTAGAGCGCTGCTGGAG 683
Qy 201 LeuLeuArgProGlyGlyIleLeuAlaValLeuArgValLeuTirParglyLysValLeu 220
Db 684 CTGTGCGACCGGAGGATCTCTCGCGCTCTCTCAGAGTCTCTGTGGCGGGAAGGTGCTG 743
Qy 221 GlnProProLysGlyAspValAlaAlaGluCysValArgAsnLeuAsnGluArgLeu 240
Db 744 CAACCTCCGAAGGGGAGCGTGGCGCGGAGTGTGTGGCAACCTTAAAGCAAGCATCCGG 803
Qy 241 ArgAspValArgValTyrIleSerLeuLeuProLeuGlyAspGlyLeuThrLeuAlaPhe 260
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Db 864 AAGATC 869

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AX697237
LOCUS AX697237
DEFINITION Sequence 305 from Patent WO0078961.
ACCESSION AX697237
VERSION AX697237.1 GI:29498404
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS Ferrara,N., Stewart,T.A., Williams,P.M., Baker,K.P., Desnoyers,L.,
Eaton,D.L., Gao,W.Q., Pan,J., Botstein,D., Fong,S., Goddard,A.,
Godowski,P.J., Gurney,A.L., Smith,V., Tumas,D., Wood,W.I.,
Grimaldi,C.J., Hillan,K.J., Paoni,N.F., Roy,M.A. and Watanabe,C.K.
Secreted and transmembrane polypeptides and nucleic acids encoding
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Patent: WO 0078961-A 305 28-DEC-2000;
Genentech Inc. (US)
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Pred. No.: 6.4e-95 Length: 989
Score: 1343.00 Matches: 262
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-017-407A-306 (1-262) x AX697237 (1-989)

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Qy 21 LeuGlyAlaAlaPheAlaThrClyLeuPheLeuGlyArgArgCysProTirPargly 40
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Qy 41 ArgArgGluGlnCysLeuLeuProGluAspSerArgLeuTirParglyLeuSer 60
Db 204 CGCGAGAGCAGTGTCTCTTCCCCCGAGGACGCGCTGTGGCAGTATCTTCTGAGC 263
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Db 264 CGCTCCATGGCGGAGCACCGCGCTCGGAGCCTTGGGCTGTGACCTTGGAGCAGCG 323
Qy 81 GlnGlyAspSerMetThrCysGluGlnAlaGlnLeuLeuAlaAsnLeuAlaArgLeu 100
Db 324 CAGGGGATTTATGATGACCTTGGAGCAGCGGCCAGCTCTTGGCCAACTTGGCGGGCTC 383
Qy 101 IleGlnAlaLysLysAlaLeuAspLeuGlyThrPheThrGlyTyrSerAlaLeuAlaLeu 120
Db 384 ATCCAGGCGCAGAGCGCTGAGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGG 443
Qy 121 AlaLeuAlaLeuProAlaAspGlyArgValThrCysGluValAlaAsnGluArgLeu 140
Db 444 GCCCTGGCGTCTCCCGGAGCGGCGCTGTGGTGTGACCTCGAGGTGTGAGCGAGCGCG 503
Qy 141 GluLeuGlyArgProLeuTirPargGlnAlaGluAlaGluHisLysIleAspLeuArgLeu 160
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Db	684	CTGCTGCGACCGGAGGATCTCTCGCTCTCTCAGAGTCTGTGGCGCGGAGAGTCTG	743
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DEFINITION		complete cds.	
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SOURCE		Homo sapiens	
ORGANISM		Homo sapiens	
REFERENCE			
AUTHORS			
1 (bases 1 to 989)			
Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J.,			
Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Deuel,B.,			
Dowd,P., Eaton,D., Foster,J., Grimaldi,C., Gu,Q., Hass,P.E.,			
Heldens,S., Huang,A., Kim,H.S., Klimowski,L., Jin,Y., Johnson,S.,			
Lee,J., Lewis,L., Liao,D., Mark,M., Robbie,E., Sanchez,C.,			
Schoenfeld,J., Seehagiri,S., Simmons,L., Singh,J., Smith,V.,			
Stinson,J., Vagts,A., Vandlen,R., Watanabe,C., Wieand,D., Woods,K.,			
Xie,M.H., Yansura,D., Yi,S., Yu,G., Yuan,J., Zhang,M., Zhang,Z.,			
Goddard,A., Wood,W.I. and Godowski,P.			
The Secreted Protein Discovery Initiative (SPDI), a Large-Scale			
Effort to Identify Novel Human Secreted and Transmembrane Proteins:			
A Bioinformatics Assessment			
Genome Res. 13 (10), 2265-2270 (2003)			
JOURNAL			
PUBMED			
12975309			
2 (bases 1 to 989)			
Clark,H.F.			
Direct Submission			
Submitted (01-AUG-2003) Department of Bioinformatics, Genentech,			
Inc., 1 DNA Way, South San Francisco, CA 94080, USA			
JOURNAL			
Inc., 1 DNA Way, South San Francisco, CA 94080, USA			
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ORIGIN

Alignment Scores:

Pred. No.: 6.4e-95 Length: 989

Score: 1343.00 Matches: 262

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 9 Gaps: 0

US-10-017-407A-306 (1-262) x AY358476 (1-989)

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Db 84 ATGACCAGCGCGTGGCCGGCTCTCCGTGCCCGCGCGCTGGCCCTGAGCGCA 143

QY 21 LeuGlyAlaAlaPheAlaThrGlyLeuPheLeuGlyArgArgCysProThrPArgGly 40

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LOCUS

AX338454

1037 bp

DNA

linear

PAT 09-JAN-2002

AX338454

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DEFINITION Sequence 1 from Patent WO0183719.
ACCESSION AX338454
VERSION AX338454.1 GI:18128893
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Meyers, R.A. and Williamson, M.
TITLE 25692, a novel human o-methyltransferase family member and uses thereof
JOURNAL Patent: WO 0183719-A 1 08-NOV-2001;
FEATURES Millenium Pharmaceuticals, Inc. (US)
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ACCESSION BC047774
VERSION BC047774.1 GI:28839536
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1041)
AUTHORS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klauser, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Sheezy, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., Richards, S.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywicki, M.I., Skalska, U., Smalls, D.E.,
Schnerch, A., Schein, J.B., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
2 (bases 1 to 1041)
Strausberg, R.
Direct Submission
Submitted (03-MAR-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome

```

Center, Stanford University School of Medicine, Stanford, CA 94305
 Web site: <http://www-shgc.stanford.edu>
 Contact: (Dickson, Mark) mcd@paxil.stanford.edu
 Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAK Plate: 98 Row: 9 Column: 5
 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 21389376.

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Alignment Scores:
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 Query Match: 100.00% Indels: 0
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 VERSION
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 ORGANISM

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 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
 AUTHORS
 1 Watanabe, K., Kumagai, A., Itakura, S., Yamazaki, M., Tashiro, H.,
 Ota, T., Suzuki, Y., Obayashi, M., Nishi, T., Shibahara, T., Tanaka, T.,
 Nakamura, Y., Isogai, T. and Sugano, S.
 NEDO human cDNA sequencing project

TITLE
 JOURNAL
 REFERENCE
 AUTHORS
 2 (bases 1 to 988)
 Sugano, S., Suzuki, Y., Ota, T., Obayashi, M., Nishi, T., Isogai, T.,
 Shibahara, T., Tanaka, T. and Nakamura, Y.
 Direct Submission

TITLE
 JOURNAL
 Submitted (14-FEB-2002) Sumio Sugano, Institute of Medical Science,
 University of Tokyo, Laboratory of Genome Structure, Human Genome
 Center, Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan
 (E-mail: flicdn@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286,
 Fax:81-3-5449-5416)

COMMENT
 NEDO human cDNA sequencing project supported by Ministry of
 Economy, Trade and Industry of Japan; cDNA full insert sequencing;
 Research Association for Biotechnology; cDNA library construction,
 5'- & 3'-end one pass sequencing; Department of Virology and Human
 Genome Center, Institute of Medical Science, University of Tokyo
 (partly supported by Science and Technology Agency).

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cDNA Library Preparation: Michael Brownstein / Ted Udin	
Laboratory	
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DNA Sequencing by: Genome Sequence Centre,	
BC Cancer Agency, Vancouver, BC, Canada	
info@bcgsc.bc.ca	
Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield,	
Andy Chan, Steve S. Chand, William Chow, Allison Cloutier, Ruth	
Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao,	
Kim MacDonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Morin,	
Teika Olson, Diana Palmquist, Anca Petrescu, Anna Liisa Prabhu,	
Parvaneh Saedi, JR Santos, Angelique Schnerch, Ursula Skalska,	
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Db	394 GCCTTGGCGCTTCGGAGGCTGGCGCGCTGGTGTGACCTGGAGGTTGAGCGAGCGCCCG 453
Qy	141 GluLeuGlyArgProLeuTrpArgGlnAlaGluAlaGluHisLysLysLeuAspLeuArgLeu 160
Db	454 AAGCTGGGACGCCCATGTGGAGCAGCAGAGTGGAGCAGAGATCGACCTTCGGCTG 513
Qy	161 LysProAlaLeuGluThrLeuAspGluLeuLeuAlaAlaGlyGluAlaGlyThrPheAsp 180
Db	514 CAGCCCGCCCTGCAGACATTCGATGAGCTCTAGCGCGCGCGAGCGCGAACCCTTCGAC 573
Qy	181 ValAlaValValAspAlaAlaAspLysGluAsnCysSerAlaLafyTyxGluArgCysLeuGln 200
Db	574 ATAGCCGTGTGGAGCGCGCAAGAGAACTGTACCGCTACTACGAGCGCTGTCTGCAG 633
Qy	201 LeuLeuArgProGlyGlyLysLeuAlaValLeuArgValLeuTrpArgGlyLysValLeu 220
Db	634 CTCCTACGTCCTCGGAGCGTGTCTGCTACTCAGAGTCTGTGGCGCGGAGAGTGCTG 693
Qy	221 GlnProLysGlyAspValAlaAlaGluCysValArgAsnLeuAsnGluArgGileArg 240
Db	694 CAGCCTCAGCCAGCAAGACTGTGTGATGTGTGCGGACCTGAACGACGATCCTG 753
Qy	241 ArgAspValArgValTrpLysSerLeuLeuProLeuGlyAspGlyLeuThrLeuAlaPhe 260
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Qy	261 LysIle 262
Db	814 AAGATC 819
RESULT 12	
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DEFINITION	
Human DNA sequence from clone RP11-375G3 on chromosome 10, complete	
sequence.	
ACCESSION	
AL390034	
VERSION	
AL390034.23	
KEYWORDS	
HTG.	
SOURCE	
Homo sapiens (human)	
ORGANISM	
Homo sapiens	
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
REFERENCE	
1 (bases 1 to 38679)	
AUTHORS	
Wray, P.	
TITLE	
Direct Submission	
JOURNAL	
Submitted (01-JAN-2002) Wellcome Trust Sanger Institute, Hinxton,	
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:	
humquerry@sanger.ac.uk	
Clonerequest@sanger.ac.uk	
On Jan 2, 2002 this sequence version replaced gi:18032099.	
During sequence assembly data is compared from overlapping clones.	
Where differences are found these are annotated as variations	
together with a note of the overlapping clone name. Note that the	
variation annotation may not be found in the sequence submission	
corresponding to the overlapping clone, as we submit sequences with	
only a small overlap as described above.	
This sequence was finished as follows unless otherwise noted: all	
regions were either double-stranded or sequenced with an alternate	
chemistry or covered by high quality data (i.e., phred quality >=	
30); an attempt was made to resolve all sequencing problems, such	
as compressions and repeats; all regions were covered by at least	
one plasmid subclone or more than one M13 subclone; and the	
assembly was confirmed by restriction digest. The following	
abbreviations are used to associate primary accession numbers given	
in the feature table with their source databases: Em, EMBL; Sw, S-	
WISSPROT; Tr, TREMBL; Wp, WORMPEP; Information on the WORMPEP	
database can be found at	
http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence	
was generated from part of bacterial clone contigs of human	
chromosome 10, constructed by the Sanger Centre Chromosome 10	
Mapping Group. Further information can be found at	
http://www.sanger.ac.uk/HGP/Chr10	
RP11-375G3 is from the library RPCI-11.2 constructed by the group	
of Pieter de Jong. For further details see	
http://www.chori.org/bacpac/home.htm	
VECTOR: pBACes.6	
IMPORTANT: This sequence is not the entire insert of clone	
RP11-375G3 It may be shorter because we sequence overlapping	
sections only once, except for a short overlap.	
The true left end of clone RP11-399K21 is at 36680 in this	
sequence. The true right end of clone RP11-48715 is at 2000 in this	
sequence.	
Location/Qualifiers	
FEATURES	


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/Note="Sequence from uni-directional dGTP big dye
terminator reads only."

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Score:          1028.00      Matches:    261
Percent Similarity: 42.10%      Conservative: 0
Best Local Similarity: 42.10%      Mismatches: 1
Query Match:      76.55%      Indels:     359
DB:               9          Gaps:        6

US-10-017-407A-306 (1-262) x AL390034 (1-38679)

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Qy      21 LeuGlyAlaAlaPheAlaThrGlyLeuPheLeu----- 31
Db      9388 CTGGCGCGCGCTTCGCCCACTGGCCTCTTCCTGGGTGAGCAGGACCTGGTCCCGCGGGC 9329

Qy      31 ----- 31
Db      9328 GGGTGGCGGGCGCAGAGTAGGGCGCGGTGGCTCAGGTTAATCCAAACACCTCTCCCC 9269

Qy      32 ---- GlyArgArgCysProTrpArgGlyArgGluGlnCysLeuLeuProGln 50
Db      9268 GTCAGGAGGCGGTGTCCTCCCATGGCGAGGCGCGGAGAGTGCTGCTTCCCGCCGGA 9209

Qy      50 uAspSerArgLeuTrpGlnTyrLeuLeuSerArgSerMetArgGluHisProAlaLeuAr 70
Db      9208 GGACAGCGCGCTGTGGCAGTATCTTCAGCGGCTCCATGGGGAGCACCCGGCGGCTGG 9149

Qy      70 gSerLeuArgLeu----- 74
Db      9148 AAGCCTGAGGCTGGTCAGCAGGGCGCGGACGAAACGGGGTCCCTCTCGACCCCTCGC 9089

Qy      74 ----- 74
Db      9088 GGTCACAGTGGCTGTGTGA CTTGGGCTGGGCCCTTGGCCCTTCCCTGGGCTTCGGGCTTC 9029

Qy      74 ----- 74
Db      9028 CCTGGCCGGGTGGGTGGGCTTCGGAAGGGCCAGTCCCCCAGGCCACGCCAGAACCG 8969

Qy      74 ----- 74
Db      8968 CGCCCTGGGGCTTGGGACCCCGCAGGCGAAGTGGGTGACCTGCATGGCTGGTGCCACC 8909

Qy      75 -----LeuThrLeuGluGlnProGlnGlyAspSerMetMetThrCysGln 89
Db      8908 CTCTCTTTTCAGCAGCTGACCTCTGGAGCAGCGCAGGGGATTTCTATGATGACCTGCGA 8849

Qy      89 uGlnAlaGlnLeuLeuAlaAsnLeuAlaArgLeuGlnAlaLysLysAlaLeuAspLe 109
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Qy      109 u----- 109
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Qy      110 -----GlyThrPheThrGlyTyrSerAlaLeuAla 120
Db      8728 GGGCTAGCCGCTGTGTCTGTGCTCCAGGACCTTCA CGGGCTACTCCGCGCTTGGGCC 8669

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Qy      120 euAlaLeuAlaLeuProAlaAspGlyArgValValThrCysGluValAlaAspAlaGlnProP 140
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Qy      140 roGluLeuGlyArgProLeuTrpArg----- 148
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Qy      149 -----GlnAlaGluAlaGluHisLysIleAsp 157
Db      8548 GCGGGGGCGCAACGGCTGACCCGCTCCTCGGACGGCGGAGGCGGAGCAACAAGATCGAC 8489

Qy      158 LeuArgLeuLysProAlaLeuGluThrLeu----- 167
Db      8488 CTCCGGCTGAAGCCCGCTTGGAGACCTTGGAGACCTTGGAGACCTTGGAGAGGCTTTGA 8430

Qy      167 ----- 167
Db      8429 AGCCATTCAATTGCAACGAGGCTGCTGTGGCCGAGCTGTGACTGGGCTTGC CGGGCAG 8370

Qy      167 ----- 167
Db      8369 GTTAAGGCGAGGCGCGGTTGTTCACAGACCCCGGGCCGCGCTGGGAGGGCCCTCAGGGCGC 8310

Qy      168 -----AspGluLeuLeuAla 172
Db      8309 CCGGGCGCGGACTCAGCCGACCTGCTCCCTCCCTCCCGCAAGACGAGCTGTGGCG 8250

Qy      173 AlaGlyGluAlaGlyThrPheAspValAlaValValAspAlaAspLysGluAsnCysSer 192
Db      8249 CCGGGCGAGGCGCGACCTTCAGCTGGCCGCTGGTGGTGGTGGTGGTGGTGGTGGTGGT 8190

Qy      193 AlaTyrTyrGluArgCysLeuGlnLeuLeuArgProGlyGlyIleLeuAlaValLeuArg 212
Db      8189 GCCTACTACGAGCGCTGCTGAGCTGTGCTGAGCCCGAGGAGTCTCGCGTCTCTCAGA 8130

Qy      212 ----- 212
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Qy      212 ----- 212
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Qy      212 ----- 212
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Qy      212 ----- 212
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Qy      213 -----ValLeuTrpArgGlyLysValLeuGlnProProLys 224
Db      7769 CCGGTTGGCCCGGCTCCCGCAGGCTCTGTGGCGGGAAGGTCTGCACCTCCGAAA 7710

Qy      225 GlyAspValAlaAlaGluCysValArgAsnLeuAsnGluArgGlyIleArgArgAspValArg 244
Db      7709 GGGGACGTGGGGCGGAGTGTGCGAAACCTAAACGAAACGATCCGCGGGAGCTCAGG 7650

Qy      245 ValTyrIleSerLeuLeuProLeuGlyAspGlyLeuThrLeuAlaPheLysIle 262
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RESULT 13

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LOCUS
DEFINITION Homo sapiens chromosome 10 clone RP11-770D23 map 10, WORKING DRAFT
SEQUENCE, 28 unordered pieces.
AC027393
ACCESSION
VERSION HTG; HTGS_PHASE1; HTGS_DRAFT.
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Birren, B., Linton, L., Nusbaum, C. and Lander, E.
TITLE Homo sapiens chromosome 10, clone RP11-770D23
JOURNAL
REFERENCE

2 (bases 1 to 169612)
Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,
Anderson, S., Baldwin, J., Barna, N., Bastien, V., Bida, F.,
Boguslavsky, L., Boukhgalter, B., Brown, A., Burkett, G.,
Campopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S.,
Collamore, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J.S.,
Dodge, S., Domino, M., Doyle, M., Ferreira, P., FitzHugh, W., Gage, D.,
Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L.,
Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L.,
Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A.,
Klein, J., LaRocque, K., Lamazares, R., Landers, T., Lehoczy, J.,
Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N.,
McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R.,
Melidrim, J., Meneus, L., Mihova, T., Miranda, C., Mlenga, V., Morrow, J.,
Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P.,
O'Neill, D., Olivat, T.M., Oliver, J., Peterson, K., Pierre, N.,
Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D.,
Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B.,
Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,
Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigglio, J.,
Vassiliou, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J.,
Young, G., Zainoun, J., Zimmer, A. and Zody, M.

Direct Submission
Submitted (30-MAR-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 169612)

Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,
Anderson, S., Baldwin, J., Barna, N., Bastien, V., Bida, F.,
Boguslavsky, L., Boukhgalter, B., Brown, A., Burkett, G.,
Campopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S.,
Collamore, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J.S.,
Dodge, S., Domino, M., Doyle, M., Ferreira, P., FitzHugh, W., Gage, D.,
Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L.,
Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L.,
Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A.,
Klein, J., LaRocque, K., Lamazares, R., Landers, T., Lehoczy, J.,
Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N.,
McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R.,
Melidrim, J., Meneus, L., Mihova, T., Miranda, C., Mlenga, V., Morrow, J.,
Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P.,
O'Neill, D., Olivat, T.M., Oliver, J., Peterson, K., Pierre, N.,
Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D.,
Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B.,
Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,
Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigglio, J.,
Vassiliou, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J.,
Young, G., Zainoun, J., Zimmer, A. and Zody, M.

Direct Submission
Submitted (24-AUG-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On May 25, 2000 this sequence version replaced gi:7652066.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR

Web site: <http://www-seq.wi.mit.edu>
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L6572
Center clone name: 770 D 23

----- Summary Statistics
Sequencing vector: M13; M77815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 155213 bases at least Q40
Consensus quality: 162022 bases at least Q30
Consensus quality: 164973 bases at least Q20
Insert size: 179000; agarose-fp
Insert size: 166912; sum-of-contigs
Quality coverage: 4.1 in Q20 bases; agarose-fp
Quality coverage: 4.4 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 28 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 1191: contig of 1191 bp in length
1192 1291: gap of 100 bp
1292 2404: contig of 1113 bp in length
2405 2504: gap of 100 bp
2505 3705: contig of 1201 bp in length
3706 3805: gap of 100 bp
3806 4734: contig of 929 bp in length
4735 4834: gap of 100 bp
4835 6570: contig of 1736 bp in length
6571 6670: gap of 100 bp
6671 8583: contig of 1913 bp in length
8584 10290: contig of 1607 bp in length
10291 10390: gap of 100 bp
10391 11938: contig of 1548 bp in length
11939 12038: gap of 100 bp
12039 15839: contig of 3801 bp in length
15840 15939: gap of 100 bp
15940 19203: contig of 3264 bp in length
19204 19303: gap of 100 bp
19304 22581: contig of 3278 bp in length
22582 22681: gap of 100 bp
22682 24947: contig of 2266 bp in length
24948 25047: gap of 100 bp
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28168 28267: gap of 100 bp
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32084 32183: gap of 100 bp
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35334 35634: gap of 100 bp
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41518 41617: gap of 100 bp
41618 47143: contig of 5526 bp in length
47144 47243: gap of 100 bp
47244 51694: contig of 4451 bp in length
51695 51795: gap of 100 bp
51795 57670: contig of 5776 bp in length
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57671 63190: contig of 5520 bp in length
63191 63290: gap of 100 bp
63291 70708: contig of 7418 bp in length
70709 70808: gap of 100 bp
70809 78988: contig of 8180 bp in length
78989 79088: gap of 100 bp
79089 86527: contig of 7439 bp in length
86528 86628: gap of 100 bp
86628 99114: contig of 12487 bp in length
99115 99214: gap of 100 bp

* 99215 110221: contig of 11007 bp in length
 * 110222 110321: gap of 100 bp
 * 110322 123287: contig of 12966 bp in length
 * 123287 123387: gap of 100 bp
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FEATURES

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Alignment Scores:

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 Score: 1028.00 Matches: 261
 Percent Similarity: 42.10% Conservative: 0
 Best Local Similarity: 42.10% Mismatches: 1
 Query Match: 76.55% Indels: 359
 DB: 2 Gaps: 6

US-10-017-407A-306 (1-262) x AC027393 (1-169612)

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Db 142098 ATGACCCAGCGGTGCGGCTCTCCGTGCCCGCGGCTGGCTGGGCTCAGCCGCA 142039

Qy 21 LeuGlyAlaAlaPhaAlaThrGlyLeuPheLeu----- 31

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Db 142038 CTGGGGCGCGCCTTCGCCACTGGCCTCTTCCTGGGTGACGAGCCTGGTCCGGGGCGG 141979

Qy 31 ----- 31

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Qy 70 gSerLeuArgLeu----- 74

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Qy 74 ----- 74

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Qy 75 -----LeuThrLeuGluGlnProGlnGlyAppSerMetMetThrCysG 89

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Qy 110 -----GlyThrPheThrGlyTyrSerAlaLeuAla 120

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Qy 120 euAlaLeuAlaLeuProAlaLeuGlyArgValValThrCysGluValaLeuAlaGlnProp 140

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Qy 158 LeuArgLeuLysProAlaLeuGluThrLeu----- 167

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Qy 167 ----- 167

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Qy 167 ----- 167

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Db 140839 GCCTACTACGAGCGCTGCTGCAGCTGTGTGACCGCGAGGCATCCTCGCGTCTCTAGA 140780
QY 212 ----- 212
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QY 245 ValTyrIleSerLeuLeuProLeuGlyAspGlyLeuThrLeuAlaPheIle 262
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Fragment Name Begin End
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AY294423_1 100001 210000
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Continuation (4 of 4) of AY294423 from base 300001 (AY294423 Mus musculus chromosome 17

Alignment Scores:
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QY 21 LeuGlyAlaAlaPheAlaThrGlyLeuPheLeuGly----- 32
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QY 33 -----ArgArgCys----- 35
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QY 44 GlnCysLeuLeuProProGluAspSerArgLeuTyrGlnTyrLeuLeuSerArgSerMet 63
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QY 64 ArgGluHisProAlaLeuArgSerLeuArgLeu----- 74
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QY 109 Leu----- 109
Db 77673 CT-GGGTAGGAACACGAGCCATGGTCTCTGGAACACAGGGTCAAGGGCAGCCCTGCAC 77615
QY 110 -----GlyThrPheThrGlyTyrSerAlaLeu 118
Db 77614 CTTGACCTGAGCTTGACAGTGTCCCTTCCACAGTACTTTCACGGGCTACTCGGCCCTG 77555
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QY 167 ----- 167
Db 77316 GAGGACCCAGACAGACTGTCCAAACCCCGGGGAAACAACTGGGCGACCTGAGCAGCC 77257
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QY 172 AlaAlaGlyGluAlaGlyThrPheAspValAlaValValAspAlaAspLysGluAsnCys 191
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 Db 76896 CATCTGTAGGTCCTGTGGCGGAGAGTGTCTGCAGCCTCAGCCAGGACCAAGACTGTT 76837
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 sequence.
 ACCESSION AC132590
 VERSION AC132590.3 GI:38564396
 KEYWORDS HTG
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 161371)
 AUTHORS Swearengen-Shahid,S., Shahid,S., Meyer,R. and Haglund,K.
 TITLE The sequence of Mus musculus BAC clone RP24-273G1
 JOURNAL Unpublished (2001)
 REFERENCE 2 (bases 1 to 161371)
 AUTHORS Wilson,R.
 TITLE Sequencing of Mus musculus
 JOURNAL Unpublished (2001)
 REFERENCE 3 (bases 1 to 161371)
 AUTHORS McPherson,J.D. and Waterston,R.H.
 TITLE Direct Submission
 JOURNAL Submitted (01-SEP-2002) Genome Sequencing Center, 4444 Forest Park
 Parkway, St. Louis, MO 63108, USA
 REFERENCE 4 (bases 1 to 161371)
 AUTHORS McPherson,J.D. and Waterston,R.H.
 TITLE Direct Submission
 JOURNAL Submitted (10-OCT-2002) Genome Sequencing Center, 4444 Forest Park
 Parkway, St. Louis, MO 63108, USA
 REFERENCE 5 (bases 1 to 161371)
 AUTHORS Wilson,R.K.
 TITLE Direct Submission
 JOURNAL Submitted (27-NOV-2003) Genome Sequencing Center, 4444 Forest Park
 Parkway, St. Louis, MO 63108, USA
 REFERENCE 6 (bases 1 to 161371)
 AUTHORS Wilson,R.
 TITLE Direct Submission
 JOURNAL Submitted (01-JAN-2004) Department of Genetics, Washington
 University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
 COMMENT On Nov 27, 2003 this sequence version replaced gi:23683300.
 ----- Genome Center
 Center: Washington University Genome Sequencing Center
 Center code: WUGSC
 Web site: http://genome.wustl.edu

Contact: submissions@watson.wustl.edu
 ----- Summary Statistics
 Center project name: M_BB0273G01

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. Wes Warren, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu>

SOURCE INFORMATION:

The RPCI-24 BAC Library has been constructed by Pieter de Jong and coworkers (<http://www.chori.org>) from male C57BL/6J mouse spleen and/or brain genomic DNA. The clone and detailed information can be obtained from Pieter de Jong and coworkers at <http://www.chori.org>

NEIGHBORING SEQUENCE INFORMATION:

This sequence is the entire insert of the clone. This clone is overlapped by AC129590.

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Alignment Scores:
Pred. No.: 6.75e-56 Length: 161371
Score: 870.50 Matches: 223
Percent Similarity: 44.84% Conservative: 16
Best Local Similarity: 41.84% Mismatches: 23
Query Match: 64.82% Indels: 275
DB: 10 Gaps: 7

US-10-017-407A-306 (1-262) x AC132590 (1-161371)

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Db 45149 GAGCGCTGCTGCCACCTGAGACAAATCCCTGTGGCAGTATCTGCTGAGCGGCTCCATG 45208
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: January 12, 2005, 21:38:38 ; Search time 2958 Seconds
(without alignments)
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Title: US-10-017-407a-306

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Total number of hits satisfying chosen parameters: 65645750

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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7	1181.5	88.0	1321	3	CR625911
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BP433057	BP433057
BI411825	602966437
BP463671	BP463671
BM768764	K-EST0051
EX339546	EX339546
BG339399	602437508
BM976177	UI-CF-EN1
BQ746381	UI-M-ER0-
BE279279	601157608
BG339315	602437607
CK464189	935151 MA
BQ072503	AGENCOURT
BM769685	K-EST0052
CN157520	946232 MA
CN159458	948536 MA
BB666437	BB666437
CK622065	ml32b11.y
AI929359	au59e03.y
BQ918468	AGENCOURT
AM157329	au94f01.x
CK463833	934767 MA
CK771494	959788 MA
AM163385	au94f01.y
CN157439	946147 MA
CN159383	948451 MA
CN161942	951279 MA
CN163323	952815 MA
CK838500	UI-R-AF1-
CN166896	998978 MA
AM163525	au95h04.y
BE014998	126934 MA
AI692198	wd37h07.x
BF341318	602013260
BI340505	365795 MA
AM157252	au93e01.x
BG910899	602812540
BE665755	154904 MA
BE665750	154898 MA
BE237447	146741 MA
CB720369	AMGNNUC.N
BI198020	602762169
BE684896	186649 MA
AM003514	wg66g10.x
BI341406	368809 MA
BG895491	358968 MA
CB716330	AMGNNUC.C
CD674768	fa15a05.y
BG081244	H3062H08-
AI765658	wi82g12.x
BF193231	244743 MA
AM157459	au95h04.x
BM826016	K-EST0097
BG680071	602628219
AK046931	Mus muscu
BE797685	601584583
BQ083301	K-EST0145
CQ651631	OST413096
CF360100	821402 MA
BE287985	601093725
BE286087	601095931
BI680796	459974 MA
EX524890	EX524890

83	710	52.9	446	4	BM825668	BM825668 K-EST0097	156	569.5	42.4	1244	3	CR732330	CR732330 Tetraodon
C 84	707	52.6	620	1	AA584408	AA584408 m81b03.b	157	569	42.4	1186	3	CR640728	CR640728 Tetraodon
C 85	707	52.6	638	1	AI924025	AI924025 wn73606.x	158	569	42.4	1208	3	CR700159	CR700159 Tetraodon
C 86	701	52.1	1056	5	EX3339545	EX3339545 BX3339545	159	569	42.4	1222	3	CR696179	CR696179 Tetraodon
C 87	700	52.1	575	1	AI810740	AI810740 t040a11.x	160	568	42.3	582	5	BQ615284	BQ615284 fab24d05.
C 88	699.5	52.1	599	4	BG498801	BG498801 602544450	161	568	42.3	596	4	BM574082	BM574082 fx59h01.y
C 89	693.5	51.6	970	5	BX422891	BX422891 BX422891	162	568	42.3	790	4	BJ719956	BJ719956 BJ719956
C 90	690	51.4	449	2	AW163255	AW163255 au93601.y	163	568	42.3	1228	3	CR731482	CR731482 Tetraodon
C 91	682	50.8	516	4	BG285119	BG285119 602409396	164	568	42.3	1243	3	CR638609	CR638609 Tetraodon
C 92	680.5	50.7	629	1	AI989669	AI989669 w35a05.x	165	568	42.3	1247	3	CR727337	CR727337 Tetraodon
C 93	663	49.4	506	4	BI340371	BI340371 365618 MA	166	567.5	42.3	1218	3	CR727683	CR727683 Tetraodon
C 94	658.5	49.0	505	1	AA016453	AA016453 mh40c05.f	167	567.5	42.3	1220	3	BF522579	BF522579 UI-R-C3-t
C 95	652	48.5	413	5	BQ082692	BQ082692 K-EST0144	168	567	42.2	379	2	CA374473	CA374473 648906 NC
C 96	643	47.9	442	7	CK457735	CK457735 922062 MA	169	567	42.2	746	6	CR732881	CR732881 Tetraodon
C 97	640	47.9	442	7	CK458804	CK458804 923214 MA	170	567	42.2	1216	3	CR682009	CR682009 Tetraodon
C 98	643	47.7	977	4	BI198073	BI198073 602762269	171	566.5	42.2	1161	3	CA382012	CA382012 661717 NC
C 99	638	47.5	474	4	BM141962	BM141962 if24h03.y	172	566	42.1	724	6	CG889814	CG889814 338070 BA
C 100	638	47.2	502	7	CK819655	CK819655 if22d02.y	173	564	42.0	458	4	CR687110	CR687110 Tetraodon
C 101	634	47.2	525	4	BM129725	BM129725 if22d02.y	174	563	41.9	1074	6	CA490947	CA490947 AGENCOURT
C 102	633.5	47.2	754	5	BF158933	BF158933 BP158933	175	562.5	41.9	1074	6	BM529070	BM529070 fx61f11.y
C 103	630	46.9	565	4	BM753400	BM753400 K-EST0030	176	562	41.8	538	1	AI659582	AI659582 tt87c02.x
C 104	628.5	46.8	664	2	BF181707	BF181707 601805520	177	560	41.7	538	1	CA353706	CA353706 625267 NC
C 105	627	46.7	411	4	BM768965	BM768965 K-EST0052	178	560	41.7	678	6	CR685515	CR685515 Tetraodon
C 106	621	46.2	740	5	EX074246	EX074246 BX074246	179	559.5	41.7	1433	3	BQ450896	BQ450896 fab12d03.
C 107	617.5	46.0	421	1	AJ679437	AJ679437 BJ79437	180	559	41.6	581	5	BQ450896	BQ450896 fab12d03.
C 108	612	45.6	519	4	BM141699	BM141699 if24h03.x	181	559	41.6	653	4	BM426804	BM426804 pgf2n.pk0
C 109	611	45.5	1000	5	EX422892	EX422892 BX422892	182	556.5	41.4	1198	3	CR695082	CR695082 Tetraodon
C 110	608	45.3	769	6	CA346219	CA346219 677059 NC	183	553.5	41.2	871	3	CR653669	CR653669 Tetraodon
C 111	605	45.0	539	2	BF769048	BF769048 BB769048	184	553.5	41.2	878	3	CR654482	CR654482 Tetraodon
C 112	604	45.0	515	6	CF181537	CF181537 818378 MA	185	553	41.2	428	5	BY041621	BY041621 BX041621
C 113	600	44.7	414	1	AI325680	AI325680 mm60d11.y	186	552.5	41.1	885	3	CR636332	CR636332 Tetraodon
C 114	598	44.5	402	6	CB769191	CB769191 AMGNNUC:N	187	551.5	41.1	1200	3	CR698066	CR698066 Tetraodon
C 115	598	44.5	499	4	BG95780	BG95780 359409 MA	188	551	41.0	569	5	BQ480163	BQ480163 faa86g07.
C 116	593	44.2	414	1	AI892364	AI892364 mm60d11.y	189	549.5	40.9	913	3	CR638711	CR638711 Tetraodon
C 117	592.5	44.1	1235	3	CR721460	CR721460 Tetraodon	190	547	40.7	1188	3	CR690884	CR690884 Tetraodon
C 118	592	44.1	507	4	BM129438	BM129438 if22d02.x	191	546.5	40.7	860	3	CR655148	CR655148 Tetraodon
C 119	591.5	44.0	1171	3	CR731130	CR731130 Tetraodon	192	546.5	40.7	861	3	CR634105	CR634105 Tetraodon
C 120	590	43.9	1232	3	CR646763	CR646763 Tetraodon	193	546.5	40.7	882	3	CR645383	CR645383 Tetraodon
C 121	590	43.9	1232	3	CR722216	CR722216 Tetraodon	194	546.5	40.7	1186	3	CR690706	CR690706 Tetraodon
C 122	589	43.9	881	6	CF250863	CF250863 esa018.al	195	545.5	40.6	860	3	CR656656	CR656656 Tetraodon
C 123	588	43.8	1275	3	CR686979	CR686979 Tetraodon	196	545.5	40.6	863	3	CR651698	CR651698 Tetraodon
C 124	587	43.7	1133	3	CR640078	CR640078 Tetraodon	197	545.5	40.6	874	3	CR649975	CR649975 Tetraodon
C 125	586.5	43.7	1183	3	CR696893	CR696893 Tetraodon	198	545.5	40.6	876	3	CR656653	CR656653 Tetraodon
C 126	586.5	43.7	1194	3	CR725106	CR725106 Tetraodon	199	545.5	40.6	881	3	CR656653	CR656653 Tetraodon
C 127	584.5	43.5	1211	3	CR728184	CR728184 Tetraodon	200	544.5	40.5	862	3	CR650550	CR650550 Tetraodon
C 128	584	43.5	470	6	CA777819	CA777819 ip21g07.y	201	544.5	40.5	873	3	CR733986	CR733986 Tetraodon
C 129	584	43.5	747	6	CA388383	CA388383 670627 NC	202	544	40.5	454	5	BU500439	BU500439 AGENCOURT
C 130	582.5	43.4	1216	3	CR685301	CR685301 Tetraodon	203	542.5	40.4	864	3	CR653465	CR653465 Tetraodon
C 131	581.5	43.3	1238	3	CR682588	CR682588 Tetraodon	204	542.5	40.4	884	3	CR653782	CR653782 Tetraodon
C 132	581	43.3	1229	3	CR701700	CR701700 Tetraodon	205	542.5	40.4	904	3	CR639009	CR639009 Tetraodon
C 133	579.5	43.1	1224	3	CR662508	CR662508 Tetraodon	206	542.5	40.4	910	3	CR637704	CR637704 Tetraodon
C 134	579.5	43.1	1224	3	CR698208	CR698208 Tetraodon	207	542.5	40.4	924	3	CR655129	CR655129 Tetraodon
C 135	577	43.0	413	5	BY094423	BY094423 BY094423	208	542.5	40.4	1181	3	CR692840	CR692840 Tetraodon
C 136	577	43.0	487	7	CK819654	CK819654 if22d02.x	209	542.5	40.4	796	7	CF931709	CF931709 EST0141.A
C 137	576	42.9	528	1	AI548694	AI548694 UI-R-C3-t	210	542	40.4	905	4	BM439118	BM439118 Iplvr0184
C 138	575	42.9	1292	3	CR681700	CR681700 Tetraodon	211	542	40.4	1211	3	CR698267	CR698267 Tetraodon
C 139	575	42.8	1218	3	CR687075	CR687075 Tetraodon	212	542	40.4	858	3	CR641707	CR641707 Tetraodon
C 140	575	42.8	1290	3	CR647544	CR647544 Tetraodon	213	541.5	40.3	863	3	CR637158	CR637158 Tetraodon
C 141	574.5	42.8	1144	3	CR700317	CR700317 Tetraodon	214	541.5	40.3	1189	3	CR734171	CR734171 Tetraodon
C 142	574	42.7	459	1	AI929284	AI929284 au9e03.x	215	541.5	40.3	555	4	BM154433	BM154433 fv85a10.y
C 143	573	42.7	582	4	BM574123	BM574123 fx59d04.y	216	541	40.3	555	4	BM186124	BM186124 fv98c04.y
C 144	572	42.6	458	6	CB739243	CB739243 AMGNNUC:N	217	541	40.3	1188	3	CR698292	CR698292 Tetraodon
C 145	572	42.6	1226	3	CR683190	CR683190 Tetraodon	218	541	40.3	1263	3	CR727342	CR727342 Tetraodon
C 146	572	42.6	1245	3	CR685973	CR685973 Tetraodon	219	540.5	40.2	581	5	BQ783563	BQ783563 fab31c01.
C 147	571.5	42.6	1156	3	CR660388	CR660388 Tetraodon	220	540	40.2	720	6	CA360096	CA360096 633318 NC
C 148	571.5	42.6	1178	3	CR633873	CR633873 Tetraodon	221	539	40.1	375	2	BE653217	BE653217 UI-N-AMO-
C 149	571.5	42.6	1201	3	CR633873	CR633873 Tetraodon	222	538	40.1	756	4	BJ739050	BJ739050 BJ739050
C 150	571.5	42.6	1205	3	CR692309	CR692309 Tetraodon	223	538	40.1	764	4	BJ716953	BJ716953 BJ716953
C 151	571.5	42.6	1215	3	CR676419	CR676419 Tetraodon	224	538	40.1	765	6	CA341770	CA341770 671433 NC
C 152	571.5	42.6	1572	3	CR693937	CR693937 Tetraodon	225	537	40.0	553	4	BM186049	BM186049 fv97a10.y
C 153	571	42.5	453	1	AI969924	AI969924 wg77f05.x	226	537	40.0	868	7	CK406586	CK406586 AUF_Ifllvr
C 154	570.5	42.5	1150	3	CR684437	CR684437 Tetraodon	227	537	40.0	869	7	CK409595	CK409595 AUF_Ifllvr
C 155	570.5	42.5	1162	3	CR683289	CR683289 Tetraodon	228	537	40.0				

229	537	40.0	943	7	CK409493	AUF_Iflvr	CK409493	AUF_Iflvr	302	444	33.1	566	7	CK885643	SGP166021
230	535	39.8	1215	3	CK726092	Tetraodon	CR726092	Tetraodon	303	444	33.1	781	5	BU296625	603733078
231	532	39.6	688	6	CK350955	NC	CK350955	621897 NC	304	443	33.0	362	5	BY045218	BY045218
232	531.5	39.5	531.5	9	CQ567423	OSR193749	CQ567423	OSR193749	305	441	32.8	344	5	BY057551	BY057551
233	530	39.6	426	2	BE233897	140418 MA	BE233897	140418 MA	306	441	32.8	543	6	C23048	C23048
234	529	39.4	479	2	AW251950	UI-R-BJO-	AW251950	UI-R-BJO-	307	438	32.6	370	1	AI341293	AI341293
235	528	39.3	855	7	CN885363	58335 126	CN885363	58335 126	308	437.5	32.6	917	7	CK406909	AUF_Iflvr
236	527	39.2	537	4	BM534699	fx70d07.Y	BM534699	fx70d07.Y	309	436	32.5	808	7	CN977279	27484 125
237	526	39.1	921	7	CK409380	AUF_Iflvr	CK409380	AUF_Iflvr	310	434	32.3	336	5	BY048400	BY048400
238	525	39.0	921	7	CK406607	AUF_Iflvr	CK406607	AUF_Iflvr	311	433	32.2	413	5	AW252346	UI-R-BJO-
239	524	39.0	400	5	BY050241	BY050241	BY050241	BY050241	312	432	32.2	499	1	AL919863	AL919863
240	524	39.0	854	3	CR651708	Tetraodon	CR651708	Tetraodon	313	431	32.1	613	7	CK896516	SGP159062
241	524	39.0	934	7	CK406893	AUF_Iflvr	CK406893	AUF_Iflvr	314	430	32.0	298	2	AW664650	hi84b01.x
242	522	38.9	422	2	BF593185	7050a03.x	BF593185	7050a03.x	315	427	31.8	610	7	CK896728	SGP159280
243	521	38.8	678	7	CN974704	23486 125	CN974704	23486 125	316	426	31.7	411	2	AW251159	UI-R-BJO-
244	520	38.7	869	7	CN985211	57529 127	CN985211	57529 127	317	423	31.5	627	5	BQ036498	SL5-0017
245	519	38.6	629	1	AU179577	AU179577	AU179577	AU179577	318	420	31.3	598	7	CK895980	SGP158514
246	518	38.6	460	1	AI340993	qo82g09.x	AI340993	qo82g09.x	319	420	31.3	847	7	CN175403	AGENCOURT
247	518	38.6	614	1	AU180003	AU180003	AU180003	AU180003	320	419	31.2	615	3	CR647326	Tetraodon
248	518	38.6	896	7	CK407472	AUF_Iflvr	CK407472	AUF_Iflvr	321	419	31.2	937	6	CA458592	AGENCOURT
249	512	38.1	421	2	AW299522	x640h01.x	AW299522	x640h01.x	322	416.5	31.0	671	5	EX864474	EX864474
250	512	38.1	645	4	BJ705610	BJ705610	BJ705610	BJ705610	323	416	31.0	737	2	AW012934	Ldt-0102
251	512	38.1	660	4	BJ727162	BJ727162	BJ727162	BJ727162	324	413	30.8	635	8	AZ958898	M0226D22
252	511	38.0	902	7	CK409572	AUF_Iflvr	CK409572	AUF_Iflvr	325	409.5	30.5	720	7	CN989253	65281 125
253	511	38.0	956	7	CK406337	AUF_Iflvr	CK406337	AUF_Iflvr	326	408	30.4	416	5	BQ479917	faa84a07
254	509.5	37.9	691	4	BU708514	BU708514	BU708514	BU708514	327	408	30.4	439	5	BY447416	BY447416
255	509	37.9	448	1	AI349083	qo83g09.x	AI349083	qo83g09.x	328	407.5	30.3	766	5	BU010720	QGJ14E17
256	509	37.9	643	6	CB512007	ssalrgb53	CB512007	ssalrgb53	329	407	30.3	539	6	CA333551	haa85C09
257	509	37.9	722	5	BQ208081	UI-R-BJO-	BQ208081	UI-R-BJO-	330	406	30.2	526	5	BY468703	BY468703
258	509	37.9	837	6	C23373	C23373 Japa	C23373	C23373 Japa	331	404	30.1	351	5	BY085557	BY085557
259	508.5	37.9	1205	3	CR652934	Tetraodon	CR652934	Tetraodon	332	404	30.1	808	7	CN991683	68533 125
260	507	37.8	384	1	AA068794	mm60dl1.x	AA068794	mm60dl1.x	333	403	30.0	406	4	BI288752	UI-R-DKO-
261	504	37.5	415	2	AW299513	AW299513	AW299513	AW299513	334	403	30.0	599	1	AI981881	pat.pk006
262	504	37.5	923	7	CK407551	AUF_Iflvr	CK407551	AUF_Iflvr	335	403	30.0	635	7	CN984292	53247 126
263	503	37.5	612	4	BI304044	UI-R-DRO-	BI304044	UI-R-DRO-	336	401.5	29.9	753	6	CA782445	sat28h08
264	503	37.5	875	7	CN978664	29797 125	CN978664	29797 125	337	401	29.9	243	4	BI832844	603082670
265	495	36.9	415	1	AI340991	qo82g07.x	AI340991	qo82g07.x	338	401	29.9	878	7	CO366616	RTK1_29_A
266	495	36.9	638	4	BU711589	BU711589	BU711589	BU711589	339	399	29.7	362	2	BF509580	UI-H-B14-
267	494	36.8	905	7	CK407588	AUF_Iflvr	CK407588	AUF_Iflvr	340	399	29.7	882	7	CK605765	gmrhRW6-
268	492	36.6	670	6	CA355616	627543 NC	CA355616	627543 NC	341	398	29.6	1045	3	CN80A6FG	Arabiadops
269	490	36.5	731	4	BJ722907	BJ722907	BJ722907	BJ722907	342	397	29.6	341	1	AI650609	wb01f04.x
270	489	36.5	866	7	CN175149	AGENCOURT	CN175149	AGENCOURT	343	397	29.6	857	7	CN172476	AGENCOURT
271	489	36.5	587	7	CK896420	SGP158963	CK896420	SGP158963	344	396.5	29.5	779	4	EG6647257	ESTS08886
272	488	36.3	642	1	AI477552	fb58g04.Y	AI477552	fb58g04.Y	345	396	29.5	826	7	CK189143	EST778458
273	486	36.2	401	6	CB969999	AMGNNUC:N	CB969999	AMGNNUC:N	346	396	29.5	866	6	CB650869	OSJNEB15J
274	485.5	36.2	527	5	BQ615750	fab14b01	BQ615750	fab14b01	347	396	29.5	873	7	CK189144	EST778459
275	484	36.0	371	5	BY048974	BY048974	BY048974	BY048974	348	395	29.4	365	6	CB050636	NISC_G118
276	481	35.8	704	2	BF228537	EST00248	BF228537	EST00248	349	395	29.4	365	6	CB050637	NISC_G118
277	479	35.7	434	2	BF787832	BF787832	BF787832	BF787832	350	395	29.4	635	6	C23181	C23181 Japa
278	478	35.6	405	1	AI912836	tz86c05.x	AI912836	tz86c05.x	351	394.5	29.4	720	7	CO532807	CO532807
279	477	35.5	374	5	BY037587	BY037587	BY037587	BY037587	352	394	29.3	398	4	BM573972	fx57d11.Y
280	477	35.5	579	7	CK895655	SGP158175	CK895655	SGP158175	353	394	29.3	593	7	CK888688	SGP160680
281	477	35.5	874	7	CN169125	AGENCOURT	CN169125	AGENCOURT	354	394	29.3	1064	7	CK163121	FGAS01573
282	476	35.4	513	5	BQ783421	fab29f02	BQ783421	fab29f02	355	393	29.3	683	2	BB594747	BB594747
283	471.5	35.1	1206	3	CK641100	Tetraodon	CK641100	Tetraodon	356	392.5	29.2	818	6	CF203341	UI-R-EAO-
284	471	35.1	360	5	BY057583	BY057583	BY057583	BY057583	357	392	29.2	419	7	CN542838	UI-R-EAO-
285	470	35.0	746	7	CN988270	64067 125	CN988270	64067 125	358	392	29.2	465	4	BJ498661	BJ498661
286	468	34.8	436	2	AW251225	UI-R-BJO-	AW251225	UI-R-BJO-	359	392	29.2	499	4	BJ527812	BJ527812
287	464	34.5	598	7	CK895107	SGP154357	CK895107	SGP154357	360	392	29.2	515	4	BJ490344	BJ490344
288	463	34.5	661	4	BI468189	EST00596	BI468189	EST00596	361	392	29.2	562	4	BJ496988	BJ496988
289	461	34.3	551	7	CK896911	SGP159468	CK896911	SGP159468	362	391.5	29.2	833	6	CF215293	CF215293
290	459.5	34.2	1211	3	CK683715	Tetraodon	CK683715	Tetraodon	363	391.5	29.2	924	7	CF652643	68-J02013
291	458	34.1	372	5	BY042000	BY042000	BY042000	BY042000	364	391.5	29.2	942	7	CF516928	CF516928
292	457.5	34.1	812	7	CO804908	AGENCOURT	CO804908	AGENCOURT	365	391.5	29.2	1003	3	CN80A315	Arabiadops
293	454	33.8	292	4	BM856156	K-EST0139	BM856156	K-EST0139	366	391.5	29.2	1024	5	BY398556	BY398556
294	453.5	33.8	644	6	CA333572	haa85h10	CA333572	haa85h10	367	391	29.1	370	5	BY398556	BY398556
295	453	33.7	503	4	BQ669239	DRNIG10 R	BQ669239	DRNIG10 R	368	390.5	29.1	810	6	CF213611	CGF100079
296	451	33.6	375	5	BY041991	BY041991	BY041991	BY041991	369	390	29.0	488	6	CD737778	4023355 1
297	451	33.6	963	7	CK409756	AUF_Iphdk	CK409756	AUF_Iphdk	370	390	29.0	658	4	BJ510111	BJ510111
298	445	33.1	423	2	AW252701	UI-R-BJO-	AW252701	UI-R-BJO-	371	390	29.0	712	7	CN975952	CN975952
299	445	33.1	473	6	CA395926	c870g11.Y	CA395926	c870g11.Y	372	389.5	29.0	789	4	BI308775	EST530185
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524	353	26.3	860	6	CB893812	EST646604	CB893812	EST646604	524	353	26.3	860	6	CB893812	EST646604	CB893812	EST646604	524	353	26.3	860	6	CB893812	EST646604	CB893812	EST646604
525	352.5	26.2	715	5	BQ123287	EST608863	BQ123287	EST608863	525	352.5	26.2	715	5	BQ123287	EST608863	BQ123287	EST608863	525	352.5	26.2	715	5	BQ123287	EST608863	BQ123287	EST608863
C 526	352.5	26.2	864	6	CB823986	EST_5210	CB823986	EST_5210	C 526	352.5	26.2	864	6	CB823986	EST_5210	CB823986	EST_5210	C 526	352.5	26.2	864	6	CB823986	EST_5210	CB823986	EST_5210
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528	352	26.2	686	5	BP184507	BP184507	BP184507	BP184507	528	352	26.2	686	5	BP184507	BP184507	BP184507	BP184507	528	352	26.2	686	5	BP184507	BP184507	BP184507	BP184507
C 529	352	26.2	774	9	CG694438	OGUJH61TH	CG694438	OGUJH61TH	C 529	352	26.2	774	9	CG694438	OGUJH61TH	CG694438	OGUJH61TH	C 529	352	26.2	774	9	CG694438	OGUJH61TH	CG694438	OGUJH61TH
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532	351.5	26.2	588	4	BM520677	sa197b12	BM520677	sa197b12	532	351.5	26.2	588	4	BM520677	sa197b12	BM520677	sa197b12	532	351.5	26.2	588	4	BM520677	sa197b12	BM520677	sa197b12
533	351.5	26.2	693	6	CA153085	CA153085	CA153085	CA153085	533	351.5	26.2	693	6	CA153085	CA153085	CA153085	CA153085	533	351.5	26.2	693	6	CA153085	CA153085	CA153085	CA153085
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535	351.5	26.2	754	7	CN012179	WHE3893_E	CN012179	WHE3893_E	535	351.5	26.2	754	7	CN012179	WHE3893_E	CN012179	WHE3893_E	535	351.5	26.2	754	7	CN012179	WHE3893_E	CN012179	WHE3893_E
536	351.5	26.2	764	5	BQ804819	WHE33559_C	BQ804819	WHE33559_C	536	351.5	26.2	764	5	BQ804819	WHE33559_C	BQ804819	WHE33559_C	536	351.5	26.2	764	5	BQ804819	WHE33559_C	BQ804819	WHE33559_C
C 537	351	26.1	665	6	CD860328	TE_002B22	CD860328	TE_002B22	C 537	351	26.1	665	6	CD860328	TE_002B22	CD860328	TE_002B22	C 537	351	26.1	665	6	CD860328	TE_002B22	CD860328	TE_002B22
538	350.5	26.1	620	2	AW585897	ESF317520	AW585897	ESF317520	538	350.5	26.1	620	2	AW585897	ESF317520	AW585897	ESF317520	538	350.5	26.1	620	2	AW585897	ESF317520	AW585897	ESF317520
539	350.5	26.1	667	2	BF636068	BF636068	BF636068	BF636068	539	350.5	26.1	667	2	BF636068	BF636068	BF636068	BF636068	539	350.5	26.1	667	2	BF636068	BF636068	BF636068	BF636068
540	350.5	26.1	697	2	BF634788	BF634788	BF634788	BF634788	540	350.5	26.1	697	2	BF634788	BF634788	BF634788	BF634788	540	350.5	26.1	697	2	BF634788	BF634788	BF634788	BF634788
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542	350.5	26.1	795	5	BQ255166	BQ255166	BQ255166	BQ255166	542	350.5	26.1	795	5	BQ255166	BQ255166	BQ255166	BQ255166	542	350.5	26.1	795	5	BQ255166	BQ255166	BQ255166	BQ255166
543	350.5	26.1	877	6	CA755835	MTWAE30TK	CA755835	MTWAE30TK	543	350.5	26.1	877	6	CA755835	MTWAE30TK	CA755835	MTWAE30TK	543	350.5	26.1	877	6	CA755835	MTWAE30TK	CA755835	MTWAE30TK
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545	349.5	26.0	590	4	BM660518	602436489	BM660518	602436489	545	349.5	26.0	590	4	BM660518	602436489	BM660518	602436489	545	349.5	26.0	590	4	BM660518	602436489	BM660518	602436489
546	349.5	26.0	631	4	BG045213	sa239a10	BG045213	sa239a10	546	349.5	26.0	631	4	BG045213	sa239a10	BG045213	sa239a10	546	349.5	26.0	631	4	BG045213	sa239a10	BG045213	sa239a10
547	349.5	26.0	713	6	CD869948	AZ02_113A	CD869948	AZ02_113A	547	349.5	26.0	713	6	CD869948	AZ02_113A	CD869948	AZ02_113A	547	349.5	26.0	713	6	CD869948	AZ02_113A	CD869948	AZ02_113A
548	349.5	26.0	729	6	CD885596	CD885596	CD885596	CD885596	548	349.5	26.0	729	6	CD885596	CD885596	CD885596	CD885596	548	349.5	26.0	729	6	CD885596	CD885596	CD885596	CD885596
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C 551	349	26.0	553	5	BQ036499	BQ036499	BQ036499	BQ036499	C 551	349	26.0	553	5	BQ036499	BQ036499	BQ036499	BQ036499	C 551	349	26.0	553	5	BQ036499	BQ036499	BQ036499	BQ036499
552	349	26.0	711	6	CD873066	AZ02_122E	CD873066	AZ02_122E	552	349	26.0	711	6	CD873066	AZ02_122E	CD873066	AZ02_122E	552	349	26.0	711	6	CD873066	AZ02_122E	CD873066	AZ02_122E
553	349	26.0	731	6	CD885623	G118_001P	CD885623	G118_001P	553	349	26.0	731	6	CD885623	G118_001P	CD885623	G118_001P	553	349	26.0	731	6	CD885623	G118_001P	CD885623	G118_001P
554	349	26.0	762	6	CB649583	OSJNEB13J	CB649583	OSJNEB13J	554	349	26.0	762	6	CB649583	OSJNEB13J	CB649583	OSJNEB13J	554	349	26.0	762	6	CB649583	OSJNEB13J	CB649583	OSJNEB13J
C 555	348.5	25.9	605	4	BM660519	952039C01	BM660519	952039C01	C 555	348.5	25.9	605	4	BM660519	952039C01	BM660519	952039C01	C 555	348.5	25.9	605	4	BM660519	952039C01	BM660519	952039C01
556	348.5	25.9	689	4	BG544230	BG544230	BG544230	BG544230	556	348.5	25.9	689	4	BG544230	BG544230	BG544230	BG544230	556	348.5	25.9	689	4	BG544230	BG544230	BG544230	BG544230
557	348.5	25.9	693	1	AU270835	AU270835	AU270835	AU270835	557	348.5	25.9	693	1	AU270835	AU270835	AU270835	AU270835	557	348.5	25.9	693	1	AU270835	AU270835	AU270835	AU270835
558	348.5	25.9	717	4	BI434036	BI434036	BI434036	BI434036	558	348.5	25.9	717	4	BI434036	BI434036	BI434036	BI434036	558	348.5	25.9	717	4	BI434036	BI434036	BI434036	BI434036
559	348.5	25.9	737	2	BE559087	BE559087	BE559087	BE559087	559	348.5	25.9	737	2	BE559087	BE559087	BE559087	BE559087	559	348.5	25.9	737	2	BE559087	BE559087	BE559087	BE559087
560	347.5	25.9	612	4	BG045242	sa439d08	BG045242	sa439d08	560	347.5	25.9	612	4	BG045242	sa439d08	BG045242	sa439d08	560	347.5	25.9	612	4	BG045242	sa439d08	BG045242	sa439d08
C 561	347.5	25.9	622	1	A1637136	603001A11	A1637136	603001A11	C 561	347.5	25.9	622	1	A1637136	603001A11	A1637136	603001A11	C 561	347.5	25.9	622	1	A1637136	603001A11	A1637136	603001A11
562	347.5	25.9	630	2	AW757356	AW757356	AW757356	AW757356	562	347.5	25.9	630	2	AW757356	AW757356	AW757356	AW757356	562	347.5	25.9	630	2	AW757356	AW757356	AW757356	AW757356
563	347.5	25.9	639	2	BE203346	BE203346	BE203346	BE203346	563	347.5	25.9	639	2	BE203346	BE203346	BE203346	BE203346	563	347.5	25.9	639	2	BE203346	BE203346	BE203346	BE203346
564	347.5	25.9	657	5	BQ624016	USDA-FP_0	BQ624016	USDA-FP_0	564	347.5	25.9	657	5	BQ624016	USDA-FP_0	BQ624016	USDA-FP_0	564	347.5	25.9	657	5	BQ624016	USDA-FP_0	BQ624016	USDA-FP_0
565	347.5	25.9	676	2	BF642362	BF642362	BF642362	BF642362	565	347.5	25.9	676	2	BF642362	BF642362	BF642362	BF642362	565	347.5	25.9	676	2	BF642362	BF642362	BF642362	BF642362
566	347.5	25.9	686	2																						

667	337.5	25.1	673	7	CN190619	CN190619	UCRCS06_0	740	331.5	24.7	681	5	BQ987553	BQ987553	QGF12119.
668	337.5	25.1	674	2	AW560150	AW560150	EST315198	741	331.5	24.7	683	2	AW030736	AW030736	EST273991
669	337.5	25.1	683	2	BF520049	BF520049	EST457517	742	331.5	24.7	683	4	BI922821	BI922821	EST542725
670	337.5	25.1	683	6	CD930335	CD930335	GR45.110P	743	331.5	24.7	714	6	CA918225	CA918225	EST642372
671	337.5	25.1	699	5	BQ624767	BQ624767	USDA-FP_0	744	331.5	24.7	726	5	BQ938107	BQ938107	WHE2906_F
672	337.5	25.1	718	6	CD938268	CD938268	OV.109I23	745	331.5	24.7	750	5	CF921444	CF921444	gmthrw3-
673	337.5	25.1	718	6	CD938289	CD938289	OV.109K04	746	331	24.6	606	2	BE021597	BE021597	sm60804.Y
674	337.5	25.1	746	7	CK215205	CK215205	FGAS02715	747	331	24.6	946	6	CA270677	CA270677	SCRULB206
675	337	25.1	629	6	CD478576	CD478576	eca01-14m	748	330.5	24.6	519	2	BF636493	BF636493	NF088G06D
676	337	25.1	732	7	CF433087	CF433087	EST674432	749	330.5	24.6	596	2	BE403578	BE403578	WHE0434_C
677	337	25.1	732	7	CF433087	CF433087	EST674432	750	330.5	24.6	531	2	BF473218	BF473218	WHE0922_H
678	336.5	25.1	543	1	AI939180	AI939180	sc67h02_Y	751	330.5	24.6	652	7	CN192437	CN192437	UCRCS06_0
679	336.5	25.1	617	2	BE405650	BE405650	WHE1209_G	752	330.5	24.6	658	7	CF836276	CF836276	UCRCS03_0
680	336.5	25.1	618	2	BE405650	BE405650	WHE1209_G	753	330.5	24.6	658	7	CN191414	CN191414	UCRCS06_0
681	336.5	25.1	653	4	BI957460	BI957460	WHE1209_G	754	330.5	24.6	731	1	AJ803420	AJ803420	AJ803420
682	336.5	25.1	704	6	CD817128	CD817128	HN20.040N	755	330.5	24.6	772	6	CD839679	CD839679	RFO2.116D
683	336.5	25.1	786	7	CN137489	CN137489	OXI_57_D0	756	330.5	24.6	1121	6	CA131093	CA131093	SCBFR106
684	336.5	25.1	797	7	CK193862	CK193862	FGAS00228	757	330	24.6	569	7	CK439809	CK439809	G00021b.B
685	336	25.0	442	7	CN967135	CN967135	14632_100	758	330	24.6	706	7	CF517412	CF517412	CAPO005_I
686	336	25.0	442	7	CN967135	CN967135	14632_100	759	330	24.6	712	7	CF389766	CF389766	RTRW2_19
687	336	25.0	675	4	RM814917	RM814917	EST593011	760	330	24.6	712	7	CF473897	CF473897	RTRW2_21
688	336	25.0	733	5	BQ838231	BQ838231	WHE2908_A	761	330	24.6	718	7	CF478998	CF478998	RTRW3_13
689	336	25.0	733	5	BQ838231	BQ838231	WHE2908_A	762	330	24.6	747	7	CF396117	CF396117	RTRW3_13
690	336	25.0	750	6	CD898674	CD898674	WHE2908_A	763	329.5	24.5	562	2	BF484304	BF484304	WHE2321_F
691	335.5	25.0	530	6	CD319523	CD319523	OSTR163G7	764	329.5	24.5	638	4	BI959367	BI959367	WHE2321_F
692	335.5	25.0	559	2	AW103253	AW103253	sd86f04_Y	765	329.5	24.5	639	4	BI959367	BI959367	WHE2321_F
693	335.5	25.0	623	8	BK641943	BK641943	OGAMK72TC	766	329.5	24.5	651	1	AL504625	AL504625	WHE2321_F
694	335.5	25.0	731	7	CK240495	CK240495	VRJ324_Vi	767	329.5	24.5	651	1	AL504625	AL504625	WHE2321_F
695	335.5	25.0	737	2	AW348485	AW348485	GM210002B	768	329.5	24.5	672	2	AW442463	AW442463	WHE2321_F
696	335.5	25.0	747	7	CF474427	CF474427	RTRW2_20	769	329.5	24.5	684	4	BM110489	BM110489	WHE2321_F
697	335	24.9	337	2	AW356352	AW356352	38646_NAR	770	329.5	24.5	693	2	BM284958	BM284958	WHE2321_F
698	335	24.9	344	7	CF478537	CF478537	RTRW3_20	771	329.5	24.5	631	4	BM284958	BM284958	WHE2321_F
699	334.5	24.9	531	4	BI426741	BI426741	sa6f5902_	772	329	24.5	672	2	AW218547	AW218547	EST303730
700	334.5	24.9	598	4	BI321639	BI321639	sa6f5902_	773	329	24.5	640	2	AW218547	AW218547	EST303730
701	334.5	24.9	644	6	CD930761	CD930761	WHE2909_A	774	328.5	24.5	646	2	AW218547	AW218547	EST303730
702	334.5	24.9	646	5	BQ838318	BQ838318	WHE2909_A	775	328.5	24.5	646	2	AW218547	AW218547	EST303730
703	334.5	24.9	724	7	CF921036	CF921036	gmthrw3-	776	328.5	24.5	649	6	CF227474	CF227474	WHE2321_F
704	334	24.9	646	5	BI762428	BI762428	BP176248	777	328.5	24.5	655	4	BI960120	BI960120	HVSMEN002
705	334	24.9	659	1	AJ615423	AJ615423	AJ615423	778	328.5	24.5	762	7	CO171539	CO171539	NDL1_22_C
706	334	24.9	661	4	BJ247474	BJ247474	BJ247474	779	328.5	24.5	797	7	CF838015	CF838015	UCRCS02_0
707	334	24.9	692	6	CD868552	CD868552	AZ02.109E	780	328.5	24.5	800	7	CF833320	CF833320	UCRCS02_0
708	333.5	24.8	630	4	BG449728	BG449728	NF007D11I	781	328.5	24.5	800	7	CF833320	CF833320	UCRCS02_0
709	333.5	24.8	632	2	BE325133	BE325133	SCBGR104	782	328.5	24.5	859	6	CB823461	CB823461	EST_4685
710	333.5	24.8	654	6	CA131555	CA131555	SCBGR104	783	328	24.4	743	6	CA180815	CA180815	WHE2321_F
711	333.5	24.8	662	2	BF597864	BF597864	su89c03_Y	784	327.5	24.4	621	5	BQ743179	BQ743179	WHE2321_F
712	333.5	24.8	682	2	BF641947	BF641947	NF011B12I	785	327.5	24.4	623	6	CA821361	CA821361	WHE2321_F
713	333.5	24.8	684	5	BH875316	BH875316	V005C03_P	786	327.5	24.4	635	1	AJ560090	AJ560090	WHE2321_F
714	333.5	24.8	694	5	BH875316	BH875316	V005C03_P	787	327.5	24.4	635	1	AJ560090	AJ560090	WHE2321_F
715	333.5	24.8	699	1	AJ615461	AJ615461	AJ615461	788	327.5	24.4	654	6	CD839660	CD839660	SCSBA0108
716	333.5	24.8	708	7	CN184479	CN184479	UCRCS04_0	789	327.5	24.4	667	6	CA196132	CA196132	SCSBA0108
717	333.5	24.8	709	5	BO752659	BO752659	WHE4117_F	790	327	24.3	762	7	CF472622	CF472622	RTRW1_10
718	333.5	24.8	716	5	BH874994	BH874994	V001B12_P	791	327	24.3	629	4	BI959561	BI959561	HVSMEN002
719	333.5	24.8	722	5	BF630744	BF630744	HVSMEN001	792	326.5	24.3	636	6	CA020338	CA020338	HZ36A04r
720	333.5	24.8	756	2	BF630744	BF630744	HVSMEN001	793	326.5	24.3	637	5	BO623195	BO623195	USDA-FP_0
721	333	24.8	417	1	A1477667	A1477667	FD58904_X	794	326.5	24.3	643	5	BU977235	BU977235	HALL1B05f
722	333	24.8	664	5	BP184560	BP184560	BP184560	795	326.5	24.3	648	4	BI959235	BI959235	HVSMEN001
723	333	24.8	667	4	BI957447	BI957447	HVSMEN000	796	326.5	24.3	650	7	CK987645	CK987645	SP7-A3(P1
724	333	24.8	738	7	CK861883	CK861883	33001_In	797	326.5	24.3	656	7	CK987645	CK987645	SP7-A3(P1
725	333	24.8	743	4	BJ252414	BJ252414	BJ252414	798	326.5	24.3	675	7	CF932162	CF932162	PI-A3-REV
726	333	24.8	766	7	CO173178	CO173178	NDL1_34_B	799	326.5	24.3	712	6	CD841037	CD841037	PI-A4_A
727	333	24.8	882	7	CN201625	CN201625	Tor1690_G	800	326.5	24.3	719	7	CF833209	CF833209	RFO2.121J
728	332.5	24.8	671	4	BF642662	BF642662	NF072H07I	801	326.5	24.3	719	7	CF833209	CF833209	RFO2.121J
729	332.5	24.8	674	2	BM063898	BM063898	K501060G0	802	326.5	24.3	774	6	CA065807	CA065807	WHE2321_F
730	332.5	24.8	725	6	CD823678	CD823678	BN25.049J	803	326.5	24.3	823	2	BF264389	BF264389	WHE2321_F
731	332.5	24.8	739	7	CN190771	CN190771	UCRCS06_0	804	326.5	24.3	836	5	BY398227	BY398227	WHE2321_F
732	332.5	24.8	807	7	CK932928	CK932928	CGF10043A	805	326.5	24.3	1086	7	CK213734	CK213734	WHE2321_F
733	332.5	24.8	817	7	CK932928	CK932928	CGF10043A	806	326.5	24.3	336	5	BY398227	BY398227	WHE2321_F
734	332	24.7	208	2	BE853865	BE853865	ux22608_Y	807	326	24.3	360	6	CA065807	CA065807	WHE2321_F
735	332	24.7	511	4	BG653155	BG653155	sa82f01_	808	326	24.3	366	7	CK194117	CK194117	WHE2321_F
736	331.5	24.7	511	4	BG653155	BG653155	sa82f01_	809	326	24.3	817	7	CK194117	CK194117	WHE2321_F
737	331.5	24.7	649	6	CD879761	CD879761	AZ04.106E	810	325.5	24.2	543	4	BM738368	BM738368	WHE2321_F
738	331.5	24.7	665	1	AI898029	AI898029	EST267472	811	325.5	24.2	574	4	BM738368	BM738368	WHE2321_F
739	331.5	24.7	681	5	BQ875399	BQ875399	QGI8A03_Y	812	325.5	24.2	610	5	BQ467961	BQ467961	HR01H17f

813	325.5	24.2	624	6	CA021273	CA021273	HZ39J21r	886	319	23.8	853	2	BF256079	BF256079	HVSMEf000	
814	325.5	24.2	630	7	CN010185	WHE3867_G	CN010185	WHE3867_G	887	318.5	23.7	549	4	BG155028	BG155028	sab40b01.
815	325.5	24.2	647	7	BI960119	HVSMEN002	BI960119	HVSMEN002	888	318.5	23.7	570	6	CA279207	CA279207	SCBFLB209
816	325.5	24.2	660	7	CF418675	USDA-FP_1	CF418675	USDA-FP_1	889	318.5	23.7	608	7	CK750439	CK750439	PSM01-6n8
817	325.5	24.2	681	1	AV782400	AV782400	AV782400	AV782400	890	318.5	23.7	609	4	BM065108	BM065108	KSO1075A0
818	325.5	24.2	698	5	BUB96211	X037C08_P	BUB96211	X037C08_P	891	318.5	23.7	623	4	BM111532	BM111532	EST559068
819	325.5	24.2	714	1	AJ778942	AJ778942	AJ778942	AJ778942	892	318.5	23.7	687	6	CA192398	CA192398	SCCST3C0
820	325.5	24.2	734	9	CG327759	OGXFO38TH	CG327759	OGXFO38TH	893	318.5	23.7	694	6	BJ261281	BJ261281	BJ261281
821	325.5	24.2	788	7	CF669731	RTCNM1_45	CF669731	RTCNM1_45	894	318.5	23.7	745	6	CA918812	CA918812	EST636530
822	325.5	24.2	684	6	CA142702	SCMNT1_45	CA142702	SCMNT1_45	895	318.5	23.7	753	7	CF436915	CF436915	EST673260
823	325.5	24.2	757	7	CF395287	RTD82_10	CF395287	RTD82_10	896	318.5	23.7	856	7	CK202105	CK202105	FGAS01062
824	324.5	24.2	557	2	BE404145	WHE1201_G	BE404145	WHE1201_G	897	318	23.7	695	5	BX252395	BX252395	BM252395
825	324.5	24.2	591	5	BQ753204	WHE4124_C	BQ753204	WHE4124_C	898	318	23.7	720	6	CA221618	CA221618	SCSFLA03
826	324.5	24.2	624	5	BQ744417	WHE4115_D	BQ744417	WHE4115_D	899	318	23.7	787	5	BQ515541	BQ515541	EST622956
827	324.5	24.2	627	5	BQ788936	WHE4155_E	BQ788936	WHE4155_E	900	317.5	23.6	510	2	AW424002	AW424002	sh59c10.Y
828	324.5	24.2	628	5	BQ744183	WHE4112_F	BQ744183	WHE4112_F	901	317.5	23.6	711	5	BQ139680	BQ139680	GM023A10P
829	324.5	24.2	664	6	CD079415	MAB3-9995U	CD079415	MAB3-9995U	902	317.5	23.6	720	7	CF921163	CF921163	gmrbw3
830	324.5	24.2	680	4	B1179085	EST520030	B1179085	EST520030	903	317.5	23.6	756	6	CD849237	CD849237	DH0AC017Z
831	324.5	24.2	694	4	BG646445	EST508064	BG646445	EST508064	904	317	23.6	468	7	CK895492	CK895492	SGP158009
832	324.5	24.2	707	4	BG587428	EST489200	BG587428	EST489200	905	317	23.6	605	6	CA155532	CA155532	SCACR2310
833	324.5	24.2	719	7	CN146340	WOUNDI_39	CN146340	WOUNDI_39	906	317	23.6	663	6	CA280962	CA280962	SCRFSD101
834	324	24.1	588	2	BE493850	WHE1276_H	BE493850	WHE1276_H	907	317	23.6	681	4	BM267355	BM267355	MEST365-F
835	324	24.1	624	5	BP184421	BP184421	BP184421	BP184421	908	317	23.6	893	4	BI952091	BI952091	HVSMEM000
836	324	24.1	640	5	BQ743388	WHE4103_D	BQ743388	WHE4103_D	909	316.5	23.6	515	7	CK864045	CK864045	35355_In
837	324	24.1	641	4	BM813932	EST592025	BM813932	EST592025	910	316.5	23.6	559	2	BE802841	BE802841	sr45d12.Y
838	324	24.1	649	6	CA290596	SCUTSD102	CA290596	SCUTSD102	911	316.5	23.6	566	2	BE942838	BE942838	EST422417
839	324	24.1	791	3	CNS0AB15	Arabidops	BX818211	Arabidops	912	316.5	23.6	571	7	CN008321	CN008321	WHE2639_H
840	323.5	24.1	546	4	BG096397	EST460916	BG096397	EST460916	913	316.5	23.6	578	2	AW695176	AW695176	GM092D12S
841	323.5	24.1	566	5	BQ762267	EBrc01_SQ	BQ762267	EBrc01_SQ	914	316.5	23.6	580	7	CN517425	CN517425	QO092_B3
842	323.5	24.1	669	6	CD073590	MAB3-0001U	CD073590	MAB3-0001U	915	316.5	23.6	590	2	BF006247	BF006247	EST434745
843	323.5	24.1	669	7	CF507287	USDA-FP_1	CF507287	USDA-FP_1	916	316.5	23.6	595	6	CF092647	CF092647	QHN12F02.
844	323.5	24.1	709	6	CA146291	SCVPR207	CA146291	SCVPR207	917	316.5	23.6	598	2	BE124003	BE124003	EST394128
845	323.5	24.1	796	2	BE034896	ML05H01_M	BE034896	ML05H01_M	918	316.5	23.6	637	5	BQ765794	BQ765794	EBrc03_SQ
846	323.5	24.1	846	7	CK195394	FGAS00383	CK195394	FGAS00383	919	316.5	23.6	643	7	CF518411	CF518411	CAPO007_I
847	323	24.1	803	7	CK200685	FGAS00920	CK200685	FGAS00920	920	316	23.5	669	6	CA187131	CA187131	SCUTST308
848	322.5	24.0	633	7	CF418893	USDA-FP_1	CF418893	USDA-FP_1	921	316	23.5	691	1	AJ613139	AJ613139	BJ313139
849	322.5	24.0	674	7	CK739670	USDA-FP_6	CK739670	USDA-FP_6	922	316	23.5	836	9	CG323590	CG323590	OGWIE57TV
850	322.5	24.0	840	7	CO234257	WHE3952_B	CO234257	WHE3952_B	923	315.5	23.5	526	6	CF059783	CF059783	QCS16904.
851	322	24.0	640	6	CA191213	SCCOT2C0	CA191213	SCCOT2C0	924	315.5	23.5	539	2	AW980337	AW980337	EST391490
852	322	24.0	649	6	CD904272	G356.112P	CD904272	G356.112P	925	315.5	23.5	561	4	BM732615	BM732615	sal79d10.
853	322	24.0	716	4	BI960085	HVSMEN002	BI960085	HVSMEN002	926	315.5	23.5	631	2	AW776700	AW776700	EST335765
854	322	24.0	736	2	BF630555	HVSMEN001	BF630555	HVSMEN001	927	315.5	23.5	702	6	CA179873	CA179873	SCCST200
855	322	24.0	807	7	CF443345	EST679690	CF443345	EST679690	928	315	23.5	442	7	CN966263	CN966263	13760.100
856	321.5	23.9	647	7	CN012727	WHE3952_B	CN012727	WHE3952_B	929	315	23.5	660	5	BQ086305	BQ086305	WHE3577_C
857	321.5	23.9	686	7	CF833210	UCRCS02_0	CF833210	UCRCS02_0	930	315	23.5	739	9	CN013071	CN013071	QXSDT72TV
858	321.5	23.9	754	4	BG584701	EST486462	BG584701	EST486462	931	315	23.5	852	9	CG320079	CG320079	OGXDT72TV
859	321.5	23.9	770	4	BI967327	GM830001B	BI967327	GM830001B	932	315	23.5	880	9	CG229531	CG229531	QGS3060TH
860	321	23.9	616	4	BZ259369	BZ259369	BZ259369	BZ259369	933	314.5	23.4	540	4	BG789661	BG789661	saes3e08.
861	321	23.9	678	6	CA071322	SCACAM107	CA071322	SCACAM107	934	314.5	23.4	562	2	AW683492	AW683492	NF012H09L
862	321	23.9	737	7	CF397756	RTD83_1_C	CF397756	RTD83_1_C	935	314.5	23.4	598	5	BU008292	BU008292	QGH7C13.Y
863	321	23.9	881	7	CK196097	FGAS00454	CK196097	FGAS00454	936	314.5	23.4	616	5	BQ788665	BQ788665	WHE4152_E
864	320.5	23.9	637	7	CN189395	UCRCS06_0	CN189395	UCRCS06_0	937	314.5	23.4	625	2	AW034347	AW034347	EST277918
865	320.5	23.9	643	2	AW695080	NF091D1S	AW695080	NF091D1S	938	314.5	23.4	708	6	CF213537	CF213537	CGF100060
866	320.5	23.9	681	4	BI959659	HVSMEN002	BI959659	HVSMEN002	939	314.5	23.4	776	7	CN987035	CN987035	62721.125
867	320.5	23.9	744	4	BM408348	EST582675	BM408348	EST582675	940	314	23.4	484	2	BF627066	BF627066	HVSMEM000
868	320.5	23.9	904	2	BF972265	602240747	BF972265	602240747	941	313.5	23.3	672	5	BQ460884	BQ460884	HE01017r
869	320	23.8	712	5	BUG72830	NL_6_90_D	BUG72830	NL_6_90_D	942	313.5	23.3	573	2	BE998050	BE998050	EST4229773
870	320	23.8	770	3	CNS0A8E83	ArabIdops	BX818064	ArabIdops	943	313.5	23.3	605	5	BQ970451	BQ970451	QHB42B22.
871	320	23.8	835	4	BM407184	EST581511	BM407184	EST581511	944	313.5	23.3	612	5	BQ699842	BQ699842	NXRVI22_D
872	319.5	23.8	605	1	A1486500	EST2444821	A1486500	EST2444821	945	313.5	23.3	635	5	BQ888753	BQ888753	P012B02_P
873	319.5	23.8	662	6	CA916813	EST640960	CA916813	EST640960	946	313	23.3	486	3	CR640865	CR640865	Tetraxodon
874	319.5	23.8	666	4	CB869763	HC12G06V	CB869763	HC12G06V	947	313	23.3	702	6	CA262688	CA262688	SCPIB202
875	319.5	23.8	670	4	BG455746	NF066H01P	BG455746	NF066H01P	948	313	23.3	709	4	BI073165	BI073165	PIP2A_F04
876	319.5	23.8	740	7	CN011226	WHE3881_F	CN011226	WHE3881_F	949	313	23.3	881	7	CK202172	CK202172	FGAS01069
877	319.5	23.8	748	5	BUG35690	004G05_In	BUG35690	004G05_In	950	312.5	23.3	539	7	CO415038	CO415038	Mdfw2041m
878	319.5	23.8	789	5	BUG94945	X017B10_P	BUG94945	X017B10_P	951	312.5	23.3	540	4	BI788174	BI788174	ea967f01.
879	319	23.8	644	1	A1895091	EST264534	A1895091	EST264534	952	312.5	23.3	545	2	AW620537	AW620537	ej06d09.Y
880	319	23.8	675	6	CA209393	SCCST3C1	CA209393	SCCST3C1	953	312.5	23.3	577	5	BQ490451	BQ490451	24-R01178
881	319	23.8	684	1	AL821924	AL821924	AL821924	AL821924	954	312.5	23.3	606	7	CF807049	CF807049	p8H019xK
882	319	23.8	711	4	BJ253542	BJ253542	BJ253542	BJ253542	955	312.5	23.3	656	2	BF650456	BF650456	NF097D11E
883	319	23.8	756	6	CB680447	OSUNEf05C	CB680447	OSUNEf05C	956	312.5	23.3	670	5	BUB16246	BUB16246	N062C10_P
884	319	23.8	756	7	CF428636	PHI_9_G09	CF428636	PHI_9_G09	957	312.5	23.3	676	6	CD817919	CD817919	BN20.043K
885	319	23.8	819	7	CN127149	RHOH1_21_	CN127149	RHOH1_21_	958	312.5	23.3	704	5	BUB14263	B	

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959	312.5	23.3	706	6	CF233163	PLAJX0002	1032	305	22.7	646	7	CK860977	32005	IN
960	312.5	23.3	754	1	AJ806917	AJ806917	1033	305	22.7	713	6	AW221136	ESTZFL404	
961	312.5	23.3	815	2	BE642551	CR12_6_F2	1034	304.5	22.7	569	2	AW736350	SCST32269	
962	312.5	23.3	817	7	CK193931	FGAS00235	1035	304.5	22.7	594	2	CK319292	RTPD9504	
963	312.5	23.3	963	7	CG935465	SL1-0818	1036	304.5	22.7	745	7	CF397680	RTD3_1_C	
964	312	23.2	647	4	BJ264257	BZ264257	1037	304.5	22.7	768	6	CD839106	RF02_114A	
965	312	23.2	726	6	CA158055	SCBZR2305	1038	304.5	22.7	831	7	CK201781	FGAS01030	
966	312	23.2	816	8	BZ541105	OGAET43TC	1039	304	22.6	302	2	BF605771	272357_MA	
967	311.5	23.2	605	6	CA733178	w1p1c.pk0	1040	304	22.6	592	4	BM660366	952037B06	
968	311.5	23.2	611	4	BI957501	RVSMD000	1041	304	22.6	622	6	CA182599	SCBSTR314	
969	311.5	23.2	622	7	CF395203	HYDS2_10	1042	304	22.6	647	6	CA285613	SCBSTR107	
970	311	23.2	742	6	CA146092	SCVPR207	1043	304	22.6	661	6	CA107862	TALR1141H	
971	310.5	23.1	559	4	BI894075	SA159906	1044	304	22.6	677	6	CG905724	SCBSTR105	
972	310.5	23.1	608	7	CK318739	X9P02911	1045	304	22.6	685	6	CA121225	SCBGLR109	
973	310.5	23.1	616	5	B0139156	USDA-FP_1	1046	303.5	22.6	511	7	CF603338	BACCA01_0	
974	310.5	23.1	624	7	CF4117506	NFO11F12P	1047	303.5	22.6	618	7	CF6010871	WHE3877_C	
975	310.5	23.1	638	4	BI957710	HVSMEN00	1048	303.5	22.6	632	1	AI486948	ESTZ45270	
976	310.5	23.1	650	2	BF646063	USDA-FP_1	1049	303.5	22.6	609	1	AU263882	AU263882	
977	310.5	23.1	735	5	B0835879	RF066810E	1050	303	22.6	679	6	CD823836	BN25_050C	
978	310.5	23.1	756	7	CK879029	TO79G08_P	1051	303	22.6	814	7	CK201094	FGAS00961	
979	310	23.1	447	7	CK879029	SGP143200	1052	302.5	22.5	577	2	AW703717	sk23607.Y	
980	310	23.1	654	6	CK175542	SCJLST101	1053	302.5	22.5	588	1	AL808354	AL808354	
981	310	23.1	699	5	BK251392	BK251392	1054	302.5	22.5	659	6	CA089962	SCSGAM207	
982	310	23.1	802	2	BF261040	354522_MA	1055	302	22.5	636	4	BJ259464	BJ259464	
983	309.5	23.0	505	4	BG835402	EST313943	1056	302	22.5	674	5	EX251216	EX251216	
984	309.5	23.0	565	2	AW625126	EST313943	1057	302	22.5	675	5	EX250520	EX250520	
985	309.5	23.0	613	4	BI309404	EST313943	1058	302	22.5	675	5	EX250520	EX250520	
986	309.5	23.0	691	7	CN524624	GO15M16	1059	302	22.5	689	5	CA142664	SCMCR210	
987	309.5	23.0	756	6	CD842950	CD842950	1060	302	22.5	692	6	CA142664	SCMCR210	
988	309.5	23.0	781	5	B0895541	WHE2309_A	1061	302	22.5	784	6	CD840817	FGAS01088	
989	309	23.0	489	7	CF931812	EST0244_A	1062	302	22.5	814	7	CK203270	W500111_B	
990	309	23.0	536	2	BF484161	WHE2309_A	1063	301.5	22.4	548	1	AI899227	ESTZ68670	
991	309	23.0	638	7	CF972935	PSU_108E	1064	301.5	22.4	588	1	AL822798	AL822798	
992	309	23.0	718	6	CD888511	GI18_108E	1065	301.5	22.4	643	5	B0880080	UM41TB11	
993	308.5	23.0	507	7	CF972935	PSU_108E	1066	301	22.4	600	2	AW306980	8F51C05.Y	
994	308.5	23.0	585	2	AW690185	NF029D09S	1067	301	22.4	622	4	BI679740	949078E04	
995	308.5	23.0	712	7	CO361980	NF029D09S	1068	301	22.4	652	6	CD847394	DM08582H	
996	308.5	23.0	759	6	CD879592	NDL2_8_G1	1069	301	22.4	666	7	CO532808	3530_1_21	
997	308.5	23.0	834	7	CF233249	AZ04_105M	1070	301	22.4	702	7	CO230270	W500111_B	
998	308.5	23.0	872	7	CO489149	QO258.B7	1071	300.5	22.4	560	4	BM85724	8AM04D08	
999	308	22.9	520	1	AU164541	AU164541	1072	300.5	22.4	578	4	BM086659	WHE31461_D	
1000	308	22.9	626	2	BE423372	WHE0065_D	1073	300.5	22.4	591	1	AA660318	00189_MER	
1001	307.5	22.9	535	5	BQ624278	USDA-FP_0	1074	300.5	22.4	600	4	AA660318	00189_MER	
1002	307.5	22.9	598	2	AW071192	sk22a02.Y	1075	300.5	22.4	636	7	CK606552	gmhrhw6-	
1003	307.5	22.9	673	5	BQ991852	QGF24A02	1076	300.5	22.4	637	7	CK606552	gmhrhw6-	
1004	307.5	22.9	765	2	BE705618	SC01_03G1	1077	300.5	22.4	661	7	CK987646	SP7-B5(P1	
1005	307.5	22.9	772	6	CF229531	PCAXN0026	1078	300.5	22.4	690	6	BQ518761	ESTZ62176	
1006	307.5	22.9	775	6	CD839277	RFO2_114K	1079	300.5	22.4	800	5	BQ518761	ESTZ62176	
1007	307	22.9	605	6	CD895487	GL74_001P	1080	300	22.3	550	6	CA107671	SCUHR107	
1008	306.5	22.8	503	1	AI898952	ESTZ68395	1081	300	22.3	679	6	CA253440	SCUHR1410	
1009	306.5	22.8	534	2	AW287882	ESTZ68395	1082	300	22.3	685	5	BUL03556	SCCCHR100	
1010	306.5	22.8	535	2	BE574803	N100726e	1083	300	22.3	685	5	BUL03556	SCCCHR100	
1011	306.5	22.8	546	1	AL827353	H20_TripH	1084	299.5	22.3	516	6	EM402624	SLA006D04	
1012	306.5	22.8	580	1	AU261430	AU261430	1085	299.5	22.3	551	1	AL828595	AL828595	
1013	306.5	22.8	618	4	BQ453059	NF089HILL	1086	299.5	22.3	584	1	AI898101	ESTZ67544	
1014	306.5	22.8	664	4	BT308484	EST529894	1087	299.5	22.3	603	7	CF445936	ESTZ682955	
1015	306.5	22.8	668	5	BUR87057	R054A07_P	1088	299.5	22.3	605	7	CF445936	ESTZ682955	
1016	306.5	22.8	694	4	BUR87057	R054A07_P	1089	299.5	22.3	627	7	BG299397	HVSMEN001	
1017	306	22.8	626	4	BM895773	952065C05	1090	299.5	22.3	699	7	CF653377	USDA-FP_0	
1018	306	22.8	664	1	AJ802646	AJ802646	1091	299	22.3	689	7	CF653377	USDA-FP_0	
1019	306	22.8	692	6	CA168805	SCBSTR101	1092	298.5	22.2	531	2	BE124333	ESTZ393368	
1020	306	22.8	698	1	AJ803239	AJ803239	1093	298.5	22.2	534	1	AI443130	ESTZ393368	
1021	306	22.8	727	6	CA219139	SCRFAD111	1094	298.5	22.2	590	5	BUS77914	8AR34D04	
1022	306	22.8	805	8	B2533265	WHE2602_F	1095	298.5	22.2	600	9	CR180853	Forward_B	
1023	305.5	22.7	454	4	EM136098	WHE2602_F	1096	298.5	22.2	612	7	CK745975	Forward_B	
1024	305.5	22.7	476	6	CA117774	SCBGLR104	1097	298.5	22.2	630	7	CK745975	Forward_B	
1025	305.5	22.7	544	4	BM527684	SA164F09	1098	298.5	22.2	640	6	CA835476	CA835476	
1026	305.5	22.7	561	1	AL819807	AL819807	1099	298.5	22.2	766	6	CF236578	CF236578	
1027	305.5	22.7	564	4	BM085705	SAJ28G08	1100	298.5	22.2	805	2	AW350997	GM210010A	
1028	305.5	22.7	572	5	BQ473426	SAJ28G08	1101	298.5	22.2	823	2	BF256995	HVSMEN001	
1029	305.5	22.7	696	6	CA085150	SCBSTR206	1102	298.5	22.2	1049	7	CK163799	FGAS01643	
1030	305.5	22.7	802	6	CA180913	SCACST316	1103	298	22.2	592	4	BI478930	949071A06	
1031	305.5	22.7	851	7	CK201455	FGAS00997	1104	298	22.2	673	6	CA234708	SCJLSB106	

c1105	298	22.2	724	4	BJ572947	1178	290.5	21.6	820	7	CF443771	CF443771	EST80116
1106	297.5	22.2	509	4	BJ549094	1179	290	21.6	648	5	BQ743293	BQ743293	WHE4102.D
1107	297.5	22.2	561	2	BE450736	1180	290	21.6	655	4	BI960535	BI960535	HVSMEN002
1108	297.5	22.2	636	6	CD934106	1181	290	21.6	673	6	CA220527	CA220527	SCRJFLA02
1109	297.5	22.2	659	2	BF646182	1182	290	21.6	679	6	CA141617	CA141617	SCRJFLA205
1110	297.5	22.2	688	1	AV821843	1183	290	21.6	705	2	AW278810	AW278810	sf98906.Y
1111	297.5	22.2	713	7	CN146262	1184	290	21.6	707	7	CN988152	CN988152	63924.125
1112	297.5	22.2	744	6	CD430220	1185	290.5	21.6	561	4	EM269671	EM269671	sak02904.
1113	297	22.1	622	6	CA137725	1186	289.5	21.6	646	7	CO488997	CO488997	QO02510.B
1114	297	22.1	673	4	BN371957	1187	289	21.5	895	7	CO529747	CO529747	3530.1.19
c1115	297	22.1	927	7	CO480346	1188	289	21.5	650	2	BF260414	BF260414	HVSMENf002
1116	296.5	22.1	477	1	AU262139	1189	289	21.5	676	7	CF671538	CF671538	RTCNT1.57
1117	296.5	22.1	537	7	BE490625	1190	289	21.5	702	7	CN123933	CN123933	RHOH1.D
1118	296.5	22.1	586	7	CF419317	1191	289	21.5	732	3	CNS0A750	CNS0A750	ArabiDops
1119	296.5	22.1	664	1	AL820289	1192	289	21.5	826	7	CN128942	CN128942	RHOH1.32
1120	296.5	22.1	687	6	CD820187	1193	288.5	21.5	540	4	BI779178	BI779178	EBR001.SQ
1121	296.5	22.1	834	7	CO369560	1194	288.5	21.5	559	1	AU263008	AU263008	AU263008
1122	296	22.0	646	2	AW695899	c1195	288.5	21.5	636	6	CD932185	CD932185	GR45.117C
1123	296	22.0	670	5	BU998750	c1196	288	21.4	690	6	CD918343	CD918343	G608.109A
1124	296	22.0	691	6	CA182059	1197	288	21.4	696	6	CA280310	CA280310	SCVFLB2C0
c1125	296	22.0	742	5	BQ634193	c1198	287.5	21.4	510	4	BN357022	BN357022	151V-H8.T
1126	296	22.0	1090	7	CK216386	1199	287.5	21.4	550	2	AW278618	AW278618	sf45h04.Y
1127	295.5	22.0	511	4	BG262486	1200	287.5	21.4	554	5	BX682301	BX682301	EX682301
1128	295.5	22.0	529	2	BF598865	1201	287.5	21.4	577	4	BM086141	BM086141	eah36a07.
1129	295.5	22.0	564	2	BE998654	1202	287.5	21.4	634	6	CA136726	CA136726	SCQRT103
1130	295.5	22.0	589	6	CA018785	1203	287.5	21.4	634	6	CA823264	CA823264	R23C02.tw
1131	295.5	22.0	605	2	AW776435	1204	287.5	21.4	643	9	CL561927	CL561927	OB_Ba002
1132	295.5	22.0	641	1	AL827928	c1205	287.5	21.4	655	5	BQ750517	BQ750517	EST83253
1133	295.5	22.0	654	7	CF575000	c1206	287.5	21.4	703	4	BM407958	BM407958	EST582285
1134	295.5	22.0	672	6	CD825507	1207	287.5	21.4	777	5	BP133915	BP133915	BP133915
1135	295	22.0	571	6	CB399845	1208	287	21.4	593	5	BU579330	BU579330	sa579a02.
1136	295	22.0	670	7	CF433879	1209	287	21.4	630	6	CA191567	CA191567	SCCRTC2C0
c1137	295	22.0	701	4	BJ569035	1210	287	21.4	691	5	BQ840928	BQ840928	WHE4205.B
1138	294.5	21.9	803	4	BI956671	1211	287	21.4	729	8	BZ635220	BZ635220	OGCAG327C
1139	294	21.9	571	1	AU246119	1212	287	21.4	753	7	CF471006	CF471006	RTD51.15
1140	294	21.9	613	6	CD911360	c1213	287	21.4	774	6	CB651301	CB651301	OSJNEB16D
1141	294	21.9	692	4	BI978962	c1214	287	21.4	795	7	CO176253	CO176253	NDL1.60.G
c1142	294	21.9	722	4	BU576352	1215	287	21.4	807	7	CF663779	CF663779	RTCNT1.5
1143	293.5	21.9	556	2	BE124175	1216	287	21.4	860	7	CO365601	CO365601	RTK1.18.C
c1144	293.5	21.9	630	7	CO174797	1217	287	21.4	919	9	CG235840	CG235840	OG3AC56TV
c1145	293.5	21.9	681	6	CF213698	1218	286.5	21.3	584	5	BQ623631	BQ623631	USDA-FP.0
1146	293.5	21.9	697	7	CK863140	1219	286.5	21.3	595	6	CB075138	CB075138	hx15g02_b
c1147	293.5	21.9	785	4	BG320047	1220	286.5	21.3	623	6	CA821671	CA821671	RSU06A03
c1148	293	21.8	781	7	CO174891	1221	286	21.3	387	1	AU179319	AU179319	AU179319
1149	292.5	21.8	489	2	BE500470	c1222	286	21.3	438	6	C23182	C23182	C23182 Japa
1150	292.5	21.8	496	2	BE330982	1223	286	21.3	568	1	AU267141	AU267141	AU267141
1151	292.5	21.8	496	5	B0247189	1224	286	21.3	569	1	AU270834	AU270834	AU270834
1152	292.5	21.8	518	4	BG300054	1225	286	21.3	577	1	AU264259	AU264259	AU264259
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1154	292.5	21.8	573	2	BF065160	1227	286	21.3	609	6	CA139015	CA139015	SCCQLR107
1155	292.5	21.8	573	6	CD877325	1228	286	21.3	649	6	CA120549	CA120549	SCCQLR107
1156	292.5	21.8	588	1	AA660308	1229	286	21.3	668	4	BI959395	BI959395	HVSMEN001
1157	292.5	21.8	590	4	BI779395	1230	286	21.3	866	7	CF667338	CF667338	RTCNT1.29
1158	292.5	21.8	617	5	BQ611858	1231	285.5	21.3	517	4	BI205825	BI205825	EST523865
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1163	291.5	21.7	580	4	BM100502	1236	285	21.2	641	6	CB651300	CB651300	OSJNEB16D
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1176	290.5	21.6	711	6	CA921232	1249	284	21.1	619	5	BU030545	BU030545	OHJ15L05.
c1177	290.5	21.6	765	7	CO369642	1250	284	21.1	692	7	CK099634	CK099634	A078P58.5

[illegible]

1397	271.5	20.2	448	1	AU182287	AU182287	1470	266	19.8	456	2	BE050598	BE050598	2a67f09.b
1398	271.5	20.2	569	5	B0691157	B0691157	1471	266	19.8	587	6	CA208078	CA208078	SCMCSB111
1399	271.5	20.2	570	2	BE315693	NF025B04L	1472	266	19.8	614	7	CF476774	CF476774	RTW3_3.C
1400	271.5	20.2	586	7	CF471684	RTD31_6.C	1473	266	19.8	722	6	CD843176	CD843176	CD843176.F02.130N
1401	271.5	20.2	562	4	BI271859	NF013H06F	1474	266	19.8	705	6	CD838653	CD838653	RFO2.132B
1402	271.5	20.2	664	7	CF470189	RTD51_18	1475	266	19.8	773	7	CN988195	CN988195	63972.125
1403	271.5	20.2	712	7	CN949776	XXXP184.N	1476	265.5	19.8	450	2	AW102314	AW102314	sd86b06.y
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1405	271	20.2	569	7	CN517932	QO092.B3	1478	265.5	19.8	536	4	BM178915	BM178915	saJ61a08.
1406	271	20.2	647	6	CD845559	RFO2.143N	1479	265.5	19.8	569	1	AJ798214	AJ798214	AJ798214
1407	271	20.2	774	7	CO176680	NDL1_63.B	1480	265.5	19.8	621	4	BJ577619	BJ577619	UIJ7619
1408	271	20.2	805	7	CO176182	NDL1_60.G	1481	265	19.7	193	2	BS863248	BS863248	UIJ-M-BHO-
1409	271	20.2	812	8	BZ635847	OGCCR44TM	1482	265	19.7	577	6	CD933864	CD933864	GR45.122E
1410	270.5	20.1	493	4	BG263195	WHE2339.B	1483	265	19.7	715	6	CD840162	CD840162	RFO2.118D
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1415	270.5	20.1	648	6	CD878345	AZO4.102I	1488	264.5	19.7	641	5	BH94619	BH94619	XO12C02.P
1416	270	20.1	498	2	BF293046	WHE2159.G	1489	264.5	19.7	692	6	CB653599	CB653599	OSUNEC04M
1417	270	20.1	543	5	BQ660910	HM01A23w	1490	264	19.7	412	4	BQ68207	BQ68207	H3062H08-
1418	270	20.1	569	4	BI321039	saf47d06.	1491	264	19.7	626	1	AJ615113	AJ615113	AJ615113
1419	270	20.1	649	4	BI958809	HVSMEN001	1492	264	19.7	725	7	CO168700	CO168700	NDL1_1.H0
1420	270	20.1	656	7	CF669134	RTCNT1_40	1493	263.5	19.6	554	6	CA686379	CA686379	wlm96.DKO
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1428	270	20.1	741	7	CF478061	RTW3_17								
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1436	269.5	20.1	651	7	CF479933	POL1_62.E								
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1438	269	20.0	559	2	AW625461	EST319368								
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1440	269	20.0	722	6	CD838645	RFO2.112B								
1441	269	20.0	773	7	CA132666	Ox1_7.B07								
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1449	268.5	20.0	716	6	CD840581	RFO2.1190								
1450	268	20.0	440	4	BI450513	kt26509.y								
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1466	266.5	19.8	612	5	BQ587490	E012341-0								
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ALIGNMENTS

RESULT 1	BM451059	889 bp	linear	EST 05-FEB-2002
BM451059	AGENCYCOURT_6392456	NIH_MGC_67	Homo sapiens	cDNA clone IMAGE:5494999
LOCUS	5', mRNA	sequence.		
DEFINITION	BM451059	889 bp	mRNA	
ACCESSION	BM451059.1	GI:18500099		
VERSION	EST.			
KEYWORDS	EST.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
TITLE	1 (bases 1 to 889)			
JOURNAL	NIH-MGC http://mgc.nci.nih.gov/.			
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC)			
	Unpublished (1999)			
	Contact: Robert Strausberg, Ph.D.			
	Email: cgapbs-remail.nih.gov			
	Tissue Procurement: ATCC			
	cDNA Library Preparation: Life Technologies, Inc.			
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)			
	DNA Sequencing by: Agencourt Bioscience Corporation			
	Clone distribution: MGC clone distribution information can be			
	found through the I.M.A.G.E. Consortium/ILNL at:			
	http://image.llnl.gov			
	Plate: L1AM12121 row: d column: 08			
	High quality sequence stop: 665.			
FEATURES	Location/Qualifiers			
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	/tissue_type="retinoblastoma"			
	/lab_host="DH10B (phage-resistant)"			
	/clone_lib="NIH_MGC_67"			
	Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.			

Average insert size 1.75 kb. Library constructed by Life Technologies."

ORIGIN	Alignment Scores:	2.86e-125	Length:	889
	Pred. No.:	1330.00	Matches:	262
	Percent Similarity:	99.62%	Conservative:	0
	Best Local Similarity:	99.62%	Mismatches:	0
	Query Match:	99.03%	Indels:	1
	DB:	4	Gaps:	0
US-10-017-407A-306 (1-262) x BM051236 (1-889)				
QY	1	MetThrGlnProValProArgLeuSerValProAlaLeuAlaLeuAlaLeuGlySerAlaAla	20	
Db	13	ATGACCCAGCGGTGCGCGGCTCTCCGTCGCCCGCGGCTGGCCCTGAGCGCA	72	
QY	21	LeuGlyAlaAlaPheAlaThrGlyLeuPheLeuGlyArgArgCysProProTrpArgGly	40	
Db	73	CTGGCGCGCGCTTCCGCACTGGCTCTTCTGCGGAGCGGTGCCCCCATGCGAGGC	132	
QY	41	ArgArgGluGlnCysLeuLeuProGluAspSerArgLeuTrpGlnTyrLeuLeuSer	60	
Db	133	CGCGAGAGCAGTGTCTTCCCCCGAGGACCGCGCTGTGCGATATCTTCTGAGC	192	
QY	61	ArgSerMetArgGluHisProAlaLeuArgSerLeuArgLeuLeuThrLeuGlnPro	80	
Db	193	CGCTCATCGGAGGACCCGCGGCTGCGAGCTGAGCTGTGACCTGGAGCAGCG	252	
QY	81	GlnGlyAspSerMetThrCysGlnGlnAlaGlnLeuLeuAlaAsnLeuAlaArgLeu	100	
Db	253	CAGGGGATTTCTATGATGACCTGCGAGGAGCGGCTTCTGGCCAACTGGCGGGCTC	312	
QY	101	IleGlnAlaGlyAlaLeuAspLeuGlyThrPheThrGlyTyrSerAlaLeuAlaLeu	120	
Db	313	ATCCAGGCCAGAGGCGGTGAGCTGGGACCTTCCGCGGCTACTCCGCGCTGGCCCTG	372	
QY	121	AlaLeuAlaLeuProAlaAspGlyArgValValThrCysGluValAspAlaGlnPro	140	
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QY	161	LysProAlaLeuGluThrLeuAspGluLeuLeuAlaAlaGlyClnAlaGlyThrPheAsp	180	
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QY	181	ValAlaValValAspAlaAspLysGluAsnCysSerAlaTyrTyrGluArgCysLeuGln	200	
Db	553	GTGGCCGTGTGGATGGGACAGAGAACTGTCCGCTACTACGAGCGCTCGCTGCGAG	612	
QY	201	LeuLeuArgProGlyGlyIleLeuAlaValLeuArgValLeuTrpArgGlyLysValLeu	220	
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QY	221	GlnProProLysGlyAspValAlaAlaGlyCysValArgAsnLeuAsnGluArgIleArg	240	
Db	673	CAACCTCCGAAAGGAGGAGCTGGCGCGGAGTGTGTGGAACCTTAACGAAACGATCCGG	732	
QY	241	ArgAspValArgValTyrIleSerLeuLeuProLeuGlyAspGlyLeuThrLeu-Alaph	260	
Db	733	CGGGACGTGAGGCTTACATGAGCTCTGCCCCCTGGCGGATGACTCACCTTGGGCTT	792	
QY	260	elysile 262		
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RESULT 2
BM051236
LOCUS

EST 07-NOV-2001

DEFINITION

603634191F1 NIH_MGC_43 Homo sapiens cDNA clone IMAGE:5424766 5', mRNA sequence.

ACCESSION BM051236

VERSION BM051236.1 GI:16780503

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 814)
NIH-MGC <http://mgc.nci.nih.gov/>

AUTHORS

National Institutes of Health, Mammalian Gene Collection (MGC)

TITLE

Unpublished (1999)

JOURNAL

COMMENT

Contact: Robert Strausberg, Ph.D.
Email: cgabbs@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>

Plate: LLCM1886 row: e column: 23

High quality sequence stop: 811.

FEATURES

source

1..814
Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5424766"
/tissue_type="normal pigmented retinal epithelium"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_43"
/notes="Organ: eye; Vector: pORF7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library. |"

ORIGIN

Alignment Scores:
Pred. No.: 4.54e-118 Length: 814
Score: 1259.00 Matches: 259
Percent Similarity: 97.74% Conservative: 0
Best Local Similarity: 97.74% Mismatches: 1
Query Match: 93.75% Indels: 5
DB: 4 Gaps: 0

US-10-017-407A-306 (1-262) x BM051236 (1-814)

QY 3 GlnProValProArgLeuSerValProAlaLeuAlaLeuGlySerAlaAlaLeuGly 22

Db 4 CAGCGGTGCGCGGCTCTCGGTGCGCGCGCTGCGCGCTGCGCGCTGCGCGCTGCGC 63

QY 23 AlaAlaPheAlaThrGlyLeuPheLeuGlyArgArgCysProProTrpArgGlyArg 42

Db 64 GCGCGCTTGGCCACCTGCGCTCTTCTGGGAGGCGGTGCCCCCATGCGAGCGCGGCGA 123

QY 43 GluGlnCysLeuLeuProGluAspSerArgLeuTrpGlnTyrLeuLeuSerArgSer 62

Db 124 GAGCAGTGGCTGCTTCCCCCGAGGACAGCGCGCTGTGGCAGTATCTTCTGAGCGCGTCC 183

QY 63 MetArgGluHisProAlaLeuArgSerLeuArgLeuLeuThrLeuGlnGlnProGlnGly 82

Db 184 ATGCGGGAGCACCGCGCTGCGAGGCTGTGAGCTGTGACCTTGAGAGCAGCGCGAGGG 243

QY 83 AspSerMetMetThrCysGluGlnAlaGlnLeuLeuAlaAsnLeuAlaArgLeuLeuGln 102

Db 244 GATTCTATGATGACCTGCGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 303


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QY 103 AlaLysLysAlaLeuAspLeuGlyThrPheThrGlyTyrSerAlaLeuAlaLeuAlaLeu 122
Db 304 GCCAAGAAGGCGCTGGACCTGGGCACTTACGGGGCTACTCGCCCTGGCCCTGGCCCTG 363

QY 123 AlaLeuProAlaAspGlyArgValThrCysGluValAspAlaGlnProProGluLeu 142
Db 364 GCGTGGCCCGGAGCGGCGGCTGTGACCTGGAGGTGGAGCGCGACGCCCGCGAGCTG 423

QY 143 GlyArgProLeuTTPArgGlnAlaGluAlaGluHisLysIleAspLeuArgLeuLysPro 162
Db 424 GGACGGCCCTGTGTGAGGAGCGCGGAGCGGAGCAAGATCGACCTCGGCTGAAGGCC 483

QY 163 AlaLeuGluThrLeuAspGluLeuLeuAlaGly-GluAla-GlyThrPheAspValA 182
Db 484 GCTTGGAGACCTCGAGAGCTGTGTGGCGGGCCGAGGCGCGGCACTTCGACGTTGG 543

QY 182 laValValAspAlaAspLysGluAenCysSerAlaTyrTyrGluArgCysLeuGln-Leu 201
Db 544 CCGTGTGTGATCGGACAGGAGAACTGCTCGCCCTACTACGAGCGCTGCTGCACTTG 603

QY 202 LeuArgProGlyGlyIleLeuAlaValLeuArgValLeuTTPArgGlyLysValLeuGln 221
Db 604 CTGGACCGGAGGATCTCGCCCTCTCAGAGTCTGTGGCGGGGAAAGTGTGCAA 663

QY 222 ProProLysGlyAspValAlaAlaGluCys-ValArgAsnLeuAenGluArg-IleArgA 241
Db 664 CCTCGAAGGGGAGCTGGCGCGGAGTGTGTGCGAAACCTTAAACGACGCGATCCGGC 723

QY 241 rGAspValArgValTyrIleSerLeuLeuProLeuGlyAspGlyLeuAlaPheL 261
Db 724 GGGAGTCTAGGGTCTACATCATGCTCTTCCCTGGCGGAGTGGACTCACCTTGGCTTCA 783

QY 261 Ysile 262
Db 784 AGATC 788

RESULT 3
LOCUS CR602194
DEFINITION full-length cDNA clone CS0D1073YH02 of Placenta Cot 25-normalized
of Homo sapiens (human).
ACCESSION CR602194
VERSION CR602194.1 GI:50483001
KEYWORDS HTC; cNSLT cDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1308)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished
Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue
Genoscope.
2 (bases 1 to 1308)
Direct Submission
Genoscope.
SUBMITTED (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqrefgenoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
Location/Qualifiers
1..1308
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0D1073YH02"
/tissue_type="Placenta Cot 25-normalized"

FEATURES
source

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ORIGIN
Alignment Scores:
Pred. No.: 1,3e-114 Length: 1308
Score: 1228.00 Matches: 262
Percent Similarity: 62.23% Conservative: 0
Best Local Similarity: 62.23% Mismatches: 0
Query Match: 91.44% Indels: 159
DB: 3 Gaps: 2

US-10-017-407A-306 (1-262) x CR602194 (1-1308)

QY 1 MetThrGlnProValProArgLeuSerValProAlaAlaLeuAlaLeuGlySerAlaAla 20
Db 6 ATGACCCAGCGCGTGGCCCGGCTCTCCGTGGCCCGCGGCTGGCCCTGGGCTCAGCCGCA 65

QY 21 LeuGlyAlaAlaPheAlaThrGlyLeuPheLeu----- 31
Db 66 CTGGCGCGGCTTTCGCCACTGGCCCTTCTCTGGGTGAGCAGGACCTGGTCCCGGGGGC 125

QY 31 ----- 31
Db 126 GSETGGGCGGCGCAGAGTAGGGCGGCGTGGCTCAGGTTAATCCACACCCTCTCTCCC 185

QY 32 ----GlyArgArgCysProTTPArgGlyArgArgGluGlnCysLeuLeuProProGln 50
Db 186 GTCAAGGAGGCGGTGCCCCCATGCGCAGGCGCGGAGCAGTGCCTTCTCCGCCCA 245

QY 50 uAspSerArgLeuTTPGlnTyrLeuLeuSerArgSerMetArgGluHisProAlaLeuAr 70
Db 246 GGACAGCGCCTGTGGCAGTATCTTCTCAGCGCGTCCATGCGGGAGCACCCGCGCGTGG 305

QY 70 gSerLeuArgLeuLeuThrLeuGluGlnProGlnGlyAspSerMetThrCysGluGln 90
Db 306 AAGCTGAGGTGCTGACCTTGGAGCAGCGCAGGGGGATTTCTATGATGACCTTCGAGCA 365

QY 90 nAlaGlnLeuAlaAlaLeuAlaArgLeuIleGlnAlaLysLysAlaLeuAspLeuGln 110
Db 366 GCGCCAGCTCTTGGCCCAACCTTGGCGCGCTCATTCAGGCCAAGAGGCGCTGACCTGG 425

QY 110 YThrPheThrGlyTyrSerAlaLeuAlaLeuAlaLeuAlaLeuProAlaAspGlyArgVa 130
Db 426 CACCTTACAGGGCTACTCCGCCCTGGCCCTGGCCCTGGCCCTGGCCGAGCGGCGGT 485

QY 130 lValThrCysGluValAspAlaGlnProProGluLeuGlyArgProLeuTTPArgGlnAl 150
Db 486 GGTGACCTGCGAGGTGGAGCGCGCAGCCCGCGAGCTGGGACGGCCCTTGTGGAGGCGGC 545

QY 150 aGluAlaGluHisLysIleAspLeuArgLeuLysProAlaLeuGluThrLeuAspGluLe 170
Db 546 CGAGCGGAGCACAAGATCGACCTCGGCTGAAGCCCGCTTGGAGACCTTCGACGAGCT 605

QY 170 uLeuAlaAlaGlyGluAlaGlyThrPheAspValAlaValAlaAspAlaAspLysGluAs 190
Db 606 GCTGGCGGCGGCGAGGCGCGCACCTTCGAGCTGGCCCTGGTGGTGGATGGGCAAGAGAAA 665

QY 190 nCysSerAlaTyrTyrGluArgCysLeuGlnLeuLeuArgProGlyGlyIleLeuAlaVa 210
Db 666 CTGCTCCGCCCTACTACGAGCGCTGCCTGCAGCTGCTGCGACCCCGGAGGAGCATCTCGCCGT 725

QY 210 lLeuArg----- 212
Db 726 CTTCAGATGAAGGATCCACTCGCGGGGAGGAGAAAGCACCTGTGCGGCGCGGTGCCCA 785

QY 212 ----- 212
Db 786 TCTTTTCCCTTGACTCTCTTTATACCCCAAGCCCCACCCAGTCCAGTCAAGTACAGCTAC 845

QY 212 ----- 212
Db 846 ACCCCCTCCGGGGCTCCGGCCCGGTACCCAGGCTTTTCTCGGCTTTGTTCTGTCTCCA 905

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QY 212 ----- 212
Db 906 GCTCTGTACCTCTGCGCGGACCTCTCCCTCGAGGCGCGCTCCCGCCGACACAC 965
QY 212 ----- 212
Db 966 TCCCTCGAGACCGCGCTTCCGTCTGGCACCTCTCCCTCCAGACCGCGCTCCGCGCG 1025
QY 212 ----- 212
Db 1026 GGCACCTCCCTCCAGTCCCGGCTTCCGCGCGGACACCTCCCTCCGAGCGCGCGCTC 1085
QY 213 ----- 213
Db 1086 CCACGCGCGGTGCGCGCGCGCTCCCGCGAGTCTGTGGCGGGAAGGTGTGCAACC 1145
QY 222 oProlyGlyAspValAlaAlaGluCysValArgAsnLeuAsnGluArgAs 242
Db 1146 TCCGAAAGGGACGTGGCGCGCGAGTGTGTGCGGAAACCTAAACGACCATCCGCGCGGA 1205
QY 242 pValArgValTyrIleSerLeuProLeuGlyAspGlyLeuThrLeuAlaPheLysI 262
Db 1206 CCGTACGGGTCTACATCAGCTCTCTCCCTCGCGATGACTCACCCTTGGCTTCAAGAT 1265
QY 262 e 262
Db 1266 C 1266

RESULT 4
BF663323 1006 bp mRNA linear EST 21-DEC-2000
LOCUS 602144463F1 NTH_MGC_48 Homo sapiens cDNA clone IMAGE:4297911 5',
DEFINITION mRNA sequence.
ACCESSION BF663323
VERSION 1 (bases 1 to 1006)
KEYWORDS NTH-MGC http://mgi.nci.nih.gov/
SOURCE National Institutes of Health, Mammalian Gene Collection (MGC)
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1006)
AUTHORS NTH-MGC http://mgi.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-x@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: King Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLCMI152 row: m column: 16
High quality sequence stop: 745.
FEATURES
Location/Qualifiers
1..1006
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4297911"
/tissue_type="Primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NTH MGC 48"
/notes="Organ: B-cells; Vector: pOTB7; Site 1: XhoI;
Site 2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by King
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NTH_MGC Library."

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ORIGIN

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Alignment Scores: 2.43e-113 Length: 1006
Pred. No.: 1214.00 Matches: 251
Score: 96.56% Conservative: 2
Percent Similarity: 95.80% Mismatches: 5
Best Local Similarity: 90.39% Indels: 5
Query Match: 2 Gaps: 0
DB:

US-10-017-407A-306 (1-262) x BF663323 (1-1006)
QY 1 MetThrGlnProValProArgLeuSerValProAlaAlaLeuAlaLeuGlySerAlaAla 20
Db 7 ATGACCCAGCGCTGCCCGCGCTCTCCGTGCGCGCGCGCTGGCCCTGGGCTCAGCCGCA 66
QY 21 LeuGlyAlaAlaPheAlaThrGlyLeuPheLeuGlyArgCysProProTrpArgGly 40
Db 67 CTGGCGCGCGCTTCCGCACTGGCCCTCTTCTGGGAGGCGGTGCCCCCATGGCGAGGC 126
QY 41 ArgArgGluGlnCysLeuLeuProGluAspSerArgLeuTrpGlnTyrIleLeuSer 60
Db 127 CGCGGAGAGCAGTGGCTCTTCCCGGAGGACAGCGCGCTGTGGCAGTATCTTCTGAGC 186
QY 61 ArgSerMetArgGluHisProAlaLeuArgSerLeuArgLeuLeuThrLeuGlnPro 80
Db 187 CGCTCCATCGGAGACACCGCGCGCTGCGAAGCTGAGGCTGTGACCTCTGGCAGCGC 246
QY 81 GlnGlyAspSerMetThrCysGluGlnAlaGlnLeuLeuAlaAsnLeuAlaArgLeu 100
Db 247 CAGCGGATTCATGATGACCTGCGAGGAGCGCGCTCTTGGCCAACTGGCGCGGCTC 306
QY 101 IleGlnAlaLysLysAlaLeuAspLeuGlyThrPheThrGlyTyrSerAlaLeuAlaLeu 120
Db 307 ATCCAGGCAAGAAGCGCTGGACCTTCCGCGCGCTTCCGCGCGCTTCCGCGCGCTG 366
QY 121 AlaLeuAlaLeuProAlaAspGlyArgValValThrCysGluValAlaAspAlaGlnPro 140
Db 367 GCCCTGGCGCTTCCCGCGCGCGCGCGCTGTGTGACCTGGAGGTGGACGCGCGCGCG 426
QY 141 GluLeuGlyArgProLeuTrpArgGlnAlaGluAlaGluHisLysIleAspLeuArgLeu 160
Db 427 GAGCTGGAGCGCGCTGTGGAGCGAGCGCGCGCGCGAGCACAAGATCGACCTCCGGCTG 486
QY 161 LysProAlaLeuGluThrLeuAspGluLeuAlaAlaGlyGluAlaGlyThrPheAsp 180
Db 487 AAGCGCGCTTGGAGACCTTGGACAGCTGTGTGGCGCGCGCGCGCGCGCGCGCGCAC 546
QY 181 ValAlaValAlaAspAlaAspLysGluAsnCysSerAlaTyrTyrGluArgCysLeuGln 200
Db 547 GTGGCGCTGTGTGGATGCGGACAGGAGAACTGTCTCCGCTACTACGAGCGCTGTCTGAG 606
QY 201 LeuLeuArgProGlyGlyIleLeuAlaValLeuArgVal-LeuTrpArgGlyLysValle 220
Db 607 CTGCTGCGACCGCGAGGCGCATCTCGCGCTCTCAGAGTCTTGTGTGGCGGGAAGGTGCT 666
QY 220 uGlnProProLysGlyAspValAlaAlaAlaGluCysValArgAsnLeu-AsnGluArgIle 239
Db 667 GAAACT-CCGAAAGGGAGCGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCATC 725
QY 240 ArgArgAspValArgValTyrIleSerLeuLeu-ProLeuGlyAspGlyLeuThrLeu 258
Db 726 CGGCGGACCGGAGGCTTACATCAGGCTTCTGGCGCGCTTGGCGCGCTGAGATCATCCCTT 783

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RESULT 5

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BF664198
LOCUS 602145812F1 NTH_MGC_48 Homo sapiens cDNA clone IMAGE:4309298 5',
DEFINITION mRNA sequence.
ACCESSION BF664198
VERSION BF664198.1 GI:11938093
KEYWORDS EST. Homo sapiens (human)
SOURCE

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BF664198 921 bp mRNA linear EST 21-DEC-2000
LOCUS 602145812F1 NTH_MGC_48 Homo sapiens cDNA clone IMAGE:4309298 5',
DEFINITION mRNA sequence.
ACCESSION BF664198
VERSION BF664198.1 GI:11938093
KEYWORDS EST. Homo sapiens (human)
SOURCE

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ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE NIH-MGC http://mgi.nci.nih.gov/.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM182 row: h column: 03
High quality sequence stop: 726.
FEATURES
Location/Qualifiers
1..921
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4309298"
/tissue_type="primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 48"
/note="Organ: B-cells; Vector: pOTB7; Site 1: XhoI;
Site 2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
ORIGIN
Alignment Scores:
Pred. No.: 9.73e-111 Length: 921
Score: 1188.00 Matches: 244
Percent Similarity: 98.01% Conservative: 2
Best Local Similarity: 97.21% Mismatches: 5
Query Match: 88.46% Indels: 3
DB: 2 Gaps: 0

US-10-017-407A-306 (1-262) x BF664198 (1-921)

Qy 1 MetThrGlnProValProArgLeuSerValProAlaLeuAlaLeuGlySerAlaAla 20
Db 7 ATGACCCAGCGGTGCGCCGGCTCTCCGTGCGCGCGCGCTGGCCCTGGGCTCAGCGCA 66
Qy 21 LeuGlyAlaAlaPheAlaThrGlyLeuPheLeuGlyArgArgCysProProTyrArgGly 40
Db 67 CTGGCGCGCGCTTGGCCACTTGGCTCTTCTTGGCGAGCGGTGCGCCCTGCGAGGC 126
Qy 41 ArgArgGluGlnCysLeuLeuProProGluAspSerArgLeuTyrGlnTyrLeuLeuSer 60
Db 127 CGCGGAGAGCAGTGGCTCTTCCCGCGAGACAGCCCGCTGTGCGAGTATCTTCTGAGC 186
Qy 61 ArgSerMetArgGluHisProAlaLeuArgSerLeuArgLeuLeuThrLeuGluGlnPro 80
Db 187 CGCTCCATGCGGAGCACCGCGCTGCGAAGCCTGAGGCTGCTGACCTTGGAGCAGCG 246
Qy 81 GlnGlyAspSerMetMetThrCysGluGlnAlaGlnLeuLeuAlaAsnLeuAlaArgLeu 100
Db 247 CAGGCGGATTTCTATGATGACCTTGGAGCAGGCCAGCTCTTGGCCAACTTGGCGGGCTC 306
Qy 101 IleGlnAlaValLeuAlaLeuAspLeuGlyThrPheThrGlyTyrSerAlaLeuAlaLeu 120
Db 307 ATCAGGCCAGAGAGCGCTGACCTGGGCGACTTCACGGGCTACTCGCCCTGGCCCTG 366
Qy 121 AlaLeuAlaLeuProAlaAspGlyArgValValThrCysGluValValAspAlaGlnPro 140

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ORIGIN


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Db 635 CGCCCTGGGGCTTGGAGCCCGGCGGAGGTTGGTGACCTGATGGCTGGTCCACC 694
QY 75 -----LeuThrLeuGluGlnProGlnGlyAspSerMetThrCysG1 89
Db 695 CTCTCTTTTACGCGAGCTGACCTGGAGCAGCGCGAGGGGATTCTATGATGACCTGCGA 754
QY 89 ucInAlaGlnLeuAlaAenLeuAlaAglLeuIleGlnAlaLysLysAlaLeuAspLe 109
Db 755 GAGGCGCCAGCTCTTGGCCAACTGGCGGGCTCATCCAGGCGCAAGAGCGCTGACCT 814
QY 109 uGlyThrPheThrGlyTyrSerAlaLeuAlaLeuAlaLeuAlaLeuProAlaAspGlyAr 129
Db 815 GGGCACTTTCAGGGCTACTCGCCCTGGCCCTGGCCCTGGCCCTGGCCGCGGAGCGGG 874
QY 129 gValValThrCysGluValAspAlaGlnProProGluLeuGlyArgProLeuTrpArg-- 148
Db 875 COTGTGACCTGCGAGGTGGAGCGCAGCGCCCGGAGCTGGGACGGCCCTGTGGAGGCA 934
QY 148 ----- 148
Db 935 GGTGAGCGCCCGCTAGCTCTGAGCGCCCGAGCGGGGGCGCAACGCTGACCCGCTCC 994
QY 149 -----GlnAlaGluAlaGluHisLysIleAspLeuArgLeuLysProAlaLeuGluThrL 167
Db 995 CTCCCGCAGCGGAGCGGAGCACAGATCGACCTCGGCTGAGCCCGCCCTTGGAGACC 1054
QY 167 euAspGluLeuAlaAlaGlyGluAlaGlyThrPheAspValAlaValAlaAspAlaA 187
Db 1055 TGGACGAGCTGCTGGCGGGCGGAGCGCGCACCTTCGAGTGGCCGTGGTGGATCGG 1114
QY 187 sPlyeGluAsnCysSerAlaTyrTyrGluArgCysLeuGlnLeuLeuArgProGlyGlyI 207
Db 1115 ACAAGGAGAACTGCTCCGCTACTACGAGCGCTGCTGAGCTGCTGGCGCCCGGAGGCA 1174
QY 207 leLeuAlaValLeuArgValLeuTrpArgGlyLysValLeuGlnProProLysGlyAspV 227
Db 1175 TCCTCGCGCTCTCAGAGTCTGTGGCGGGAGGTGCTGCAACCTCCGAAAGGGAGG 1234
QY 227 alAlaAlaGluCysValArgAenLeuAenGluArgIleArgArgAspValArgValTyrI 247
Db 1235 TGGCGCGCGAGTGTGTGCGAAACCTTAAACGAGCATCCGCGGGAGCTCAGGGTCTACA 1294
QY 247 leSerLeuLeuProLeuGlyAspGly 255
Db 1295 TCAGCTCTGCCCCCTGGGCGATGGA 1320

RESULT 8
LOCUS CB852718 750 bp mRNA linear EST 22-APR-2003
DEFINITION UI-CF-FN0-af1-p-08-0-UI.s1 UI-CF-FN0 Homo sapiens cDNA clone
ACCESSION CB852718
VERSION UI-CF-FN0-af1-p-08-0-UI 3', mRNA sequence.
KEYWORDS CB852718.1 GI:30047716
SOURCE EST.
ORGANISM Homo sapiens (human)
REFERENCE 1 (bases 1 to 750)
AUTHORS Ronaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene
discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 9704477
PUBMED 889548
COMMENT Contact: McCray, PB
McCray Lab
University of Iowa
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
Tel: 319 356 4866
Fax: 319 356 7171
Email: paul-mccray@uiowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
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cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
cDNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com) or from Open Biosystems
(www.openbiosystems.com).
Seq primer: M13 FORWARD
POLYA=No.

Location/Qualifiers
1..750
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clones="UI-CF-FN0-af1-p-08-0-UI"
/tissue_type="Human Lung Epithelial cells"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/clone_libs="UI-CF-FN0"
/note="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a
modified polylinker; Site_1: EcoR I; Site_2: Not I;
UI-CF-FN0 is a subtracted cDNA library derived from two
normalized Human lung epithelial cell libraries (EN1 and
DUI) The library was subtracted according to according to
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. For additional information, contact:
bento-soares@uiowa.edu
TAG_SEQ=None found"

ORIGIN

Alignment Scores:
Pred. No.: 4,79e-110 Length: 750
Score: 1180.00 Matches: 228
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 87.86% Indels: 0
DBs: 6 Gaps: 0

US-10-017-407A-306 (1-262) x CB852718 (1-750)

QY 32 GlyArgArgCysProTrpArgGlyArgGluGlnCysLeuLeuProGluAsp 51
Db 30 GGGAGGCGTGCCTCCATGCGAGCGCGGAGAGCAGTGCCTGCTTCCCCCGAGGAC 89
QY 52 SerArgLeuTrpGlnTyrLeuLeuSerArgSerMetArgGluHisProAlaLeuArgSer 71
Db 90 AGCGCGCTGTGGCAGTATCTTCTGAGCGCTCCATGCGGAGCACCCGCGCTGCGAAGC 149
QY 72 LeuArgLeuThrLeuGluGlnProGlnGlyAspSerMetThrCysGluGlnAla 91
Db 150 CTGAGGCTGCTGAGCCCTGGAGCAGCGCGGGGGATTCTATGATGACCTGGAGCAGGCC 209
QY 92 GlnLeuAlaAenLeuAlaAglLeuIleGlnAlaLysLysAlaLeuAspLeuGlyThr 111
Db 210 CAGCTCTTGGCCACCTGGCGCGCTCATCCAGGCCAAGAGGCGCTGACCTGGGCGACC 269
QY 112 PheThrGlyTyrSerAlaLeuAlaLeuAlaLeuAlaLeuProAlaAspGlyArgVal 131
Db 270 TTCAGGCGCTACTCGCCCTGCGCCCTGCGCTGCGCGCTGCGCGAGCGCGCTGGTG 329
QY 132 ThrCysGluValAspAlaGlnProGluLeuGlyArgProLeuTrpArgGlnAlaGlu 151
Db 330 ACCTGCGAGGGTGGAGCGGAGCGCGCGGAGCTGGAGCGGCCCTGTGGAGGAGGCCGAG 389
QY 152 AlaGluHisLysIleAspLeuArgLeuLysProAlaLeuGluThrLeuAspGluLeu 171
Db 390 GCGGAGCACAGATCGACCTCCGCTGAGCCCGCCCTTGGAGACCTGGAGCGCTGTG 449
QY 172 AlaAlaGlyGluAlaGlyThrPheAspValAlaValAlaAspAlaAspLysGluAsn 191
Db 450 GCGGCGGCGGAGGCGCGCACCTTCGACGTGGCCCGTGGTGGATGCGGACAGGAGAAC 509
QY 192 SerAlaTyrTyrGluArgCysLeuGlnLeuLeuArgProGlyGlyIleLeuAlaVal 211
Db 510 TCCGCTACTACGAGCGCTGCTGAGCTGTGCGACCCCGGAGGCATCTCTGCGCTCCTC 569

QY 212 ArgValLeuTrpArgGlyLysValLeuGlnProProLysGlyAspValAlaAlaGluCys 231
 Db 570 AGAGTCTGTGGCGCGAGGTCCTCAACCTCCGAAGGGGACGTGGCGCGGAGTGT 629
 QY 232 ValArgAsnLeuAanGluAqGileArgArgAspValArgValTyrileSerLeuLeuPro 251
 Db 630 GTGGGAACCTTAAACGAACGATCCGGCGGACCTCAGGCTTACATCAGCCTCTTGCCC 689
 QY 252 LeuGlyAspGlyLeuThrLeuAla 259
 Db 690 CTGGCGGATGACTCACCCTTGCT 713

RESULT 9
 BF663695 779 bp mRNA linear EST 21-DEC-2000
 LOCUS 602145414F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4309010 5',
 DEFINITION mRNA sequence.

ACCESSION BF663695.1 GI:11937590
 VERSION
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 779)
 NIH-MGC http://mgi.nci.nih.gov/.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgaabs-r@mail.nih.gov
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
 cDNA Library Preparation: Ling Hong/Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: L1CM181 row: 1 column: 03
 High quality sequence stop: 761.

FEATURES
 Location/Qualifiers
 1..779
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:4309010"
 /tissue_type="primary B-cells from tonsils (cell line)"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH MGC 48"
 /notes="Organ: B-cells; Vector: pOTB7; Site 1: XhoI;
 Site 2: EcoRI; cDNA made by oligo-dT priming.
 Directionally cloned into EcoRI/XhoI sites using the
 following 5' adaptor: GGCACGAG(G). Size-selected >500bp
 for average insert size 1.8kb. Library constructed by Ling
 Hong in the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH_MGC Library."

ORIGIN
 Alignment Scores:
 Pred. No.: 1.02e-109 Length: 779
 Score: 1177.00 Matches: 249
 Percent Similarity: 95.06% Conservative: 1
 Best Local Similarity: 94.68% Mismatches: 5
 Query Match: 87.64% Indels: 8
 DB: 2 Gaps: 0

US-10-017-407A-306 (1-262) x BF663695 (1-779)
 QY 1 MetThrGlnProValProArgLeuSerValProAlaAlaLeuAlaLeuGlySerAlaAla 20
 Db 7 ATGACCCAGCGGTCGCCCGGCTCTCCGTGCGCGCGGCTGGCGCTTGGGCTCAGCGGCA 66

QY 21 LeuGlyAlaAlaPheAlaThrGlyLeuPheLeuGlyArgArgCysProProTrpArgGly 40
 Db 67 CTGGCGCGCGCTTCCGCACCTGGCCCTCTCTCTGGGGAGCGCGTGCCTCCATATGGCGAGC 126
 QY 41 ArgArgGluGlnCysLeuLeuProProGluAspSerArgLeuTrpGlnTyrLeuLeuSer 60
 Db 127 CGCGAGAGACAGTGGCTGCTTCCCCCGAGGACGCCGCTGTGGCAGTAITCTTCTGAGC 186
 QY 61 ArgSerMetArgGluHisProAlaLeuArgSerLeuArgLeuLeuThrLeuGluGlnPro 80
 Db 187 CGCTTCATCGGGAGCACCCCGCGCTGGCAACCTGAGGCTGCTGACCTGAGCGAGCGG 246
 QY 81 GlnGlyAspSerMetMetThrCysGlu-GlnAlaGlnLeuLeuAlaAanLeuAla-ArgL 100
 Db 247 CAGGGGGAATTCATGATGACCTCGAGCATGCGCCAGCTCTTGGCCAACTCGCTGGCGC 306
 QY 100 eulleGlnAlaLysLysAlaLeuAspLeuGlyThrPheThr-GlyTyr-SerAlaLeuAla 119
 Db 307 TCATCCAGGCCAAGAGGCGCTGGACCTGGGCACCTTCACTGGGCTACTCCGCCCTGGCC 366
 QY 120 LeuAlaLeuAla-LeuProAlaAspGlyArgValValThrCysGluValAspAlaGlnPr 139
 Db 367 CTGGCCCTGGCTGCTGCCCGCGAGCGCGCTGTGTGACCTCGAGGTGGAGCGCGAGCC 426
 QY 139 oProGluLeuGlyArgProLeuTrpArgGlnAlaGluAlaGluHisLysLysLysLeuAr 159
 Db 427 CCGGAGCTGGGACGGCCCTGTGGAGGCGAGCGCGGAGGACCAAGATCGACCTCCG 486
 QY 159 gLeuLysProAlaLeuGluThrLeuAspGluLeuLeuAlaAlaGlyGluAlaGlyThrPh 179
 Db 487 GCTGAAGCCCTTGGAGACCTCGACGAGCTGCTGGCGGGCGGAGCGCGCACCTT 546
 QY 179 eAspValAlaValVal-AspAlaAspLysGluAsnCysSerAlaLysTyrGluArgCysL 199
 Db 547 CGAGCTGGCGCTGGTGGATGCGGATGCGGACCAAGAGGAACTGCTCCGCTACTACGAGCGCTGCC 606
 QY 199 euGlnLeuLeuArgProGlyGlyLe-LeuAlaValLeuArgValLeuTrpArgGlyLys 218
 Db 607 TGCAGCTGCTGGCAGCCCGAGGCAATTCCTCGCGCTCTCAGAGTCTCTGTGGCGCGGAAG 666
 QY 219 ValLeuGlnProProLysGlyAsp-ValAlaAlaGluCysValArgAsnLeuAsnGluAr 238
 Db 667 GTGCTGCACCTCCGAAGGGGACGGTGGCGCGAGTGTGTGCGAAACCTAAACGACCG 726
 QY 238 gileArgArgAsp-ValArgValTyrileSerLeuLeuProLeuGlyAspGly 255
 Db 727 CATCCGGCGGACCGCTCAGGGTCTACATCAGCTTCTGGCCCTTGGCCGATGCC 779

RESULT 10
 BQ931589 934 bp mRNA linear EST 21-AUG-2002
 LOCUS AGENCOURT_8795361 NIH_MGC_101 Homo sapiens cDNA clone IMAGE:6427775
 DEFINITION 5', mRNA sequence.
 ACCESSION BQ931589
 VERSION BQ931589.1 GI:22346620
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 934)
 NIH-MGC http://mgi.nci.nih.gov/.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgaabs-r@mail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov
 Plate: LLC2613 row: e column: 24
 High quality sequence stop: 532.
 Location/Qualifiers
 1. .934
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:642775"
 /tissue_type="epidermoid carcinoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH MGC 101"
 /note="Organ: lung; Vector: pOTB7; Site 1: EcoRI; Site 2:
 XhoI; cDNA made by oligo-dT priming. Directionally cloned
 into EcoRI/XhoI sites using the following 5' adaptor:
 GGCACGAG(G). Library constructed by Ling Hong in the
 laboratory of Gerald M. Rubin (University of California,
 Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
 Superscript II RT (Life Technologies). Note: this is a
 NIH_MGC Library."

FEATURES

source

ORIGIN

Alignment Scores:
 Pred. No.: 3,56e-108 Length: 934
 Score: 1163.00 Matches: 246
 Percent Similarity: 94.36% Conservativeness: 5
 Best Local Similarity: 92.48% Mismatches: 8
 Query Match: 86.60% Indels: 2
 DB: 5 Gaps: 2

US-10-017-407A-306 (1-262) x BQ931589 (1-934)

Qy 2 ThrGlnProValProArgLeuSerValProAlaLeuAlaLeuGlySerAlaAlaLeu 21
 Db 1 ACCGAGCGGTGCTTCTCCGTGCGCGCGCTGGCCCTGAGCGCTGAGCGCTG 60
 Qy 22 GlyAlaAlaPheAlaThrGlyLeuPheLeuGlyArgArgCysProProTrpArgGlyArg 41
 Db 61 GCGCGCGCTTTCGCCACTGCGCTCTTCCTGGGAGCGGTGCGCGCGCTGAGCGCG 120
 Qy 42 ArgGluGlnCysLeuLeuProGluAspSerArgLeuTrpGlnTrpLeuLeuSerArg 61
 Db 121 CGAGAGCAGTGCCTGCTTCCCCCGAGGACGCGCGCTGTGCAGTAATCTTCTGAGCGCG 180
 Qy 62 SerMetArgGluHisProAlaLeuArgSerLeuArgLeuLeuThrLeuGluGlnProGln 81
 Db 181 TCCATGCGGGAGCACCGCGCGCTGCGAGCGCTGAG ---CTGACCTGAGCAGCGCGAG 236
 Qy 82 GlyAspSerMetMetThrCysGluGlnAlaGlnLeuLeuAlaAsnLeuAlaArgLeuLeu 101
 Db 237 GGGGATTCATGATGACCTGCGAGCAGCGCGCGCTTGGCGCAACCTGGCGCGGTCTATC 296
 Qy 102 GlnAlaLysLeuAlaLeuAspLeuGlyThrPheThrGlyTyrSerAlaLeuAlaLeuAla 121
 Db 297 CAGGCCAAGAAGCGCTGACCTGGGCACTTCAGGGCTACTCGGCCCTGCGCCCTGGCC 356
 Qy 122 LeuAlaLeuProAlaAspGlyArgValValThrCysGluValAspAlaGlnProProGlu 141
 Db 357 CTGGCGCTGCCCGGAGCGCGCGCTGTGTGACCTGGAGGTGGAGCGCGACCGCCCGGAG 416
 Qy 142 LeuGlyArgProLeuTrpArgGlnAlaGluAlaGluHisLysIleAspLeuArgLeuLys 161
 Db 417 CTGGAGCGCGCCCTGTGGAGCGAGCGCGCGCGGACCAAGATCGACCTCGCGGTGAAG 476
 Qy 162 ProAlaLeuGluThrLeuAspGluLeuAlaAlaGlyGluAlaGlyThrPheAspVal 181
 Db 477 CCGCGCTTGGAGACCTCGAGCAGCTGTGTGGCGCGCGCGCGCGCGCACCTTGGACGTG 536
 Qy 182 AlaValValAspAlaAspLysGluAsnCysSerAlaTyrTyrGluArgCysLeuGlnLeu 201
 Db 537 GCGGTGTGGTGGAGCGGACGAGGAGGAGTGTCTCCGCTACTACGAGCGGTGCTGAGGTG 596
 Qy 202 LeuArgProGlyGlyIleLeuAlaValLeuArgValLeuTrpArgGlyLysValLeuGln 221

Db 597 CTGGACCCGAGGAGCATCTCGCGTCTCAGATCTCTGTGCGCGGAGGTGCTGCA 656
 Qy 222 ProProLysGlyAspValAlaAlaGlyCysVal---ArgAsnLeuAsnGluArg-IleArg 240
 Db 657 CCTCCCAAGGGAACCTTGGCGCGCGGATTGTGTGCCAAACCTTAACGAGCCATCG 716
 Qy 240 gArg-AspValArg-ValTyrIleSerLeu-LeuProLeuGlyAsp-GlyLeuThrLeuA 259
 Db 717 GCGGGAGCTCAGGGGTCTACATCAGCTCCCGCGCCCTGGCGGAGGAGGACTCACCTGG 776
 Qy 259 laPheLys 261
 Db 777 CCCTTCAA 784

RESULT 11

AK007659

LOCUS

DEFINITION

AK007659

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TITLE
JOURNAL

Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Tejima, Y., Toya, T., Yamamura, T., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.

Direct Submission
Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp, URL: <http://genome.gsc.riken.jp/>, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

Please visit our web site (<http://genome.gsc.riken.jp/>) for further details.

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5', GAGAGAGAGAGATCAAGAGCTCTTTTCTTTTCTTTTWN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of subtraction to Rot = 20.0. Second strand cDNA was prepared with the primer adapter of sequence [5', GAGAGAGAGAGAGAGAGAGAGATCAAGAGCTCTTTTCTTTTCTTTTWN 3']. cDNA was cleaved with XhoI and SstI. Cloning sites, 5' end: XhoI; 3' end: SstI. Host: SOLR.

COMMENT

Location/Qualifiers
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/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="FANTOM DB:1810030M08"
/db_xref="taxon:10090"
/clone="1810030M08"
/sex="male"
/tissue_type="pancreas"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="10 day old"

misc_feature
1. .919
/note="weakly similar to PUTATIVE O-METHYLTRANSFERASE (FRAGMENT) [Rhodothermus marinus] (SPR|O9XCB3, evidence: FASTY, 55.5%ID, 97.3%length, match=331)"

FEATURES
source

misc_feature
1. .919
/note="weakly similar to PUTATIVE O-METHYLTRANSFERASE (FRAGMENT) [Rhodothermus marinus] (SPR|O9XCB3, evidence: FASTY, 55.5%ID, 97.3%length, match=331)"

ORIGIN

Alignment Scores:
Pred. No.: 1,816-1,07 Length: 919
Score: 1156.00 Matches: 224
Percent Similarity: 92.37% Conservative: 18
Best Local Similarity: 85.50% Mismatches: 20
Query Match: 86.08% Indels: 0
DB: 3 Gaps: 0

US-10-017-407a-306 (1-262) x AK007659 (1-919)

Qy 1 MetThrGlnProValProArgLeuSerValProAlaAlaLeuAlaLeuGlySerAlaAla 20
Db 37 ATGGCTCAGCCCGCTCCCTCGGCTATCTATCCAGCGCGCATGGCCCTGGGCTCGGCGCG 96
Qy 21 LeuGlyAlaAlaPheAlaThrGlyLeuPheLeuGlyArgCysProPrtPrtArgGly 40
Db 97 CTGGGCGCGCTTCGCTACTGCTCTCTGCTGGGAACGGTGGCCCTCCATGGGGTCC 156
Qy 41 ArgArgGluGlnCysLeuLeuProProGluAspSerArgLeuTrpGlnTyrLeuLeuSer 60
Db 157 AGCGCGCAAGACGCGCTGCTGCCACCTGAGCAACAATCCCTGTGGCAGTATCTGCTGAGC 216
Qy 61 ArgSerMetArgGluHisProAlaAlaLeuArgSerLeuLeuLeuThrLeuGluGlnPro 80
Db 217 CGCTCCATGAGAGAGACCCCGGCGCTGGGGAGCTTGGAGCTGCTGACCTGGAGCAGCG 276

Qy 81 GlnGlyAspSerMetMetThrCysGluGlnAlaGlnLeuLeuAlaAsnLeuAlaArgLeu 100
Db 277 CAGGGGGATTCATGATGACCTGTGAACAGGCCAGCTTCTGGCCCAACCTGGCGGGCTC 336
Qy 101 IleGlnAlaLeuAlaLeuAspLeuGlyThrPheThrGlyTyrSerAlaLeuAlaLeu 120
Db 337 ATTAAGGCCCAAGAAAGCTCTGGATCTGGGTACTTTTCAGGGGTACTCGGCCCTCGCCCTA 396
Qy 121 AlaLeuAlaLeuProAlaAspGlyArgValValThrCysGluValAspAlaGlnProPro 140
Db 397 GCCTTGGCGCTTCCGAGAGCTGCCCGCTGGTGTGACTGCGAGTTGACGACAGCCCGC 456
Qy 141 GluLeuGlyArgProLeuTrpArgGlnAlaGluAlaGluHisGlyIleAspLeuArgLeu 160
Db 457 AGCTGGGACGCCCATGTGGAGAGCGGAGAGTGGAGCAGACAGATCATGACCTCGGCTG 516
Qy 161 LysProAlaLeuGluThrLeuAspGluLeuAlaAlaGlyGluAlaGlyThrPheAsp 180
Db 517 CAGCCCGCTTCGACATCTGGATGCTCCAGCGCGGGGAGGCCCGACCTTCGAC 576
Qy 181 ValAlaValValAspAlaAspGlyGluAsnCysSerAlaTyrTyrGluArgCysLeuGln 200
Db 577 ATAGCCGTGTGTGACCGGACCAAGAGAACTGTACCGCTACTACGAGCGCTGTCTGCAG 636
Qy 201 LeuLeuArgProGlyGlyIleLeuAlaValLeuArgValLeuTrpArgGlyLysValLeu 220
Db 637 CTCTAGCTCCGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 696
Qy 221 GlnProProLysGlyAspValAlaAlaGluCysValArgAsnLeuAsnGluArgIleArg 240
Db 697 CAGCTCAGCCCGGAGCAAGACTGTTGATGTGTGGGACCTGAAAGCAAGCAATCCTG 756
Qy 241 ArgAspValArgValTyrIleSerLeuLeuProLeuGlyAspGlyLeuThrLeuAlaPhe 260
Db 757 AGGACCGCCAGGCTCTACATCAGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 816
Qy 261 LysIle 262
Db 817 AAGATC 822

RESULT 12
AK054334 2243 bp mRNA linear HTC 03-APR-2004
LOCUS AK054334.1 GI:26344156
DEFINITION Mus musculus 2 days pregnant adult female ovary cDNA, RIKEN full-length enriched library, clone:E330016L21, product:weakly similar to PUTATIVE O-METHYLTRANSFERASE (FRAGMENT) [Rhodothermus marinus], full insert sequence.

ACCESSION
VERSION AK054334.1
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
1 Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
PUBMED 10349636
2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
20499374
PUBMED 11042159
3 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Kono, H., Akiyama, J., Nishi, K., Katsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,

Yanamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaki, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, S., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A., and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multipillar sequencer
Genome Res. 10 (11), 1757-1771 (2000)

JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS

20530913
11076861

4
The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.

Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)

5

The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

6 (bases 1 to 2243)

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imocani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M., and Hayashizaki, Y.

Direct Submission

Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration and Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan [E-mail: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216]

cDNA library was prepared and sequenced in Mouse Genome

Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.

Division of Experimental Animal Research in Riken contributed to

prepare mouse tissues.

Please visit our web site for further details.

URL: http://genome.gsc.riken.jp/

URL: http://fantom.gsc.riken.jp/

Location/Qualifiers

1. .2243

/organism="Mus musculus"

/mol_type="mRNA"

/strain="C57BL/6J"

/db_xref="FANTOM_DB:E330016L21"

/db_xref="taxon:10090"

/clone="E330016L21"

/sex="female"

/tissue type="ovary"

/clone_libs="RIKEN full-length enriched mouse cDNA library"

/dev_stages="2 days pregnant adult"

40. .828

/note="unnamed protein product; putative

weakly similar to PUTATIVE O-METHYLTRANSFERASE (FRAGMENT)

[Rhodothermus marinus] (SPTR|Q9XCB3, evidence: FASTY,

55.5%ID, 97.3%length, match=331)"

/protein_id="BAC35735.1"

/codon_start=1

/db_xref="GI:26344157"

/translation="MAQPVPLSLPALALGSAALGAFATGLLKGWPPWGSRRQE

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AKKALDLGFTFGYSALALALPAGRVVTCVDEAPPKLRPMWQARVEQKIDRL

OPALQTLDELAAGEAGTFDIAVVDADKENCNTAYYERCLQLLRPGVGLVLRVLRGE

CDS

VLQPPRNKTVTCVNRNLNERILRDARVVISLLPLDDGLSLAFKI"

2223. .2228

/note="putative"

polyA_signal

polyA_site

2243

/note="putative"

ORIGIN

Alignment Scores:

Pred. NO.: 6.34e-107 Length: 2243

Score: 1156.00 Matches: 224

Percent Similarity: 92.37% Conservativeness: 18

Best Local Similarity: 85.50% Mismatches: 20

Query Match: 86.08% Indels: 0

DB: 3 Gaps: 0

US-10-017-407A-306 (1-262) x AK054334 (1-2243)

Qy 1 MetThrGlnProValProArgLeuSerValProAlaAlaLeuLeuGlySerAlaAla 20

Db 40 ATGGCTCAGCCCGCTCCCTCGGCTATCTATCCAGCCGCACCTGGCCCTGGGCTCGGCCGCG 99

Qy 21 LeuGlyAlaAlaPheAlaThrGlyLeuPheLeuGlyArgArgCysProProTirArgGly 40

Db 100 CTGGGCGCGCTTCGGTACTGGTCTCTTGTGGGGAACCGTGGCTCCATGGGGTCC 159

Qy 41 ArgArgGlnCysLeuLeuProProGluAspSerArgLeuTirGlnTyrLeuLeuSer 60

Db 160 AGGCGGCAAGAGCGCTGTCACCTGAGGACCAATCCCTGTGGCAGTATCTGTGAGC 219

Qy 61 ArgSerMetArgGluHisProAlaLeuArgSerLeuArgLeuLeuGlnPro 80

Db 220 CGCTCCATGAGAGAGACCCCGCGCTCGGAGCCTCGGACTGCTGACCTGGAGCAGCG 279

Qy 81 GlnGlyAspSerMetMetThrCysGluGlnAlaGlnLeuLeuAlaAsnLeuAlaArgLeu 100

Db 280 CAGGGGATTCATGATGACCTGTGAACAGGCCAGCTTCGGCCAACTGGCGGGGCTC 339

Qy 101 IleglnAlaLysLysAlaLeuAspLeuGlyThrPheThrGlyTyrSerAlaLeuAlaLeu 120

Db 340 ATTAAGGCCAAGAAGCTCTGGATCTGGTACTTTCAGGGCTACTCGGCTCTGGCCCTA 399

Qy 121 AlaLeuAlaLeuProAlaAspGlyArgValThrCysGluValAspAlaGlnPro 140

Db 400 GCCTTGGCGCTTCGGAGGCTGGCGCGTGGTGACCTGCGAGGTGACGAGGCCCGC 459

Qy 141 GluLeuGlyArgProLeuTirArgGlnAlaGluHisLysIleAspLeuArgLeu 160

Db 460 AAGCTGGAGCGGCCATGTGGNAGCAGCAGAGTGGAGCAGAGATCGACTTCGGCTG 519

Qy 161 LysProAlaLeuGluThrLeuAspGluLeuLeuAlaAlaGlyGluAlaGlyThrPheAsp 180

Db 520 CAGCCCGCTTCAGACATTTGGATGAGCTCTAGCGGGCGGCGGCGGAACTTCGAC 579

Qy 181 ValAlaValValAspAlaAspLysGluAsnCysSerAlaTyrTyrGluArgCysLeuGln 200

Db 580 ATACCGTGGTGGACGGCGGCAAGAGAACTGTACCGCTACTACGAGCGCTGTCTGAG 639

Qy 201 LeuLeuArgProGlyGlyIleLeuAlaValLeuArgValLeuTirArgGlyLysValLeu 220

Db 640 CTCTAGTCCCGGAGCGGCTCGCTGCTACTCAGAGTCTCTGGCGGGAAGATGCTG 699

Qy 221 GlnProLysGlyAspValAlaAlaGluCysValArgAsnLeuAsnGluArgIleArg 240

Db 700 CAGCCTCAGCCGAGAACAGACTGTTGATGTGTGGGAACTTGAACGACCATCTG 759

Qy 241 ArgAspValArgValTyrIleSerLeuLeuProLeuGlyAspGlyLeuThrLeuAlaPhe 260

Db 760 AGGAGCGCAGGGTCTACATCAGCCTCTGCGCCCTGGATGATGGCTCTCTCTTGGCCCTT 819

Qy 261 LysIle 262

Db 820 AAGATC 825

COMMENT

FEATURES

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RESULT 13

BY707694
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

BY707694 RIKEN full-length enriched, 10 day old male pancreas Mus

musculus CDNA clone 1810030M08 5', mRNA sequence.

BY707694.1 GI:27118872

musculus (house mouse)

Mus musculus

Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 910)

Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,

Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,

Schönbach, C., Gojohori, T., Baldarelli, R., Hill, D.P., Bult, C.,

Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H.,

Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusic, V.,

Chothia, C., Corbani, L.E., Cousins, S., Della, E., Dragani, T.A.,

Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T.,

Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S.,

Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A.,

Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Kongaya, A.,

Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R.,

Maltais, L., Marchionni, L., McKenrie, L., Miki, H., Nagashima, T.,

Numata, K., Okado, T., Pavan, W.J., Pertea, G., Pesole, G.,

Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramchandran, S.,

Ravasi, T., Reed, J.C., Reid, J., Reid, J., Ring, B.Z., Ringwald, M.,

Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K.,

Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M.,

Verardo, R., Wagner, L.G., Wahlestedt, C., Wang, Y., Watanabe, Y.,

Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I.,

Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P.,

Hayatsu, N., Hirozumi-Kishikawa, T., Kono, H., Nakamura, M.,

Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K.,

Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y.,

Itoh, M., Kogawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K.,

Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S.,

Rogers, J., Birney, E. and Hayashizaki, Y.

Analysis of the mouse transcriptome based on functional annotation

of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

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Contact: Yoshihide Hayashizaki

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The Institute of Physical and Chemical Research (RIKEN)

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Tel: 81-45-503-9222

Fax: 81-45-503-9216

Email: genome-res@gsr.riken.jp, URL: http://genome.gsc.riken.jp/

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P.,

Fukuda, S., Hashizume, W., Hayashida, K., Hirozumi, K., Hori, F.,

Imotani, K., Ishii, Y., Itoh, M., Kaga, I., Kawai, J., Kojima, Y.,

Kondo, S., Konno, H., Koya, S., Miyazaki, A., Murata, M., Nakamura, M.,

Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Saito, R., Sakazume, N.,

Sano, H., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M.,

Takeda, Y., Waki, K., Watahiki, A., Muramatsu, M. and Hayashizaki, Y.

Direct Submission

Computational Analysis of Full-Length Mouse cDNAs Compared with

Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)

Normalization and subtraction of cap-trapper-selected cDNAs to

prepare full-length cDNA libraries for rapid discovery of new

Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN,
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site (<http://genome.gsc.riken.go.jp>) for
further details.

FEATURES

Location/Qualifiers

1..910

/organism="Mus musculus"

/mol_type="mRNA"

/strains="C57BL/6J"

/db_xref="taxon:10090"

/clone="1810030M08"

/sex="male"

/tissue type="pancreas"

/dev stage="10 day old"

/clone lib="RIKEN full-length enriched, 10 day old male

pancreas"

ORIGIN

Alignment Scores:

Pred. No.: 2,07e-104 Length: 910

Score: 1126.00 Matches: 222

Percent Similarity: 91.98% Conservative: 19

Best Local Similarity: 84.73% Mismatches: 21

Query Match: 83.84% Indels: 1

DB: 6 Gaps: 0

US-10-017-407A-306 (1-262) x BY707694 (1-910)

Qy 1 MetThrGlnProValProArgLeuSerValProAlaAlaLeuAlaLeuGlySerAlaAla 20

Db 34 ATGGCTCAGCCCGCTCCCTGGCTATCTATCCAGCGCGCATCTGCCCTCGGGCTCGGCGCGG 93

Qy 21 LeuGlyAlaAlaPheAlaThrGlyLeuPheLeuGlyArgArgCysProProTrpArgGly 40

Db 94 CTGGCGC-CCCTCGCTACTGCTCTTGTCTGGGAAACGGTGGCTCCATGGGGGTCC 152

Qy 41 ArgArgGluGlnCysLeuLeuProGluAspSerArgLeuTrpGlnTrpLeuLeuSer 60

Db 153 AGCGCGCAGAGCGCCCTGCTGCCACCTTGAGGACAACTCCCTGTGGCAGATATCTGTGAGC 212

Qy 61 ArgSerMetArgGluHisProAlaLeuArgSerLeuArgLeuLeuThrLeuGluGlnPro 80

Db 213 CGCTCCATGAGAGAGACACCGCGCGCTGCGAGCGTGCAGCTGCTACCTTGGAGCGCGC 272

Qy 81 GlnGlyAspSerMetMetThrCysGluGlnAlaGlnLeuAlaAsnLeuAlaArgLeu 100

Db 273 CAGGGGATTCATGATGACCTGTGAACAGGCCCGAGCTTCTGGCCAACTTGGCGGGCTC 332

Qy 101 IleGlnAlaIysLysAlaLeuAspLeuGlyThrPheThrGlyTyrSerAlaLeuAlaLeu 120

Db 333 ATTAGGCCAAGAAGCTCTGGATCTGGTACTTTCAGGGGTACTCGGCCCTGGCCCTA 392

Qy 121 AlaLeuAlaLeuProAlaAspGlyArgValValThrCysGluValAspAlaGlnProPro 140

Db 393 GCCTTGGCGCTTCCGAGCGCTGGCGCGCTGGTGTGACCTGCGAGGTGACGACGACCCCGC 452

Qy 141 GluLeuGlyArgProLeuTrpArgGlnAlaGluAlaGluHisLysLysLysLysLysLys 160

Db 453 AAGCTGGGACGGCCCATGTGAAGCAGGACGAGAGTGGAGCAGAGATCGACCTTCGGCTG 512

Qy 161 LysProAlaLeuGluThrLeuAspGluLeuAlaAlaGlyGluAlaGlyThrPheAsp 180

Db 513 CAGCCCGCGCTCGACACATTCGATGAGCTCTTAGCGGGCGGCGAGCGCGAACCTTCGAC 572

Qy 181 ValAlaValValAspAlaAspLysGluAsnCysSerAlaTyrTyrGluArgCysLeuGln 200

Db 573 ATAGCGGTGGTGGACGCGACAAAGAGAACTGTACCGGCTACTACGACGCGCTGTCTGAG 632

Qy 201 LeuLeuArgProGlyGlyIleLeuAlaValLeuArgValLeuTrpArgGlyLysValLeu 220

Db 633 CTCCTACGTGCCGAGGGCTGCTCGCTGTACTCAGAGTCTCTGTGGCGGGAGAGAGTGTG 692

QY 221 GlnProProLysGlyAspValAlaAlaGluCysValArgAsnLeuAsnGluArgLeuArg 240
 Db 693 CAGCCTCAGCCAGCAAGAGCTGTGAATGTCGCGAAGCTGAACGACGATCCTG 752
 QY 241 ArgAspValArgValTyrIleSerLeuLeuProLeuGlyAspGlyLeuThrLeuAlaPhe 260
 Db 753 AGGAGCGCCAGGGTGTACATCAGCTCTCCCTCGATGATGGCTCTCCTTGGCCCTT 812

QY 261 LysIle 262
 Db 813 AAGATC 818

RESULT 14

BC019467

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

BC019467 999 bp mRNA linear HTC 25-JUN-2004
 Mus musculus catechol-O-methyltransferase domain containing 1, mRNA
 (cDNA clone IMAGE:4036276), containing frame-shift errors.

BC019467.1 GI:18043387

HTC.

Mus musculus

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 999)

Strausberg, R.D., Feingold, E.A., Grouse, L.H., Derge, J.G.,

Klauser, R.D., Collins, F.S., Wagner, K.H., Shenmen, C.M., Schuler, G.D.,

Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,

Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,

Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,

Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,

Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,

Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,

Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,

McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,

Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,

Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,

Fahey, J., Helton, E., Kettner, M., Madan, A., Rodriguez, S.,

Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,

Bouffard, G.G., Blakeley, R.W., Touchman, J.W., Green, E.D.,

Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,

Butterfield, Y.S., Krzywicki, M.I., Skalska, U., Smallov, D.E.,

Schmerch, A., Schein, J.E., Jones, S.J., and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length

human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

12477932

2 (bases 1 to 999)

Strausberg, R.

Direct Submission

Submitted (19-DEC-2001) National Institutes of Health, Mammalian

Gene Collection (MGC), Cancer Genomics Office, National Cancer

Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,

USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

Contact: MGC help desk

Email: cgapbs@mail.nih.gov

Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys

cDNA Library Preparation: Life Technologies, Inc.

DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)

Sequencing Center

Center code: BCM-HGSC

Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>

Contact: amg@bcm.tmc.edu

Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,

Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,

A.N., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found

through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Series: IRAC Plate: 37 Row: a Column: 14

This clone was selected for full length sequencing because it
 passed the following selection criteria: Similarity but not
 identity to protein
 This clone has the following problem: frame shifted.

FEATURES

source

Location/Qualifiers

1..999

/organism="Mus musculus"

/mol_type="mRNA"

/strain="mix FVB/N, C57BL/6J"

/db_xref="taxon:10090"

/clone="IMAGE:4036276"

/tissue_type="Mammary tumor. WAP-TGF alpha model. 7 months

old, gross tissue."

/clone_lib="NCI CGAP Mam5"

/lab_host="DH10B"

/note="Vector: pCMV-SPORT6"

ORIGIN

Alignment Scores:

Pred. No.: 8.06e-103 Length: 999

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Percent Similarity: 83.97% Conservatives: 17

Best Local Similarity: 78.05% Mismatches: 21

Query Match: 82.73% Indels: 26

DB: 3 Gaps: 1

US-10-017-407a-306 (1-262) x BC019467 (1-999)

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 Db 23 ATGGCTAGCCCGCTCCCTCGGCTATCTATCCAGCGCCTGCGCCCTGGGCTCGGCGCG 82
 QY 21 LeuGlyAlaAlaPheAlaThrGlyLeuPheLeuGlyArgArgCysProProTrpArgGly 40
 Db 83 CTGGCGCGCGCTTCGCTACTGCTCTCTGCTGGGAAACGGTGGCTCCATGGGGGTCC 142
 QY 41 ArgArgGluGlnCysLeuLeuProGluAspSerArgLeuTrpGlnTyrLeuLeuSer 60
 Db 143 AGCGCGCAAGACCGCTGCTGCCACCTGAGGACCAATCCCTGTGTCAGTATCTGTGAGC 202
 QY 61 ArgSerMetArgGluHisProAlaLeuArgSerLeuArgLeuLeuThrLeuGlnPro 80
 Db 203 CGCTCATGAGAGAGACCCCGCTCGGAGCTGCGACTGTGACCTTGAGGAGCGCG 262
 QY 81 GlnGlyAspSerMetThrCysGlnGlnAlaGlnLeuLeuAlaAsnLeuAlaArgLeu 100
 Db 263 CAGGGGATTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 322
 QY 101 IleGlnAlaLysLysAlaLeuAspLeuGlyThrPheThrGlyTyrSerAlaLeuAlaLeu 120
 Db 323 ATTAAGGCCAAGAAAGCTCTGGATCTGGGTACTTTTACGGGCTACTCGGGCTCGGCCCTA 382
 QY 121 AlaLeuAlaLeuProAlaAspGlyArgValValThrCysGluValAspAlaGlnProPro 140
 Db 383 GCCTTGGCGCTTCCGGAGGCTGGCGCGCTGTGTGACCTGCGAGGTTGACGCGAGCGCCCG 442
 QY 141 GluLeuGlyArgProLeuTrpArg----- 148
 Db 443 AAGTGGGAGCGGCCCATGTTGAA--GCAGGTGAGAGAGCCACACCTGCGCGCGTTCGGGCT 501
 QY 149 -----GlnAlaGluAlaGluHisLys 155
 Db 502 CCGGCTCGGGGGCGTGGCGGCTGACCGGCTCTCTTCGCGAGGAGAGAGTGGAGCAGAAG 561
 QY 156 IleAspLeuArgLeuLysProAlaLeuGluThrLeuAspGluLeuLeuAlaAlaGlyGlu 175
 Db 562 ATCCAGCTTCGGCTGCGAGCGCCCGCTGCAGACATTGGATGAGCTCTTAGCGCGCGCGGCG 621
 QY 176 AlaGlyThrPheAspValAlaValValAspAlaAspLysGluAsnCysSerAlaTyrTyr 195
 Db 622 GCCGGAACCTTCGACATAGCGCTGTGGAGCGCGGACAAAGAGAACTGTACCGCTACTAC 681
 QY 196 GluArgCysLeuGlnLeuLeuArgProGlyGlyIleLeuAlaValLeuArgValLeuTrp 215

ORIGIN		
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Pred. No.:		

Search completed: January 12, 2005, 23:45:50
Job time : 3031 secs

Search completed: January 12, 2005, 23:45:50
Job time : 3031 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.
OM protein - nucleic search, using frame_plus p2n model
Run on: January 12, 2005, 22:41:53 ; Search time 421 Seconds
(without alignments)
3266.861 Million cell updates/sec

Title: US-10-017-407A-306
Perfect score: 1343
Sequence: 1 MTQVPRLSVPAALALGSA.....VRVYISLLPLGDTLAFKI 262
Scoring table:
  BLOSUM62
  Xgapop 10.0 , Xgapext 0.5
  Ygapop 10.0 , Ygapext 0.5
  Fgapop 6.0 , Fgapext 7.0
  Delop 6.0 , Delext 7.0
  Delop 6.0 , Delext 7.0
Searched: 4134886 seqs, 2624710521 residues
Total number of hits satisfying chosen parameters: 8269772
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Command line parameters:
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-Q=/csm2_1/USPTO_spool_p/US10017407/runat_11012005_135153_22529/app_query_fasta_1.455
-DB=N_Geneseq_23Sep04 -QFMT=fastap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPCL=0
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-NO_MMAP -LARGESQUERY -NEG_SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
Database : N_Geneseq_23Sep04:
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2: Geneseq1990s:*
3: Geneseq2000s:*
4: Geneseq2001as:*
5: Geneseq2001bs:*
6: Geneseq2002as:*
7: Geneseq2002bs:*
8: Geneseq2003as:*
9: Geneseq2003bs:*
10: Geneseq2003cs:*
11: Geneseq2004s:*
12: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES
No. Score Match Length DB ID Description
RESULT 1
ID ABA05420 standard; cDNA; 789 BP.
DE Human O-methyltransferase family member 25692 coding sequence.
PN WO200193719-A2.
PD 08-NOV-2001.
PA (MILL-) MILLENNIUM PHARM INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
RESULT 2
ID AA298166 standard; cDNA; 985 BP.
DE Human signal peptide containing protein HSPB-58 cDNA SEQ ID NO:192.
PN WO20000610-A2.
PD 06-JAN-2000.
PA (INCY-) INCYTE PHARM INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
RESULT 3
ID ADO42272 standard; cDNA; 988 BP.
DE Human NOVX polynucleotide #61.
PN US2004058338-A1.
PD 25-MAR-2004.
PA (GETH-) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
RESULT 4
ID AAA37107 standard; cDNA; 989 BP.
DE Human PRO1558 (UNQ766) cDNA sequence SEQ ID NO:305.
PN WO200012708-A2.
PD 09-MAR-2000.
PA (GETH-) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
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ID AAF54419 standard; DNA; 989 BP.
DE DNA encoding protein of the invention #84.
PN WO200078961-A1.
PD 28-DEC-2000.
PA (GETH-) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
RESULT 6
ID ABK40264 standard; cDNA; 989 BP.
DE cDNA encoding human PRO1558 polypeptide.
PN WO200153486-A1.
PD 26-JUL-2001.
PA (GETH-) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
RESULT 7
ID ADO42272 standard; cDNA; 988 BP.
DE Human NOVX polynucleotide #61.
PN US2004058338-A1.
PD 25-MAR-2004.
PA (GETH-) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0

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PA (AGEE/) AGEE M L.
PA (ALSO/) ALSOBROOK J P.
PA (ANDE/) ANDERSON D W.
PA (BERG/) BERGHS C.
PA (BOLD/) BOLDOG F L.
PA (BURG/) BURGESS C E.
PA (CATT/) CATTERTON E.
PA (DIPI/) DIPIPO V A.
PA (EDIN/) EDINGER S R.
PA (EISE/) EISEN A.
PA (GANG/) GANGOLLI E A.
PA (GERL/) GERLACH V.
PA (GORM/) GORMAN L.
PA (ROTH/) ROTHBERG B G.
PA (GUOX/) GUO X S.
PA (HERR/) HERRMANN J L.
PA (HALV/) HALVORSEN Y.
PA (JIWW/) JI W.
PA (KEKU/) KEKUDA R.
PA (KHRA/) KHRAMTSOV N V.
PA (LARO/) LAROCHELLE W J.
PA (LEPL/) LEPLEY D M.
PA (LILL/) LI L.
PA (MACD/) MACDOUGALL J R.
PA (MILL/) MILLER C E.
PA (ORTT/) ORT T.
PA (PADI/) PADIGARAJAN M.
PA (PATT/) PATTURAJAN M.
PA (PENA/) PENA C E A.
PA (PEYM/) PEYMAN J A.
PA (RIEG/) RIEGER D K.
PA (ROTH/) ROTHENBERG M E.
PA (SHEN/) SHENOY S G.
PA (SMIT/) SMITHSON G.
PA (SPAD/) SPADERNA S K.
PA (SEYT/) SEYTEK K A.
PA (STON/) STONE D J.
PA (TAUP/) TAUPIER R J.
PA (VERN/) VERNET C A M.
PA (VOSS/) VOSS E Z.
PA (ZHON/) ZHONG M.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 4
ID AAA37107 standard; cDNA; 989 BP.
DE Human PRO1558 (UNQ766) cDNA sequence SEQ ID NO:305.
PN WO200012708-A2.
PD 09-MAR-2000.
PA (GETH-) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 5
ID AAF54419 standard; DNA; 989 BP.
DE DNA encoding protein of the invention #84.
PN WO200078961-A1.
PD 28-DEC-2000.
PA (GETH-) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
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RESULT 6
ID ABK40264 standard; cDNA; 989 BP.
DE cDNA encoding human PRO1558 polypeptide.
PN WO200153486-A1.
PD 26-JUL-2001.
PA (GETH-) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
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ID ADO42272 standard; cDNA; 988 BP.
DE Human NOVX polynucleotide #61.
PN US2004058338-A1.
PD 25-MAR-2004.
PA (GETH-) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0

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Thu Jan 13 11:25:08 2005

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ID ACD68458 standard; cDNA; 989 BP.
DE Novel human secreted and transmembrane protein PRO1558 cDNA.
PN US2003073130-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
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DE Human cDNA encoding secreted/transmembrane protein PRO1558.
PN US2003044841-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
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ID ACD68104 standard; cDNA; 989 BP.
DE Novel human secreted and transmembrane protein PRO1558 cDNA.
PN US2003073129-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 10
ID ADC18174 standard; cDNA; 989 BP.
DE Human PRO polynucleotide #86.
PN US2003064925-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 11
ID ADD70820 standard; cDNA; 989 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1558.
PN US2003099625-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 12
ID ADD39897 standard; cDNA; 989 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1558.
PN US2003083462-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 13
ID ADD70343 standard; cDNA; 989 BP.
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PN US2003054406-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
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PN US2003096955-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
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PN US2003096954-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
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PN US2003092061-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 17
ID ADD40374 standard; cDNA; 989 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1558.
PN US2003082627-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 18
ID ADE50595 standard; cDNA; 989 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1558.
PN US2003069179-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 19
ID ADE20207 standard; cDNA; 989 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1558.
PN US2003092883-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
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ID ADE50118 standard; cDNA; 989 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1558.
PN US2003082626-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 21
ID ADE21676 standard; cDNA; 989 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1558.
PN US2003082628-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 22
ID ADF30101 standard; cDNA; 989 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1558.
PN US2003204053-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 23
ID ADF55994 standard; cDNA; 989 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1558.

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PN US2003204054-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 24
ID ADH99498 standard; cDNA; 989 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1558.
PN US2003065142-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 25
ID ADJ37302 standard; cDNA; 989 BP.
DE Human tumour therapy associated PRO1558 cDNA.
PN US2003211096-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 26
ID ADE96678 standard; cDNA; 989 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1558.
PN US2003195347-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 27
ID ADF25989 standard; cDNA; 989 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1558.
PN US200319675-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 28
ID ADF24888 standard; cDNA; 989 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1558.
PN US200319893-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 29
ID ADF29624 standard; cDNA; 989 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1558.
PN US2003203401-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 30
ID ADE97155 standard; cDNA; 989 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1558.
PN US2003195334-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 31
ID ADH03193 standard; cDNA; 989 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1558.
PN US2003216562-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 32
ID ADH04147 standard; cDNA; 989 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1558.
PN US2003220471-A1.
PD 27-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 33
ID ADH03670 standard; cDNA; 989 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1558.
PN US2003224478-A1.
PD 04-DEC-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 34
ID ADG68226 standard; cDNA; 989 BP.
DE Human PRO polypeptide cDNA #11.
PN US2003170228-A1.
PD 11-SEP-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 35
ID ADH04624 standard; cDNA; 989 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1558.
PN US2004005626-A1.
PD 08-JAN-2004.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 36
ID ADH61625 standard; cDNA; 989 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1558.
PN US2004014130-A1.
PD 22-JAN-2004.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 37
ID ADL94824 standard; cDNA; 989 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1558.
PN US2004073015-A1.
PD 15-APR-2004.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 38
ID ADO42276 standard; cDNA; 989 BP.
DE Human NOVX polynucleotide #63.
PN US2004058338-A1.
PD 25-MAR-2004.
PA (AGEE/) AGEE M L.
PA (ALSO/) ALSOBROOK J P.
PA (ANDE/) ANDERSON D W.
PA (BERG/) BERGS C.
PA (BOLD/) BOLDOG F L.
PA (BURG/) BURGESS C E.
PA (CATT/) CATTERTON E.
PA (DIP/) DIPPEO V A.
PA (EDIN/) EDINGER S R.
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ID AAD56372 standard; DNA; 876 BP.
 DE Human secreted protein-encoding gene 11 cDNA clone HTAQO18, SEQ ID NO:32.
 PN WO2003038038-A2.
 PD 08-MAY-2003.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Percent Similarity: 82.51%
 Best Local Similarity: 82.51%
 Indels: 46
 Query Match:
 RESULT 44
 ID AAD56361 standard; DNA; 885 BP.
 DE Human secreted protein-encoding gene 11 cDNA clone HTAQO18, SEQ ID NO:21.
 PN WO2003038038-A2.
 PD 08-MAY-2003.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Percent Similarity: 82.51%
 Best Local Similarity: 82.51%
 Indels: 46
 Query Match:
 RESULT 45
 ID ADO42274 standard; cDNA; 787 BP.
 DE Human NOVX polynucleotide #62.
 PN US2004058338-A1.
 PD 25-MAR-2004.
 PA (AGEE/) AGEE M L.
 PA (ALSO/) ALSOBROOK J P.
 PA (ANDE/) ANDERSON D W.
 PA (BERG/) BERGES C.
 PA (BOLD/) BOLDOG F L.
 PA (BURG/) BURGESS C E.
 PA (CATT/) CATTERTON E.
 PA (DIPP/) DIPPO V A.
 PA (EDIN/) EDINGER S R.
 PA (EISE/) EISEN A.
 PA (ELLE/) ELLERMAN K.
 PA (GANG/) GANGOLLI E A.
 PA (GERL/) GERLACH V.
 PA (GORM/) GORMAN L.
 PA (ROTH/) ROTHEBERG B G.
 PA (GUOX/) GUO X S.
 PA (HERR/) HERRMANN J L.
 PA (HALV/) HALVORSEN Y.
 PA (JIWV/) JI W.
 PA (KEKU/) KEKUDA R.
 PA (KHRA/) KHRAMTSOV N V.
 PA (LARO/) LAROCHELLE W J.
 PA (LEPL/) LEPLY D M.
 PA (LILL/) LI L.
 PA (MACD/) MACDOUGALL J R.
 PA (MILL/) MILLER C E.
 PA (ORTT/) ORT T.
 PA (PADI/) PADIGARU M.
 PA (PENA/) PENA C E A.
 PA (PEYM/) PEYMAN J A.
 PA (RIEG/) RIEGER D K.
 PA (ROTH/) ROTHENBERG M E.
 PA (SHEN/) SHENOV S G.
 PA (SMIT/) SMITHSON G.
 PA (SPAD/) SPADERNA S K.
 PA (SPYT/) SPYTEK K A.
 PA (STON/) STONE D J.
 PA (TAUF/) TAUPIER R J.
 PA (VERN/) VERNET C A M.
 PA (VOSS/) VOSS E Z.
 PA (ZHON/) ZHONG M.
 Percent Similarity: 70.23%
 Best Local Similarity: 70.23%
 Query Match: 65.82%
 RESULT 46
 ID ADD34178 standard; DNA; 770 BP.
 DE Mouse mitochondrial DNA sequence SEQ ID NO:1956.
 PN WO2003020220-A2.
 PD 13-MAR-2003.
 PA (UYEN-) UNIV EMORY.
 Percent Similarity: 99.14%
 Best Local Similarity: 99.14%
 Indels: 2
 Query Match: 87.79%
 RESULT 43

ID ABA05419 standard; cDNA; 1037 BP.
 DE Human O-methyltransferase family member 25692 encoding cDNA.
 PN WO200183719-A2.
 PD 08-NOV-2001.
 PA (MILL-) MILLENNIUM PHARM INC.
 Percent Similarity: 100.00%
 Best Local Similarity: 100.00%
 Indels: 0
 Query Match:
 RESULT 40
 ID ABO61039 standard; cDNA; 1100 BP.
 DE Human PRO1558 protein encoding sequence.
 PN WO200231111-A2.
 PD 18-APR-2002.
 PA (HYSE-) HYSEQ INC.
 Percent Similarity: 100.00%
 Best Local Similarity: 100.00%
 Indels: 0
 Query Match:
 RESULT 41
 ID AAH33455 standard; cDNA; 967 BP.
 DE Human colon cancer antigen encoding cDNA SEQ ID NO:511.
 PN WO200122920-A2.
 PD 05-APR-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Percent Similarity: 98.85%
 Best Local Similarity: 98.85%
 Indels: 3
 Query Match:
 RESULT 42
 ID AAC76634 standard; cDNA; 812 BP.
 DE Human ORFX ORF2189 polynucleotide sequence SEQ ID NO:4377.
 PN WO200058473-A2.
 PD 05-OCT-2000.
 PA (CURA-) CURAGEN CORP.
 Percent Similarity: 99.14%
 Best Local Similarity: 99.14%
 Indels: 2
 Query Match: 87.79%
 RESULT 43

ID ABE061039 standard; cDNA; 1100 BP.
 DE Human PRO1558 protein encoding sequence.
 PN WO200231111-A2.
 PD 18-APR-2002.
 PA (HYSE-) HYSEQ INC.
 Percent Similarity: 100.00%
 Best Local Similarity: 100.00%
 Indels: 0
 Query Match:
 RESULT 41
 ID AAH33455 standard; cDNA; 967 BP.
 DE Human colon cancer antigen encoding cDNA SEQ ID NO:511.
 PN WO200122920-A2.
 PD 05-APR-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Percent Similarity: 98.85%
 Best Local Similarity: 98.85%
 Indels: 3
 Query Match:
 RESULT 42
 ID AAC76634 standard; cDNA; 812 BP.
 DE Human ORFX ORF2189 polynucleotide sequence SEQ ID NO:4377.
 PN WO200058473-A2.
 PD 05-OCT-2000.
 PA (CURA-) CURAGEN CORP.
 Percent Similarity: 99.14%
 Best Local Similarity: 99.14%
 Indels: 2
 Query Match: 87.79%
 RESULT 43

Percent Similarity: 92.49% Conservative: 13
 Best Local Similarity: 84.97% Mismatches: 13
 Query Match: 56.22% Indels: 0
 RESULT 47
 ID ACH35890 standard; cDNA; 458 BP.
 DE Human endothelial cell cDNA #4023.
 PD 17-APR-2003.
 PA (DRMA//) DRMANAC R T.
 PA (LABA//) LABAT I.
 PA (STAC//) STACHE-CHRAIN B.
 PA (DICK//) DICKSON M C.
 PA (JONE//) JONES L W.
 Percent Similarity: 99.02% Conservative: 1
 Best Local Similarity: 98.04% Mismatches: 1
 Query Match: 37.90% Indels: 0
 RESULT 48
 ID ACH35195 standard; cDNA; 474 BP.
 DE Human endothelial cell cDNA #3328.
 PD 17-APR-2003.
 PA (DRMA//) DRMANAC R T.
 PA (LABA//) LABAT I.
 PA (STAC//) STACHE-CHRAIN B.
 PA (DICK//) DICKSON M C.
 PA (JONE//) JONES L W.
 Percent Similarity: 99.02% Conservative: 1
 Best Local Similarity: 98.04% Mismatches: 1
 Query Match: 37.90% Indels: 0
 RESULT 49
 ID ADM80035 standard; DNA; 11171 BP.
 DE Spiramycin biosynthesis related DNA, SEQ ID 2.
 PN FR2845394-A1.
 PD 09-APR-2004.
 PA (AVET) AVENTIS PHARMA SA.
 PA (CNRS) CNRS.
 Percent Similarity: 50.49% Conservative: 35
 Best Local Similarity: 39.09% Mismatches: 96
 Query Match: 33.73% Indels: 56
 RESULT 50
 ID ADN97551 standard; DNA; 11171 BP.
 DE S ambofaciens spiramycin biosynthetic enzyme genomic region #2.
 PN WO2004033689-A2.
 PD 22-APR-2004.
 PA (AVET) AVENTIS PHARMA SA.
 PA (CNRS) CNRS.
 Percent Similarity: 50.49% Conservative: 35
 Best Local Similarity: 39.09% Mismatches: 96
 Query Match: 33.73% Indels: 56
 RESULT 51
 ID AAA81501 standard; DNA; 48275 BP.
 DE N. meningitidis partial DNA sequence gnm_48 SEQ ID NO:48.
 PN WO200022430-A2.
 PD 20-APR-2000.
 PA (CHIR) CHIRON CORP.
 Percent Similarity: 53.45% Conservative: 48
 Best Local Similarity: 36.90% Mismatches: 98
 Query Match: 33.54% Indels: 37
 RESULT 52
 ID AAA81489 standard; DNA; 837096 BP.
 DE N. meningitidis partial DNA sequence gnm_37 SEQ ID NO:37.
 PN WO200022430-A2.
 PD 20-APR-2000.
 PA (CHIR) CHIRON CORP.
 Percent Similarity: 53.45% Conservative: 48
 Best Local Similarity: 36.90% Mismatches: 98
 Query Match: 33.54% Indels: 37
 RESULT 53
 ID AAP21610 standard; DNA; 349980 BP.
 DE Neisseria meningitidis B nucleotide sequence SEQ ID NO:111.
 PN WO200066791-A1.
 PD 09-NOV-2000.
 PA (CHIR) CHIRON CORP.

PA (GENO-) INST GENOMIC RES.
 Percent Similarity: 53.45% Conservative: 48
 Best Local Similarity: 36.90% Mismatches: 98
 Query Match: 33.54% Indels: 37
 RESULT 54
 ID AB240101 standard; DNA; 666 BP.
 DE N. gonorrhoeae nucleotide sequence SEQ ID 4791.
 PN WO200279243-A2.
 PD 10-OCT-2002.
 PA (CHIR-) CHIRON SPA.
 Percent Similarity: 62.15% Conservative: 42
 Best Local Similarity: 42.52% Mismatches: 71
 Query Match: 32.69% Indels: 10
 RESULT 55
 ID ADM80044 standard; DNA; 675 BP.
 DE Spiramycin biosynthesis orf5*, SEQ ID 11.
 PN FR2845394-A1.
 PD 09-APR-2004.
 PA (AVET) AVENTIS PHARMA SA.
 PA (CNRS) CNRS CENT NAT RECH SCI.
 Percent Similarity: 60.99% Conservative: 33
 Best Local Similarity: 46.19% Mismatches: 80
 Query Match: 32.61% Indels: 8
 RESULT 56
 ID ADN97560 standard; DNA; 675 BP.
 DE S ambofaciens spiramycin biosynthetic gene ORF5*.
 PN WO2004033689-A2.
 PD 22-APR-2004.
 PA (AVET) AVENTIS PHARMA SA.
 PA (CNRS) CNRS.
 Percent Similarity: 60.99% Conservative: 33
 Best Local Similarity: 46.19% Mismatches: 80
 Query Match: 32.61% Indels: 8
 RESULT 57
 ID ABD04592 standard; DNA; 846 BP.
 DE Pseudomonas aeruginosa polynucleotide #3196.
 PN US6551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Percent Similarity: 55.19% Conservative: 31
 Best Local Similarity: 42.32% Mismatches: 82
 Query Match: 31.94% Indels: 26
 RESULT 58
 ID AAQ44449 standard; DNA; 2381 BP.
 DE 3-acylating enzyme coding sequence.
 PN JP06038750-A.
 PD 15-FEB-1994.
 PA (MEIJ) MEIJI SEIKA KAISHA.
 Percent Similarity: 54.12% Conservative: 37
 Best Local Similarity: 39.61% Mismatches: 94
 Query Match: 31.68% Indels: 24
 RESULT 59
 ID ADM45913 standard; DNA; 84428 BP.
 DE Streptomyces mycarofaciens midcamycin polyketide synthetase DNA.
 PN JP2004049100-A.
 PD 19-FEB-2004.
 PA (MEIJ) MEIJI SEIKA KAISHA LTD.
 Percent Similarity: 54.12% Conservative: 37
 Best Local Similarity: 39.61% Mismatches: 94
 Query Match: 31.68% Indels: 24
 RESULT 60
 ID AAX25215 standard; cDNA; 1218 BP.
 DE Maize caffeoyl-CoA 3-O-methyltransferase cDNA.
 PN WO9910498-A2.
 PD 04-MAR-1999.
 PA (PION-) PIONEER HI-BRED INT INC.
 Percent Similarity: 56.59% Conservative: 45
 Best Local Similarity: 39.15% Mismatches: 97
 Query Match: 30.75% Indels: 15
 RESULT 61
 ID AAD05742 standard; cDNA; 1218 BP.
 DE Maize caffeoyl-CoA 3-O-methyltransferase (cCoA-OMT) cDNA.
 PN WO200134817-A2.

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RESULT 76
 ID ADC68544 standard; cDNA; 1059 BP.
 DE Lolium perenne lignin biosynthesis protein cDNA SEQ ID NO:36.
 PN WO2003040306-A2.
 PD 15-MAY-2003.
 PA (GENE-) WRIGHTSON SEEDS LTD.
 PA (WRIG-) GENESIS RES & DEV CORP LTD.
 Percent Similarity: 56.43% Conservative: 42
 Best Local Similarity: 39.00% Mismatches: 87
 Query Match: 29.23% Indels: 18
 RESULT 77
 ID ADN74200 standard; cDNA; 780 BP.
 DE Thale cress cDNA repressed in E2Fa/Dpa expressing plants SeqID 2095.
 PN WO2004035798-A2.
 PD 29-APR-2004.
 PA (CROP-) CROPDESIGN NV.
 Percent Similarity: 58.85% Conservative: 48
 Best Local Similarity: 37.61% Mismatches: 82
 Query Match: 29.15% Indels: 11
 RESULT 78
 ID ADN73162 standard; cDNA; 780 BP.
 DE Thale cress cDNA upregulated in E2Fa/Dpa expressing plants SeqID 1057.
 PN WO2004035798-A2.
 PD 29-APR-2004.
 PA (CROP-) CROPDESIGN NV.
 Percent Similarity: 58.85% Conservative: 48
 Best Local Similarity: 37.61% Mismatches: 82
 Query Match: 29.15% Indels: 11
 RESULT 79
 ID AAC42559 standard; DNA; 1033 BP.
 DE Arabidopsis thaliana DNA fragment SEQ ID NO: 36009.
 PN EP1033405-A2.
 PD 06-SEP-2000.
 PA (ANY/) AN Y.
 Percent Similarity: 58.85% Conservative: 48
 Best Local Similarity: 37.61% Mismatches: 82
 Query Match: 29.15% Indels: 11
 RESULT 80
 ID ABN98364 standard; DNA; 1072 BP.
 DE Arabidopsis thaliana expressed polynucleotide SEQ ID NO 132.
 PN US2002023281-A1.
 PD 21-FEB-2002.
 PA (GORL/) GORLACH J.
 PA (ANY/) AN Y.
 PA (HAMI/) HAMILTON C M.
 PA (PRIC/) PRICE J L.
 PA (RAIN/) RAINES T M.
 PA (YUYV/) YU Y.
 PA (RAME/) RAMEAKA J G.
 PA (PAGE/) PAGE A.
 PA (MATH/) MATHEW A V.
 PA (LEDF/) LEDFORD B L.
 PA (WOES/) WOESSNER J P.
 PA (HAAS/) HAAS W D.
 PA (GARC/) GARCIA C A.
 PA (KRIC/) KRICKER M.
 PA (SLAT/) SLATER T.
 PA (DAVI/) DAVIS K R.
 PA (ALLE/) ALLEN K.
 PA (HOFF/) HOFFMAN N.
 PA (HURB/) HURBAN P.
 Percent Similarity: 58.85% Conservative: 48
 Best Local Similarity: 37.61% Mismatches: 82
 Query Match: 29.15% Indels: 11
 RESULT 81
 ID AAC4172 standard; DNA; 1180 BP.
 DE Arabidopsis thaliana DNA fragment SEQ ID NO: 41890.
 PN EP1033405-A2.
 PD 06-SEP-2000.
 Percent Similarity: 58.85% Conservative: 48
 Best Local Similarity: 37.61% Mismatches: 82
 Query Match: 29.15% Indels: 11
 RESULT 82
 ID AAC45547 standard; DNA; 1032 BP.
 DE Arabidopsis thaliana DNA fragment SEQ ID NO: 46896.
 PN EP1033405-A2.
 PD 06-SEP-2000.
 Percent Similarity: 55.14% Conservative: 49
 Best Local Similarity: 34.98% Mismatches: 88
 Query Match: 29.00% Indels: 21
 RESULT 83
 ID ABS63413 standard; cDNA; 997 BP.
 DE DNA encoding rice caffeoyl-CoA O-methyltransferase (CCOMT).
 PN US2002081693-A1.
 PD 27-JUN-2002.
 PA (CAHO/) CAHOON R E.
 PA (FADE/) FADER G M.
 PA (RAPA/) RAPALSKI J A.
 Percent Similarity: 57.47% Conservative: 40
 Best Local Similarity: 39.37% Mismatches: 82
 Query Match: 28.97% Indels: 12
 RESULT 84
 ID ABS63429 standard; cDNA; 953 BP.
 DE DNA encoding wheat caffeoyl-CoA O-methyltransferase (CCOMT).
 PN US2002081693-A1.
 PD 27-JUN-2002.
 PA (CAHO/) CAHOON R E.
 PA (FADE/) FADER G M.
 PA (RAPA/) RAPALSKI J A.
 Percent Similarity: 55.51% Conservative: 46
 Best Local Similarity: 38.60% Mismatches: 104
 Query Match: 28.82% Indels: 18
 RESULT 85
 ID ABS54115 standard; DNA; 967 BP.
 DE Tobacco caffeoyl CoA O-methyltransferase-9 (COAOMT-9) cDNA.
 PN US6441272-B1.
 PD 27-AUG-2002.
 PA (UYGE-) UNIV GEORGIA RES FOUND INC.
 Percent Similarity: 58.56% Conservative: 48
 Best Local Similarity: 36.94% Mismatches: 83
 Query Match: 28.78% Indels: 9
 RESULT 86
 ID ADM49212 standard; DNA; 798 BP.
 DE Maize gene conferring disease resistance in plants.
 PN WO2003000506-A2.
 PD 03-JAN-2003.
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 Percent Similarity: 55.56% Conservative: 48
 Best Local Similarity: 37.16% Mismatches: 91
 Query Match: 28.74% Indels: 25
 RESULT 87
 ID AAK68001 standard; DNA; 1012 BP.
 DE Pinus radiata OMT nucleotide sequence SEQ ID NO:94.
 PN WO200022099-A1.
 PD 20-APR-2000.
 PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.
 PA (GENE-) GENESIS RES & DEV CORP LTD.
 Percent Similarity: 57.56% Conservative: 51
 Best Local Similarity: 36.13% Mismatches: 88
 Query Match: 28.74% Indels: 13
 RESULT 88
 ID ADD41751 standard; DNA; 1012 BP.
 DE O-methyl transferase DNA #9.
 PN US2003131373-A1.
 PD 10-JUL-2003.
 PA (BLOK/) BLOKSBERG L N.
 PA (HAVU/) HAVUKKALA I.
 Percent Similarity: 57.56% Conservative: 51
 Best Local Similarity: 36.13% Mismatches: 88
 Query Match: 28.74% Indels: 13
 RESULT 89
 ID AAV23912 standard; DNA; 1026 BP.
 DE Plant OMT enzyme DNA sequence.
 PN WO9811205-A2.
 PD 19-MAR-1998.
 PA (GENE-) GENESIS RES & DEV CORP LTD.
 PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.

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Percent Similarity: 57.56%      Conservative: 51
Best Local Similarity: 36.13%    Mismatches: 88
Query Match: 28.74%             Indels: 13
RESULT 90
ID AA206875 standard; cDNA; 1026 BP.
DE Pine O-methyl transferase (OMT) partial cDNA 1.
PD US952486-A.
PD 14-SEP-1999.
PA (GENE-) GENESIS RES & DEV CORP LTD.
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.
Percent Similarity: 57.56%      Conservative: 51
Best Local Similarity: 36.13%    Mismatches: 88
Query Match: 28.74%             Indels: 13
RESULT 91
ID AAA67913 standard; DNA; 1026 BP.
DE Pinus radiata OMT nucleotide sequence SEQ ID NO:6.
PD WO200022099-A1.
PD 20-APR-2000.
PA (GENE-) GENESIS RES & DEV CORP LTD.
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.
Percent Similarity: 57.56%      Conservative: 51
Best Local Similarity: 36.13%    Mismatches: 88
Query Match: 28.74%             Indels: 13
RESULT 92
ID ADD41663 standard; DNA; 1026 BP.
DE O-methyl transferase DNA #1.
PD US200311373-A1.
PD 10-JUL-2003.
PA (BLOK/) BLOKSBERG L N.
PA (HAVU/) HAVUKKALA I.
Percent Similarity: 57.56%      Conservative: 51
Best Local Similarity: 36.13%    Mismatches: 88
Query Match: 28.74%             Indels: 13
RESULT 93
ID ABS63425 standard; cDNA; 1118 BP.
DE DNA encoding wheat caffeoyl-CoA O-methyltransferase (CCOMT).
PD US2002081693-A1.
PD 27-JUN-2002.
PA (CAHO/) CAHOON R E.
PA (FADE/) FADER G M.
PA (RAFA/) RAFALSKI J A.
Percent Similarity: 55.56%      Conservative: 48
Best Local Similarity: 37.16%    Mismatches: 91
Query Match: 28.74%             Indels: 25
RESULT 94
ID ABS63408 standard; cDNA; 1146 BP.
DE DNA encoding corn caffeoyl-CoA O-methyltransferase (CCOMT).
PD US2002081693-A1.
PD 27-JUN-2002.
PA (CAHO/) CAHOON R E.
PA (FADE/) FADER G M.
PA (RAFA/) RAFALSKI J A.
Percent Similarity: 55.56%      Conservative: 48
Best Local Similarity: 37.16%    Mismatches: 91
Query Match: 28.74%             Indels: 25
RESULT 95
ID AAX25208 standard; cDNA; 1160 BP.
DE Maize caffeoyl-CoA 3-O-methyltransferase cDNA.
PD WO9910498-A2.
PD 04-MAR-1999.
PA (PION-) PIONEER HI-BRED INT INC.
PA (FADE/) FADER G M.
Percent Similarity: 55.56%      Conservative: 48
Best Local Similarity: 37.16%    Mismatches: 91
Query Match: 28.74%             Indels: 25
RESULT 96
ID ABS63415 standard; cDNA; 931 BP.
DE DNA encoding soybean caffeoyl-CoA O-methyltransferase (CCOMT).
PD US2002081693-A1.
PD 27-JUN-2002.
PA (CAHO/) CAHOON R E.
PA (FADE/) FADER G M.
Percent Similarity: 55.56%      Conservative: 47
Best Local Similarity: 37.16%    Mismatches: 95
Query Match: 28.74%             Indels: 10
RESULT 97
ID ADC68545 standard; cDNA; 1063 BP.
DE S. arundinaceus lignin biosynthesis protein cDNA SEQ ID NO:37.
PD WO2003040306-A2.
PD 15-MAY-2003.
PA (GENE-) GENESIS RES & DEV CORP LTD.
PA (WRIG-) WRIGHTSON SEEDS LTD.
Percent Similarity: 54.85%      Conservative: 46
Best Local Similarity: 37.69%    Mismatches: 101
Query Match: 28.70%             Indels: 21
RESULT 98
ID ADA71075 standard; DNA; 783 BP.
DE Rice gene, SEQ ID 4398.
PD WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Percent Similarity: 52.73%      Conservative: 36
Best Local Similarity: 38.67%    Mismatches: 94
Query Match: 28.59%             Indels: 27
RESULT 99
ID AAX25210 standard; cDNA; 1003 BP.
DE Maize caffeoyl-CoA 3-O-methyltransferase cDNA.
PD WO9910498-A2.
PD 04-MAR-1999.
PA (PION-) PIONEER HI-BRED INT INC.
Percent Similarity: 52.55%      Conservative: 44
Best Local Similarity: 36.50%    Mismatches: 101
Query Match: 28.56%             Indels: 30
RESULT 100
ID ABS63409 standard; cDNA; 1057 BP.
DE DNA encoding corn caffeoyl-CoA O-methyltransferase (CCOMT).
PD US2002081693-A1.
PD 27-JUN-2002.
PA (CAHO/) CAHOON R E.
PA (FADE/) FADER G M.
PA (RAFA/) RAFALSKI J A.
Percent Similarity: 52.55%      Conservative: 44
Best Local Similarity: 36.50%    Mismatches: 101
Query Match: 28.56%             Indels: 30
RESULT 101
ID ABS63416 standard; cDNA; 929 BP.
DE DNA encoding soybean caffeoyl-CoA O-methyltransferase (CCOMT).
PD US2002081693-A1.
PD 27-JUN-2002.
PA (CAHO/) CAHOON R E.
PA (FADE/) FADER G M.
PA (RAFA/) RAFALSKI J A.
Percent Similarity: 56.43%      Conservative: 47
Best Local Similarity: 36.93%    Mismatches: 95
Query Match: 28.48%             Indels: 10
RESULT 102
ID ABS63428 standard; cDNA; 1049 BP.
DE DNA encoding wheat caffeoyl-CoA O-methyltransferase (CCOMT).
PD US2002081693-A1.
PD 27-JUN-2002.
PA (CAHO/) CAHOON R E.
PA (FADE/) FADER G M.
PA (RAFA/) RAFALSKI J A.
Percent Similarity: 55.15%      Conservative: 46
Best Local Similarity: 38.24%    Mismatches: 105
Query Match: 28.37%             Indels: 18
RESULT 103
ID ABS54114 standard; DNA; 845 BP.
DE Tobacco caffeoyl CoA O-methyltransferase-3 (CCOAMT-3) cDNA.
PD US6441272-B1.
PD 27-AUG-2002.
PA (UYGE-) UNIV GEORGIA RES FOUND INC.
Percent Similarity: 57.66%      Conservative: 47
Best Local Similarity: 36.49%    Mismatches: 85
Query Match: 28.26%             Indels: 9
RESULT 104

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ID ADA49019 standard; DNA; 1112 BP.
 DE Wheat gene conferring disease resistance in plants.
 PN WO200300906-A2.
 PD 03-JAN-2003.
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 Percent Similarity: 53.59% Conservative: 40
 Best Local Similarity: 38.43% Mismatches: 103
 Query Match: 28.22% Indels: 22
 RESULT 105
 ID AAX25209 standard; cDNA; 944 BP.
 DE Maize caffeoyl-CoA 3-O-methyltransferase cDNA.
 PN WO9910498-A2.
 PD 04-MAR-1999.
 PA (PTON-) PIONEER HI-BRED INT INC.
 Percent Similarity: 52.42% Conservative: 42
 Best Local Similarity: 36.80% Mismatches: 114
 Query Match: 28.15% Indels: 15
 RESULT 106
 ID ABN87108 standard; cDNA; 1113 BP.
 DE Lolium perenne LpCCOAWTA nucleotide sequence SEQ ID NO:1.
 PN WO200226994-A1.
 PD 04-APR-2002.
 PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.
 Percent Similarity: 56.02% Conservative: 44
 Best Local Similarity: 37.78% Mismatches: 88
 Query Match: 28.11% Indels: 18
 RESULT 107
 ID ABN87245 standard; cDNA; 1161 BP.
 DE Lolium perenne CCOAWT1 cDNA sequence SEQ ID NO:168.
 PN WO200226994-A1.
 PD 04-APR-2002.
 PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.
 Percent Similarity: 56.41% Conservative: 43
 Best Local Similarity: 38.03% Mismatches: 88
 Query Match: 28.03% Indels: 14
 RESULT 108
 ID AAQ32259 standard; cDNA; 1258 BP.
 DE Caffeoyl-CoA-3-O-methyltransferase gene (pL2-4).
 PN DB4117747-A.
 PD 03-DEC-1992.
 PA (FARB) BAYER AG.
 Percent Similarity: 57.21% Conservative: 45
 Best Local Similarity: 36.94% Mismatches: 86
 Query Match: 28.03% Indels: 9
 RESULT 109
 ID ABS63410 standard; cDNA; 923 BP.
 DE DNA encoding corn caffeoyl-CoA O-methyltransferase (CCOAWT).
 PN US2002081693-A1.
 PD 27-JUN-2002.
 PA (CAHO/) CAHOON R E.
 PA (FADE/) FADER G M.
 PA (RAPA/) RAPALSKI J A.
 Percent Similarity: 53.10% Conservative: 41
 Best Local Similarity: 37.21% Mismatches: 109
 Query Match: 28.00% Indels: 13
 RESULT 110
 ID ABN87246 standard; cDNA; 1199 BP.
 DE Lolium perenne CCOAWT2 cDNA sequence SEQ ID NO:170.
 PN WO200226994-A1.
 PD 04-APR-2002.
 PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.
 Percent Similarity: 56.36% Conservative: 42
 Best Local Similarity: 38.58% Mismatches: 85
 Query Match: 27.89% Indels: 18
 RESULT 111
 ID ABS54112 standard; DNA; 870 BP.
 DE Tobacco caffeoyl CoA O-methyltransferase-1 (CCOAWT-1) cDNA.
 PN US6441272-B1.
 PD 27-AUG-2002.
 PA (UYGE-) UNIV GEORGIA RES FOUND INC.

Percent Similarity: 58.11% Conservative: 50
 Best Local Similarity: 35.59% Mismatches: 84
 Query Match: 27.81% Indels: 9
 RESULT 112
 ID ABS54113 standard; DNA; 811 BP.
 DE Tobacco caffeoyl CoA O-methyltransferase-2 (CCOAWT-2) cDNA.
 PN US6441272-B1.
 PD 27-AUG-2002.
 PA (UYGE-) UNIV GEORGIA RES FOUND INC.
 Percent Similarity: 58.72% Conservative: 49
 Best Local Similarity: 36.24% Mismatches: 81
 Query Match: 27.74% Indels: 9
 RESULT 113
 ID AAC45004 standard; DNA; 917 BP.
 DE Arabidopsis thaliana DNA fragment SEQ ID NO: 44938.
 PN EP1033405-A2.
 PD 06-SEP-2000.
 Percent Similarity: 56.64% Conservative: 40
 Best Local Similarity: 38.94% Mismatches: 86
 Query Match: 27.48% Indels: 12
 RESULT 114
 ID ABS63424 standard; cDNA; 1018 BP.
 DE DNA encoding wheat caffeoyl-CoA O-methyltransferase (CCOAWT).
 PN US2002081693-A1.
 PD 27-JUN-2002.
 PA (CAHO/) CAHOON R E.
 PA (FADE/) FADER G M.
 PA (RAPA/) RAPALSKI J A.
 Percent Similarity: 50.55% Conservative: 42
 Best Local Similarity: 35.06% Mismatches: 84
 Query Match: 27.44% Indels: 50
 RESULT 115
 ID ADA48371 standard; DNA; 835 BP.
 DE Rice gene conferring disease resistance in plants.
 PN WO200300906-A2.
 PD 03-JAN-2003.
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 Percent Similarity: 56.76% Conservative: 46
 Best Local Similarity: 39.00% Mismatches: 89
 Query Match: 27.36% Indels: 24
 RESULT 116
 ID ABN94134 standard; DNA; 326 BP.
 DE Gene #632 used to diagnose liver cancer.
 PN WO200229103-A2.
 PD 11-APR-2002.
 PA (GENE-) GENE LOGIC INC.
 Percent Similarity: 98.65% Conservative: 0
 Best Local Similarity: 98.85% Mismatches: 0
 Query Match: 27.25% Indels: 1
 RESULT 117
 ID ABN87118 standard; cDNA; 1103 BP.
 DE Lolium perenne LpCCOAWTB nucleotide sequence SEQ ID NO:12.
 PN WO200226994-A1.
 PD 04-APR-2002.
 PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.
 Percent Similarity: 54.23% Conservative: 50
 Best Local Similarity: 35.00% Mismatches: 100
 Query Match: 26.99% Indels: 19
 RESULT 118
 ID ABZ14595 standard; DNA; 729 BP.
 DE Arabidopsis thaliana stress regulated gene SEQ ID NO 2400.
 PN WO200216655-A2.
 PD 28-FEB-2002.
 PA (SCRI) SCRIPPS RES INST.
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 Percent Similarity: 56.28% Conservative: 37
 Best Local Similarity: 39.07% Mismatches: 84
 Query Match: 26.81% Indels: 10
 RESULT 119
 ID AAC42096 standard; DNA; 1186 BP.
 DE Arabidopsis thaliana DNA fragment SEQ ID NO: 34272.
 PN EP1033405-A2.

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PD 06-SEP-2000.
Percent Similarity: 60.66%
Best Local Similarity: 37.91%
Query Match: 26.58%
Conservative: 48
Mismatch: 76
Indels: 7
RESULT 120
ID ADH02852 standard; cDNA; 1006 BP.
DE Torenia TWT5.nt cDNA #SEQ ID 11.
PN WO2003062428-A1.
PD 31-JUL-2003.
PA (ITFL-) INT FLOWER DEV PTY LTD.
Percent Similarity: 56.58%
Best Local Similarity: 36.40%
Query Match: 26.40%
Conservative: 46
Mismatch: 84
Indels: 15
RESULT 121
ID ABS63420 standard; cDNA; 912 BP.
DE DNA encoding soybean caffeoyl-CoA O-methyltransferase (CCOMT).
PN US2002081693-A1.
PD 27-JUN-2002.
PA (CAHO/) CAHOON R E.
PA (FADE/) FADER G M.
PA (RAFA/) RAFALSKI J A.
Percent Similarity: 53.71%
Best Local Similarity: 36.68%
Query Match: 26.36%
Conservative: 39
Mismatch: 96
Indels: 10
RESULT 122
ID ADK69931 standard; DNA; 1181 BP.
DE Maize W64A CCoAOMT2 gene substitution mutant #10.
PN FR2833615-A1.
PD 20-JUN-2003.
PA (GENO-) GENOPLANTE-VALOR SAS.
Percent Similarity: 48.57%
Best Local Similarity: 32.50%
Query Match: 26.32%
Conservative: 45
Mismatch: 71
Indels: 73
RESULT 123
ID ADK69906 standard; DNA; 1180 BP.
DE Maize F4 CCoAOMT2 gene, seq id 3.
PN FR2833615-A1.
PD 20-JUN-2003.
PA (GENO-) GENOPLANTE-VALOR SAS.
Percent Similarity: 41.83%
Best Local Similarity: 29.36%
Query Match: 26.28%
Conservative: 45
Mismatch: 98
Indels: 112
RESULT 124
ID ADK69932 standard; DNA; 1199 BP.
DE Maize W64A CCoAOMT2 gene insertion mutant #5.
PN FR2833615-A1.
PD 20-JUN-2003.
PA (GENO-) GENOPLANTE-VALOR SAS.
Percent Similarity: 42.90%
Best Local Similarity: 30.11%
Query Match: 26.21%
Conservative: 45
Mismatch: 97
Indels: 104
RESULT 125
ID ADK69927 standard; DNA; 1178 BP.
DE Maize W64A CCoAOMT2 gene deletion mutant #2.
PN FR2833615-A1.
PD 20-JUN-2003.
PA (GENO-) GENOPLANTE-VALOR SAS.
Percent Similarity: 48.39%
Best Local Similarity: 32.62%
Query Match: 26.14%
Conservative: 44
Mismatch: 72
Indels: 72
RESULT 126
ID ADK69925 standard; DNA; 1196 BP.
DE Maize W64A CCoAOMT2 gene insertion mutant #3.
PN FR2833615-A1.
PD 20-JUN-2003.
PA (GENO-) GENOPLANTE-VALOR SAS.
Percent Similarity: 46.67%
Best Local Similarity: 33.33%
Query Match: 26.14%
Conservative: 38
Mismatch: 74
Indels: 78
RESULT 127
ID ADK69918 standard; DNA; 1172 BP.
DE Maize W64A CCoAOMT2 gene deletion mutant #1.
PN FR2833615-A1.
PD 20-JUN-2003.
PA (GENO-) GENOPLANTE-VALOR SAS.
Percent Similarity: 48.21%
Best Local Similarity: 32.50%
Query Match: 26.10%
Conservative: 44
Mismatch: 72
Indels: 73
RESULT 128
ID ADK69919 standard; DNA; 1181 BP.
DE Maize W64A CCoAOMT2 gene substitution mutant #1.
PN FR2833615-A1.
PD 20-JUN-2003.
PA (GENO-) GENOPLANTE-VALOR SAS.
Percent Similarity: 48.21%
Best Local Similarity: 32.50%
Query Match: 26.10%
Conservative: 44
Mismatch: 72
Indels: 73
RESULT 129
ID ADK69920 standard; DNA; 1181 BP.
DE Maize W64A CCoAOMT2 gene substitution mutant #2.
PN FR2833615-A1.
PD 20-JUN-2003.
PA (GENO-) GENOPLANTE-VALOR SAS.
Percent Similarity: 48.21%
Best Local Similarity: 32.50%
Query Match: 26.10%
Conservative: 44
Mismatch: 72
Indels: 73
RESULT 130
ID ADK69928 standard; DNA; 1181 BP.
DE Maize W64A CCoAOMT2 gene substitution mutant #7.
PN FR2833615-A1.
PD 20-JUN-2003.
PA (GENO-) GENOPLANTE-VALOR SAS.
Percent Similarity: 48.21%
Best Local Similarity: 32.50%
Query Match: 26.10%
Conservative: 44
Mismatch: 72
Indels: 73
RESULT 131
ID ADK69923 standard; DNA; 1181 BP.
DE Maize W64A CCoAOMT2 gene substitution mutant #5.
PN FR2833615-A1.
PD 20-JUN-2003.
PA (GENO-) GENOPLANTE-VALOR SAS.
Percent Similarity: 48.21%
Best Local Similarity: 32.50%
Query Match: 26.10%
Conservative: 44
Mismatch: 72
Indels: 73
RESULT 132
ID ADK69904 standard; DNA; 1181 BP.
DE Maize W64A CCoAOMT2 gene, seq id 1.
PN FR2833615-A1.
PD 20-JUN-2003.
PA (GENO-) GENOPLANTE-VALOR SAS.
Percent Similarity: 48.21%
Best Local Similarity: 32.50%
Query Match: 26.10%
Conservative: 44
Mismatch: 72
Indels: 73
RESULT 133
ID ADK69922 standard; DNA; 1181 BP.
DE Maize W64A CCoAOMT2 gene substitution mutant #4.
PN FR2833615-A1.
PD 20-JUN-2003.
PA (GENO-) GENOPLANTE-VALOR SAS.
Percent Similarity: 48.21%
Best Local Similarity: 32.50%
Query Match: 26.10%
Conservative: 44
Mismatch: 72
Indels: 73
RESULT 134
ID ADK69924 standard; DNA; 1181 BP.
DE Maize W64A CCoAOMT2 gene substitution mutant #6.
PN FR2833615-A1.
PD 20-JUN-2003.
PA (GENO-) GENOPLANTE-VALOR SAS.
Percent Similarity: 48.21%
Best Local Similarity: 32.50%
Query Match: 26.10%
Conservative: 44
Mismatch: 72
Indels: 73
RESULT 135
ID ADK69929 standard; DNA; 1181 BP.
DE Maize W64A CCoAOMT2 gene substitution mutant #8.
PN FR2833615-A1.
PD 20-JUN-2003.
PA (GENO-) GENOPLANTE-VALOR SAS.
Percent Similarity: 48.21%
Best Local Similarity: 32.50%
Query Match: 26.10%
Conservative: 44
Mismatch: 72
Indels: 73

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PA (GENO-) GENOPLANTE-VALOR SAS.
 Percent Similarity: 48.21%
 Best Local Similarity: 32.50%
 Query Match: 26.10%
 RESULT 136
 ID ADK69921 standard; DNA; 1181 BP.
 DE Maize W64A CCoAOMT2 gene substitution mutant #3.
 PN FR2833615-A1.
 PD 20-JUN-2003.
 PA (GENO-) GENOPLANTE-VALOR SAS.
 Percent Similarity: 48.21%
 Best Local Similarity: 32.50%
 Query Match: 26.10%
 RESULT 137
 ID ADK69930 standard; DNA; 1181 BP.
 DE Maize W64A CCoAOMT2 gene substitution mutant #9.
 PN FR2833615-A1.
 PD 20-JUN-2003.
 PA (GENO-) GENOPLANTE-VALOR SAS.
 Percent Similarity: 48.21%
 Best Local Similarity: 32.50%
 Query Match: 26.10%
 RESULT 138
 ID ADK69917 standard; DNA; 1186 BP.
 DE Maize W64A CCoAOMT2 gene insertion mutant #1.
 PN FR2833615-A1.
 PD 20-JUN-2003.
 PA (GENO-) GENOPLANTE-VALOR SAS.
 Percent Similarity: 48.21%
 Best Local Similarity: 32.50%
 Query Match: 26.10%
 RESULT 139
 ID ADH02845 standard; cDNA; 888 BP.
 DE Petunia E20 cDNA #SEQ ID 4.
 PN WO2003062428-A1.
 PD 31-JUL-2003.
 PA (ITFL-) INT FLOWER DEV PTY LTD.
 Percent Similarity: 54.39%
 Best Local Similarity: 37.66%
 Query Match: 25.99%
 RESULT 140
 ID ADH02842 standard; cDNA; 969 BP.
 DE Petunia dife cDNA #SEQ ID 1.
 PN WO2003062428-A1.
 PD 31-JUL-2003.
 PA (ITFL-) INT FLOWER DEV PTY LTD.
 Percent Similarity: 54.39%
 Best Local Similarity: 37.66%
 Query Match: 25.99%
 RESULT 141
 ID AAA14651 standard; DNA; 77536 BP.
 DE Nucleotide sequence of the FK-520 biosynthetic gene cluster.
 Percent Similarity: 51.97%
 Best Local Similarity: 38.43%
 Query Match: 25.91%
 RESULT 142
 ID ADK69926 standard; DNA; 1199 BP.
 DE Maize W64A CCoAOMT2 gene insertion mutant #4.
 PN FR2833615-A1.
 PD 20-JUN-2003.
 PA (GENO-) GENOPLANTE-VALOR SAS.
 Percent Similarity: 47.20%
 Best Local Similarity: 31.82%
 Query Match: 25.87%
 RESULT 143
 ID ABS63422 standard; cDNA; 982 BP.
 DE DNA encoding soybean caffeoyl-CoA O-methyltransferase (CCOMT).
 PN US2002081693-A1.
 PD 27-JUN-2002.
 PA (CAHO/) CAHOON R E.
 PA (FADE/) FADER G M.
 PA (RAFA/) RAFALSKI J A.
 Percent Similarity: 55.14%
 Conservative: 37

Best Local Similarity: 37.85%
 Query Match: 25.39%
 RESULT 144
 ID AAL61224 standard; DNA; 82746 BP.
 DE Actinosynnema pretiosum anisamitocin biosynthetic gene cluster I.
 PN WO2003045312-A2.
 PD 05-JUN-2003.
 PA (UNIW) UNIV WASHINGTON.
 Percent Similarity: 52.63%
 Best Local Similarity: 40.35%
 Query Match: 25.32%
 RESULT 145
 ID ADH02867 standard; cDNA; 1079 BP.
 DE Petunia E33 (corrected) cDNA #SEQ ID 26.
 PN WO2003062428-A1.
 PD 31-JUL-2003.
 PA (ITFL-) INT FLOWER DEV PTY LTD.
 Percent Similarity: 57.59%
 Best Local Similarity: 36.61%
 Query Match: 25.28%
 RESULT 146
 ID ABN87110 standard; cDNA; 758 BP.
 DE Lolium perenne LpCCoAMTa partial nucleotide sequence SEQ ID NO:4.
 PN WO200226994-A1.
 PD 04-APR-2002.
 PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.
 Percent Similarity: 51.82%
 Best Local Similarity: 34.82%
 Query Match: 25.17%
 RESULT 147
 ID ABN87115 standard; cDNA; 793 BP.
 DE Lolium perenne LpCCoAMTa partial nucleotide sequence SEQ ID NO:9.
 PN WO200226994-A1.
 PD 04-APR-2002.
 PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.
 Percent Similarity: 55.56%
 Best Local Similarity: 37.04%
 Query Match: 24.91%
 RESULT 148
 ID ABN87126 standard; cDNA; 689 BP.
 DE Lolium perenne LpCCoAMTc nucleotide sequence SEQ ID NO:21.
 PN WO200226994-A1.
 PD 04-APR-2002.
 PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.
 Percent Similarity: 55.94%
 Best Local Similarity: 41.09%
 Query Match: 24.80%
 RESULT 149
 ID ABN87112 standard; cDNA; 765 BP.
 DE Lolium perenne LpCCoAMTa partial nucleotide sequence SEQ ID NO:6.
 PN WO200226994-A1.
 PD 04-APR-2002.
 PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.
 Percent Similarity: 58.33%
 Best Local Similarity: 39.06%
 Query Match: 24.46%
 RESULT 150
 ID ADH02847 standard; cDNA; 1077 BP.
 DE Petunia E33 cDNA #SEQ ID 5.
 PN WO2003062428-A1.
 PD 31-JUL-2003.
 PA (ITFL-) INT FLOWER DEV PTY LTD.
 Percent Similarity: 56.70%
 Best Local Similarity: 36.16%
 Query Match: 24.42%
 RESULT 151
 ID ADH02884 standard; cDNA; 943 BP.
 DE Fuchsia FMT full (3289) cDNA #SEQ ID 43.
 PN WO2003062428-A1.

PN WO200226994-A1.
 PD 04-APR-2002.
 PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.
 PA (AGRE-) AGRESEARCH LTD.
 Percent Similarity: 54.25%
 Best Local Similarity: 38.68%
 Query Match: 23.45%
 Indels: 12
 Conservative: 33
 Mismatches: 86
 Indels: 12

RESULT 160
 ID ABZ13934 standard; DNA; 699 BP.
 DE Arabidopsis thaliana stress regulated gene SEQ ID NO 1739.
 PD 28-FEB-2002.
 PA (SCRI) SCRIPPS RES INST.
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 Percent Similarity: 55.00%
 Best Local Similarity: 34.09%
 Query Match: 23.19%
 Indels: 15
 Conservative: 46
 Mismatches: 84
 Indels: 15

RESULT 161
 ID ADG87603 standard; cDNA; 699 BP.
 DE A. thaliana RPP7/RPP8-upregulated pathogen infection-related gene #45.
 PD 21-MAR-2002.
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 PA (UINC-) UNIV NORTH CAROLINA.
 PA (GLAZ/) GLAZEBROOK J.
 PA (WANG/) WANG X.
 PA (DANG/) DANG J L.
 PA (EULG/) EULGEM T.
 PA (ZHUT/) ZHU T.
 Percent Similarity: 55.00%
 Best Local Similarity: 34.09%
 Query Match: 23.19%
 Indels: 15
 Conservative: 46
 Mismatches: 84
 Indels: 15

RESULT 162
 ID ADG87604 standard; cDNA; 699 BP.
 DE A. thaliana RPP7/RPP8-upregulated pathogen infection-related gene #46.
 PD 21-MAR-2002.
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 PA (UINC-) UNIV NORTH CAROLINA.
 PA (GLAZ/) GLAZEBROOK J.
 PA (WANG/) WANG X.
 PA (DANG/) DANG J L.
 PA (EULG/) EULGEM T.
 PA (ZHUT/) ZHU T.
 Percent Similarity: 55.00%
 Best Local Similarity: 34.09%
 Query Match: 23.19%
 Indels: 15
 Conservative: 46
 Mismatches: 84
 Indels: 15

RESULT 163
 ID ADG67907 standard; DNA; 699 BP.
 DE Arabidopsis thaliana gene, SEQ ID 151.
 PD 03-JAN-2003.
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 Percent Similarity: 55.00%
 Best Local Similarity: 34.09%
 Query Match: 23.19%
 Indels: 15
 Conservative: 46
 Mismatches: 84
 Indels: 15

RESULT 164
 ID AAL61190 standard; DNA; 504 BP.
 DE Actinosynnema pretiosum O-methyltransferase gene.
 PD 05-JUN-2003.
 PA (UINW) UNIV WASHINGTON.
 Percent Similarity: 57.32%
 Best Local Similarity: 43.29%
 Query Match: 22.30%
 Indels: 3
 Conservative: 23
 Mismatches: 67
 Indels: 3

RESULT 165
 ID AAV23875 standard; DNA; 1075 BP.
 DE Plant OMT enzyme DNA sequence.
 PD 19-MAR-1998.
 PA (GENE-) GENESIS RES & DEV CORP LTD.
 PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.
 Percent Similarity: 50.41%
 Indels: 47
 Conservative: 47

PD 31-JUL-2003.
 PA (ITFL-) INT FLOWER DEV PTY LTD.
 Percent Similarity: 57.47%
 Best Local Similarity: 35.75%
 Query Match: 24.35%
 Indels: 12
 Conservative: 48
 Mismatches: 82
 Indels: 12

RESULT 152
 ID ADH02882 standard; cDNA; 841 BP.
 DE Fuchsia FMT (3282) cDNA #SEQ ID 41.
 PD 31-JUL-2003.
 PA (ITFL-) INT FLOWER DEV PTY LTD.
 Percent Similarity: 58.82%
 Best Local Similarity: 37.22%
 Query Match: 24.20%
 Indels: 10
 Conservative: 44
 Mismatches: 74
 Indels: 10

RESULT 153
 ID AAC47161 standard; DNA; 738 BP.
 DE Arabidopsis thaliana DNA fragment SEQ ID NO: 52786.
 PD 06-SEP-2000.
 PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.
 PA (AGRE-) AGRESEARCH LTD.
 Percent Similarity: 56.42%
 Best Local Similarity: 36.24%
 Query Match: 24.13%
 Indels: 10
 Conservative: 44
 Mismatches: 85
 Indels: 10

RESULT 154
 ID AAC47930 standard; DNA; 833 BP.
 DE Arabidopsis thaliana DNA fragment SEQ ID NO: 55635.
 PD 06-SEP-2000.
 PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.
 PA (AGRE-) AGRESEARCH LTD.
 Percent Similarity: 56.42%
 Best Local Similarity: 36.24%
 Query Match: 24.13%
 Indels: 10
 Conservative: 44
 Mismatches: 85
 Indels: 10

RESULT 155
 ID ABN87111 standard; cDNA; 774 BP.
 DE Lolium perenne LpCCoAMTa partial nucleotide sequence SEQ ID NO:5.
 PD 04-APR-2002.
 PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.
 PA (AGRE-) AGRESEARCH LTD.
 Percent Similarity: 57.81%
 Best Local Similarity: 38.54%
 Query Match: 24.09%
 Indels: 8
 Conservative: 37
 Mismatches: 73
 Indels: 8

RESULT 156
 ID ABN87113 standard; cDNA; 777 BP.
 DE Lolium perenne LpCCoAMTa partial nucleotide sequence SEQ ID NO:7.
 PD 04-APR-2002.
 PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.
 PA (AGRE-) AGRESEARCH LTD.
 Percent Similarity: 57.81%
 Best Local Similarity: 38.54%
 Query Match: 24.09%
 Indels: 8
 Conservative: 37
 Mismatches: 73
 Indels: 8

RESULT 157
 ID ABN87114 standard; cDNA; 792 BP.
 DE Lolium perenne LpCCoAMTa partial nucleotide sequence SEQ ID NO:8.
 PD 04-APR-2002.
 PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.
 PA (AGRE-) AGRESEARCH LTD.
 Percent Similarity: 54.63%
 Best Local Similarity: 36.11%
 Query Match: 24.01%
 Indels: 20
 Conservative: 40
 Mismatches: 78
 Indels: 20

RESULT 158
 ID ABN87122 standard; cDNA; 789 BP.
 DE Lolium perenne LpCCoAMTB partial nucleotide sequence SEQ ID NO:17.
 PD 04-APR-2002.
 PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.
 PA (AGRE-) AGRESEARCH LTD.
 Percent Similarity: 54.63%
 Best Local Similarity: 36.11%
 Query Match: 23.94%
 Indels: 20
 Conservative: 40
 Mismatches: 78
 Indels: 20

RESULT 159
 ID ABN87121 standard; cDNA; 773 BP.
 DE Lolium perenne LpCCoAMTB partial nucleotide sequence SEQ ID NO:16.
 PD 04-APR-2002.
 PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.
 PA (AGRE-) AGRESEARCH LTD.
 Percent Similarity: 52.77%
 Best Local Similarity: 37.02%
 Query Match: 23.90%
 Indels: 18
 Conservative: 37
 Mismatches: 94
 Indels: 18

Best Local Similarity: 31.30% Mismatches: 99
 Query Match: 22.23% Indels: 23
 RESULT 166
 ID AA206878 standard; cDNA; 1075 BP.
 DE Pine O-methyl transferase (OMT) partial cDNA 4.
 PN US952486-A.
 PD 14-SEP-1999.
 PA (GENE-) GENESIS RES & DEV CORP LTD.
 PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.
 Percent Similarity: 50.41% Conservative: 47
 Best Local Similarity: 31.30% Mismatches: 99
 Query Match: 22.23% Indels: 23
 RESULT 167
 ID AA67962 standard; DNA; 1075 BP.
 DE Pinus radiata OMT nucleotide sequence SEQ ID NO:55.
 PN WO20022099-A1.
 PD 20-APR-2000.
 PA (GENE-) GENESIS RES & DEV CORP LTD.
 PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.
 Percent Similarity: 50.41% Conservative: 47
 Best Local Similarity: 31.30% Mismatches: 99
 Query Match: 22.23% Indels: 23
 RESULT 168
 ID ADD41712 standard; DNA; 1075 BP.
 DE O-methyl transferase DNA #8.
 PN US2003131373-A1.
 PD 10-JUL-2003.
 PA (BLOK/) BLOKSBERG L N.
 PA (HAVU/) HAVUKKALA I.
 Percent Similarity: 50.41% Conservative: 47
 Best Local Similarity: 31.30% Mismatches: 99
 Query Match: 22.23% Indels: 23
 RESULT 169
 ID AAX28142 standard; DNA; 3072 BP.
 DE CCoAOMT promoter, PtCCoAOMT2.
 PN WO9909188-A2.
 PD 25-FEB-1999.
 PA (VLAAs) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.
 Percent Similarity: 43.80% Conservative: 41
 Best Local Similarity: 27.91% Mismatches: 63
 Query Match: 22.15% Indels: 82
 RESULT 170
 ID AC23248 standard; DNA; 509 BP.
 DE DNA clone originating in barley containing SNP encoding sequence #13239.
 PN WO2003057877-A1.
 PD 17-JUL-2003.
 PA (UYNi-) UNIV JAPAN OKAYAMA.
 Percent Similarity: 57.23% Conservative: 29
 Best Local Similarity: 39.76% Mismatches: 64
 Query Match: 22.15% Indels: 7
 RESULT 171
 ID AAQ14978 standard; DNA; 1810 BP.
 DE ACYA gene.
 PN EP459525-A.
 PD 04-DEC-1991.
 PA (SAOC) MERCIAN CORP.
 Percent Similarity: 49.76% Conservative: 22
 Best Local Similarity: 39.02% Mismatches: 69
 Query Match: 21.89% Indels: 34
 RESULT 172
 ID AAV23874 standard; DNA; 1074 BP.
 DE Plant OMT enzyme DNA sequence.
 PN WO9811205-A2.
 PD 19-MAR-1998.
 PA (GENE-) GENESIS RES & DEV CORP LTD.
 PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.
 Percent Similarity: 53.15% Conservative: 46
 Best Local Similarity: 32.43% Mismatches: 92
 Query Match: 21.67% Indels: 12
 RESULT 173
 ID AA206877 standard; cDNA; 1074 BP.
 DE Pine O-methyl transferase (OMT) partial cDNA 3.
 PN US952486-A.

PD 14-SEP-1999.
 PA (GENE-) GENESIS RES & DEV CORP LTD.
 PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.
 Percent Similarity: 53.15% Conservative: 46
 Best Local Similarity: 32.43% Mismatches: 92
 Query Match: 21.67% Indels: 12
 RESULT 174
 ID AA67961 standard; DNA; 1074 BP.
 DE Pinus radiata OMT nucleotide sequence SEQ ID NO:54.
 PN WO20022099-A1.
 PD 20-APR-2000.
 PA (GENE-) GENESIS RES & DEV CORP LTD.
 PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.
 Percent Similarity: 53.15% Conservative: 46
 Best Local Similarity: 32.43% Mismatches: 92
 Query Match: 21.67% Indels: 12
 RESULT 175
 ID ADD41711 standard; DNA; 1074 BP.
 DE O-methyl transferase DNA #7.
 PN US2003131373-A1.
 PD 10-JUL-2003.
 PA (BLOK/) BLOKSBERG L N.
 PA (HAVU/) HAVUKKALA I.
 Percent Similarity: 53.15% Conservative: 46
 Best Local Similarity: 32.43% Mismatches: 92
 Query Match: 21.67% Indels: 12
 RESULT 176
 ID ABN87120 standard; cDNA; 693 BP.
 DE Lolium perenne LpCCoAMTB partial nucleotide sequence SEQ ID NO:15.
 PN WO200226994-A1.
 PD 04-APR-2002.
 PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.
 PA (AGRE-) AGRESEARCH LTD.
 Percent Similarity: 54.15% Conservative: 32
 Best Local Similarity: 38.54% Mismatches: 81
 Query Match: 21.37% Indels: 14
 RESULT 177
 ID AAS08693 standard; DNA; 109519 BP.
 DE Micromonospora DNA encoding biosynthetic enzymes for Evernimycin.
 Percent Similarity: 47.60% Conservative: 39
 Best Local Similarity: 33.21% Mismatches: 111
 Query Match: 21.33% Indels: 31
 RESULT 178
 ID AA260809 standard; DNA; 2983 BP.
 DE Nucleotide sequence of promoter of caffeine-CoA-O-methyltransferase.
 PN WO200006752-A1.
 PD 10-FEB-2000.
 PA (VLAAs) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.
 Percent Similarity: 43.63% Conservative: 41
 Best Local Similarity: 27.80% Mismatches: 63
 Query Match: 21.22% Indels: 83
 RESULT 179
 ID ABN90073 standard; DNA; 792 BP.
 DE Arabidopsis thaliana expressed polynucleotide SEQ ID NO 841.
 PN US2002023281-A1.
 PD 21-FEB-2002.
 PA (GORL/) GORLACH J.
 PA (ANY/) AN Y.
 PA (HAMI/) HAMILTON C M.
 PA (PRIC/) PRICE J L.
 PA (RAIN/) RAINES T M.
 PA (YUYU/) YU Y.
 PA (RAME/) RAMEKA J G.
 PA (PAGE/) PAGE A.
 PA (MATH/) MATHEW A V.
 PA (LEDF/) LEDFORD B L.
 PA (WOES/) WOESSNER J P.
 PA (HAAS/) HAAS W D.
 PA (GARC/) GARCIA C A.
 PA (KRIC/) KRICKER M.
 PA (SLAT/) SLATER T.
 PA (DAVI/) DAVIS K R.
 PA (ALLE/) ALLEN K.

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PA (HOFF/) HOFFMAN N.
 PA (HURB/) HURBAN P.
 Percent Similarity: 56.35%
 Best Local Similarity: 34.25%
 Mismatches: 68
 Indels: 11
 Query Match:
 RESULT 180
 ID AAV23845 standard; DNA; 3800 BP.
 DE Plant OMT enzyme DNA sequence.
 PN WO9811205-A2.
 PD 19-MAR-1998.
 PA (GENE-) GENESIS RES & DEV CORP LTD.
 PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.
 Percent Similarity: 40.79%
 Best Local Similarity: 25.27%
 Mismatches: 63
 Indels: 101
 Query Match:
 RESULT 181
 ID AAV23845 standard; DNA; 3800 BP.
 DE Nucleotide sequence of promoter of caffeoyl-CoA-O-methyltransferase.
 PN WO200006752-A1.
 PD 10-FEB-2000.
 PA (VLA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.
 PA (VLA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.
 Percent Similarity: 40.79%
 Best Local Similarity: 25.27%
 Mismatches: 63
 Indels: 101
 Query Match:
 RESULT 182
 ID AAV23845 standard; DNA; 343 BP.
 DE Rat sequence differentially expressed in response to a hepatotoxin #275.
 PN WO200210453-A2.
 PD 07-FEB-2002.
 PA (GENE-) GENE LOGIC INC.
 PA (GENE-) GENE LOGIC INC.
 Percent Similarity: 60.00%
 Best Local Similarity: 55.65%
 Mismatches: 6
 Indels: 40
 Query Match:
 RESULT 183
 ID AAV23845 standard; DNA; 343 BP.
 DE Toxicity-related gene, SEQ ID 688.
 PN WO2003064624-A2.
 PD 07-AUG-2003.
 PA (GENE-) GENE LOGIC INC.
 PA (GENE-) GENE LOGIC INC.
 Percent Similarity: 60.00%
 Best Local Similarity: 55.65%
 Mismatches: 6
 Indels: 40
 Query Match:
 RESULT 184
 ID AAV23845 standard; DNA; 343 BP.
 DE Toxicity modelling related rat gene SEQ ID No 298.
 PN WO200295000-A2.
 PD 28-NOV-2002.
 PA (GENE-) GENE LOGIC INC.
 PA (GENE-) GENE LOGIC INC.
 Percent Similarity: 60.00%
 Best Local Similarity: 55.65%
 Mismatches: 6
 Indels: 40
 Query Match:
 RESULT 185
 ID AAV23845 standard; DNA; 780 BP.
 DE Fuchsia PMT. cDNA #SEQ ID 21.
 PN WO2003062428-A1.
 PD 31-JUL-2003.
 PA (ITEL-) INT FLOWER DEV PTY LTD.
 PA (ITEL-) INT FLOWER DEV PTY LTD.
 Percent Similarity: 57.50%
 Best Local Similarity: 39.12%
 Mismatches: 31
 Indels: 8
 Query Match:
 RESULT 186
 ID ABD00975 standard; DNA; 675 BP.
 DE Klebsiella pneumoniae polynucleotide seqid 6750.
 PN US6610836-B1.
 PD 26-AUG-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Percent Similarity: 53.33%
 Best Local Similarity: 35.56%
 Mismatches: 32
 Indels: 8
 Query Match:
 RESULT 187
 ID ADD34177 standard; DNA; 407 BP.
 DE Mouse mitochondrial DNA sequence SEQ ID NO:1955.
 PN WO2003020220-A2.
 PD 13-MAR-2003.

PA (UYEM-) UNIV EMORY.
 Percent Similarity: 85.71%
 Best Local Similarity: 79.37%
 Mismatches: 9
 Indels: 0
 Query Match:
 RESULT 188
 ID AAV23845 standard; DNA; 760 BP.
 DE Plant OMT enzyme DNA sequence.
 PN WO9811205-A2.
 PD 19-MAR-1998.
 PA (GENE-) GENESIS RES & DEV CORP LTD.
 PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.
 Percent Similarity: 58.96%
 Best Local Similarity: 37.31%
 Mismatches: 52
 Indels: 3
 Query Match:
 RESULT 189
 ID AAV23845 standard; cDNA; 760 BP.
 DE Eucalyptus O-methyl transferase (OMT) partial cDNA 4.
 PN US952486-A.
 PD 14-SEP-1999.
 PA (GENE-) GENESIS RES & DEV CORP LTD.
 PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.
 Percent Similarity: 58.96%
 Best Local Similarity: 37.31%
 Mismatches: 52
 Indels: 3
 Query Match:
 RESULT 190
 ID AAV23845 standard; cDNA; 760 BP.
 DE Eucalyptus grandis cinnamoyl-CoA reductase cDNA SEQ ID NO:58.
 PN WO200036081-A2.
 PD 22-JUN-2000.
 PA (GENE-) GENESIS RES & DEV CORP LTD.
 PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.
 Percent Similarity: 58.96%
 Best Local Similarity: 37.31%
 Mismatches: 52
 Indels: 3
 Query Match:
 RESULT 191
 ID AAV23845 standard; DNA; 760 BP.
 DE Eucalyptus grandis OMT nucleotide sequence SEQ ID NO:25.
 PN WO200022099-A1.
 PD 20-APR-2000.
 PA (GENE-) GENESIS RES & DEV CORP LTD.
 PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.
 Percent Similarity: 58.96%
 Best Local Similarity: 37.31%
 Mismatches: 52
 Indels: 3
 Query Match:
 RESULT 192
 ID AAV23845 standard; DNA; 760 BP.
 DE O-methyl transferase DNA #5.
 PN US2003131373-A1.
 PD 10-JUL-2003.
 PA (BLOK/) BLOKSBERG L N.
 PA (HAVU/) HAVUKKALA I.
 Percent Similarity: 58.96%
 Best Local Similarity: 37.31%
 Mismatches: 52
 Indels: 3
 Query Match:
 RESULT 193
 ID ABS63430 standard; cDNA; 534 BP.
 DE DNA encoding wheat caffeoyl-CoA O-methyltransferase (CCOMT).
 PN US2002081693-A1.
 PD 27-JUN-2002.
 PA (CAHO/) CAHOON R E.
 PA (FADE/) FADER G M.
 PA (RAFA/) RAPALSKI J A.
 Percent Similarity: 58.71%
 Best Local Similarity: 36.13%
 Mismatches: 35
 Indels: 8
 Query Match:
 RESULT 194
 ID AAV23845 standard; cDNA; 628 BP.
 DE Lolium perenne LpCCoAMTb partial nucleotide sequence SEQ ID NO:14.
 PN WO200226994-A1.
 PD 04-APR-2002.
 PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.
 PA (AGRE-) AGRESEARCH LTD.
 Percent Similarity: 51.93%
 Mismatches: 56
 Indels: 30

Best Local Similarity: 35.36% Mismatches: 75
Query Match: 16.46% Indels: 13
RESULT 195
ID AC123249 standard; DNA; 542 BP.
DE DNA clone originating in barley containing SNP encoding sequence #13240.
PN WO2003057877-A1.
PD 17-JUL-2003.
PA (UYNI-) UNIV JAPAN OKAYAMA.
PA (YUNI-) UNIV JAPAN OKAYAMA.
Percent Similarity: 55.70% Conservative: 28
Best Local Similarity: 37.97% Mismatches: 59
Query Match: 15.82% Indels: 13
RESULT 196
ID ABS63423 standard; cDNA; 528 BP.
DE DNA encoding soybean caffeoyl-CoA O-methyltransferase (CCOMT).
PN US2002081693-A1.
PD 27-JUN-2002.
PA (CAHO/) CAHOON R E.
PA (FADE/) FADER G M.
PA (RAPA/) RAPALSKI J A.
Percent Similarity: 59.52% Conservative: 27
Best Local Similarity: 38.10% Mismatches: 45
Query Match: 15.41% Indels: 6
RESULT 197
Percent Similarity: 54.29% Conservative: 37
Best Local Similarity: 33.14% Mismatches: 69
Query Match: 15.08% Indels: 11
RESULT 198
Percent Similarity: 54.29% Conservative: 37
Best Local Similarity: 33.14% Mismatches: 69
Query Match: 15.08% Indels: 11
RESULT 199
ID AAA68101 standard; DNA; 399 BP.
DE E. grandis caffeoyl CoA methyl transferase DNA sequence SEQ ID NO:194.
PN WO200022099-A1.
PD 20-APR-2000.
PA (GENE-) GENESIS RES & DEV CORP LTD.
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.
Percent Similarity: 62.93% Conservative: 27
Best Local Similarity: 39.66% Mismatches: 33
Query Match: 15.04% Indels: 11
RESULT 200
ID ADD41851 standard; DNA; 399 BP.
DE Caffeoyl CoA methyl transferase DNA #2.
PN US200313173-A1.
PD 10-JUL-2003.
PA (BLOK/) BLOKSBERG L N.
PA (HAVU/) HAVUKKALA I.
Percent Similarity: 62.93% Conservative: 27
Best Local Similarity: 39.66% Mismatches: 33
Query Match: 15.04% Indels: 11
RESULT 201
ID ADA31006 standard; DNA; 588 BP.
DE DNA encoding Acinetobacter baumannii protein #2293.
PN US6562958-B1.
PD 13-MAY-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Percent Similarity: 50.24% Conservative: 34
Best Local Similarity: 33.66% Mismatches: 65
Query Match: 15.00% Indels: 37
RESULT 202
ID ABN87109 standard; cDNA; 557 BP.
DE Lolium perenne LpCCoAMTa partial nucleotide sequence SEQ ID NO:3.
PN WO200226994-A1.
PD 04-APR-2002.
PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.
PA (AGRE-) AGRESEARCH LTD.
Percent Similarity: 54.35% Conservative: 28
Best Local Similarity: 34.06% Mismatches: 52
Query Match: 14.30% Indels: 11
RESULT 203
ID AAS96694 standard; DNA; 8580 BP.
DE Arabidopsis DMT4 (1DMT4) DNA.
PN WO200180626-A1.
PD 19-MAR-1998.
PA (GENE-) GENESIS RES & DEV CORP LTD.
PD 01-NOV-2001.
PA (REGC) UNIV CALIFORNIA.
Percent Similarity: 39.59% Conservative: 27
Best Local Similarity: 25.89% Mismatches: 51
Query Match: 14.11% Indels: 69
RESULT 204
ID ADM39547 standard; DNA; 8580 BP.
DE DMT polynucleotide #9.
PN US2003135890-A1.
PD 17-JUL-2003.
PA (FISC/) FISCHER R.
PA (CHOI/) CHOI Y.
PA (HANN/) HANNON M.
PA (OKAM/) OKAMURO J.
PA (TATA/) TATARINOVA T.
Percent Similarity: 39.59% Conservative: 27
Best Local Similarity: 25.89% Mismatches: 51
Query Match: 14.11% Indels: 69
RESULT 205
ID AAA68012 standard; DNA; 594 BP.
DE Eucalyptus grandis OMT nucleotide sequence SEQ ID NO:105.
PN WO200022099-A1.
PD 20-APR-2000.
PA (GENE-) GENESIS RES & DEV CORP LTD.
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.
Percent Similarity: 61.17% Conservative: 25
Best Local Similarity: 36.89% Mismatches: 38
Query Match: 13.63% Indels: 2
RESULT 206
ID ADD41762 standard; DNA; 594 BP.
DE O-methyl transferase DNA #11.
PN US200313173-A1.
PD 10-JUL-2003.
PA (BLOK/) BLOKSBERG L N.
PA (HAVU/) HAVUKKALA I.
Percent Similarity: 61.17% Conservative: 25
Best Local Similarity: 36.89% Mismatches: 38
Query Match: 13.63% Indels: 2
RESULT 207
ID ADB06101 standard; DNA; 798 BP.
DE Alloiococcus otitis antigenic protein encoding DNA SEQ ID NO:41.
PN WO2003048304-A2.
PD 12-JUN-2003.
PA (AMHP) WYETH HOLDINGS CORP.
Percent Similarity: 47.98% Conservative: 31
Best Local Similarity: 32.32% Mismatches: 72
Query Match: 13.55% Indels: 31
RESULT 208
ID ADB12064 standard; DNA; 1754382 BP.
DE Alloiococcus otitis entire genome sequence SEQ ID NO:6651.
PN WO2003048304-A2.
PD 12-JUN-2003.
PA (AMHP) WYETH HOLDINGS CORP.
Percent Similarity: 47.98% Conservative: 31
Best Local Similarity: 32.32% Mismatches: 72
Query Match: 13.55% Indels: 31
RESULT 209
ID ABS63421 standard; cDNA; 505 BP.
DE DNA encoding soybean caffeoyl-CoA O-methyltransferase (CCOMT).
PN US2002081693-A1.
PD 27-JUN-2002.
PA (CAHO/) CAHOON R E.
PA (FADE/) FADER G M.
PA (RAPA/) RAPALSKI J A.
Percent Similarity: 51.92% Conservative: 30
Best Local Similarity: 32.69% Mismatches: 56
Query Match: 13.51% Indels: 19
RESULT 210
ID AAV23843 standard; DNA; 607 BP.
DE Plant OMT enzyme DNA sequence.
PN WO9811205-A2.
PD 19-MAR-1998.
PA (GENE-) GENESIS RES & DEV CORP LTD.

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PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.
Percent Similarity: 61.22% Conservative: 23
Best Local Similarity: 37.76% Mismatches: 36
Indels: 2
Query Match:
RESULT 211
ID AAZ06844 standard; cDNA; 607 BP.
DE Eucalyptus O-methyl transferase (OMT) partial cDNA 2.
PN US5952486-A.
PD 14-SEP-1999.
PA (GENE-) GENESIS RES & DEV CORP LTD.
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.
Percent Similarity: 61.22% Conservative: 23
Best Local Similarity: 37.76% Mismatches: 36
Indels: 2
Query Match:
RESULT 212
ID AAA69594 standard; cDNA; 607 BP.
DE Eucalyptus grandis O-methyltransferase cDNA SEQ ID NO:68.
PN WO200036081-A2.
PD 22-JUN-2000.
PA (GENE-) GENESIS RES & DEV CORP LTD.
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.
Percent Similarity: 61.22% Conservative: 23
Best Local Similarity: 37.76% Mismatches: 36
Indels: 2
Query Match:
RESULT 213
ID AAA67930 standard; DNA; 607 BP.
DE Eucalyptus grandis OMT nucleotide sequence SEQ ID NO:23.
PN WO200022099-A1.
PD 20-APR-2000.
PA (GENE-) GENESIS RES & DEV CORP LTD.
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.
Percent Similarity: 61.22% Conservative: 23
Best Local Similarity: 37.76% Mismatches: 36
Indels: 2
Query Match:
RESULT 214
ID ADD41680 standard; DNA; 607 BP.
DE O-methyl transferase DNA #3.
PN US200313173-A1.
PD 10-JUL-2003.
PA (BLOK/) BLOKSBERG L N.
PA (HAVU/) HAVUKKALA I.
Percent Similarity: 61.22% Conservative: 23
Best Local Similarity: 37.76% Mismatches: 36
Indels: 2
Query Match:
RESULT 215
ID AAS59516 standard; DNA; 29255 BP.
DE Propionibacterium acnes immunogenic protein encoding DNA #11.
PN WO200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Percent Similarity: 45.54% Conservative: 38
Best Local Similarity: 28.57% Mismatches: 91
Indels: 32
Query Match:
RESULT 216
ID ACF64445 standard; DNA; 29255 BP.
DE Propionibacterium acnes DNA contig sequence #11.
PN WO200303315-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Percent Similarity: 45.54% Conservative: 38
Best Local Similarity: 28.57% Mismatches: 91
Indels: 32
Query Match:
RESULT 217
ID ADA4866 standard; DNA; 584 BP.
DE Banana gene conferring disease resistance in plants.
PN WO2003000906-A2.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Percent Similarity: 46.67% Conservative: 18
Best Local Similarity: 33.33% Mismatches: 38
Indels: 34
Query Match:
RESULT 218
ID ABS63411 standard; cDNA; 510 BP.

DE DNA encoding rice caffeoyl-CoA O-methyltransferase (CCOMT).
PN US2002081693-A1.
PD 27-JUN-2002.
PA (CAHO/) CAHOON R E.
PA (FADE/) FADER G M.
PA (RAFA/) RAFALSKI J A.
Percent Similarity: 54.93% Conservative: 27
Best Local Similarity: 35.92% Mismatches: 45
Indels: 20
Query Match:
RESULT 219
ID ABS63426 standard; cDNA; 600 BP.
DE DNA encoding wheat caffeoyl-CoA O-methyltransferase (CCOMT).
PN US2002081693-A1.
PD 27-JUN-2002.
PA (CAHO/) CAHOON R E.
PA (FADE/) FADER G M.
PA (RAFA/) RAFALSKI J A.
Percent Similarity: 48.84% Conservative: 21
Best Local Similarity: 36.63% Mismatches: 57
Indels: 32
Query Match:
RESULT 220
ID AAA31496 standard; DNA; 451 BP.
DE Plant microsatellite marker #457.
PN WO9967421-A1.
PD 29-DEC-1999.
PA (GENE-) GENESIS RES & DEV CORP LTD.
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.
Percent Similarity: 59.18% Conservative: 21
Best Local Similarity: 37.76% Mismatches: 38
Indels: 2
Query Match:
RESULT 221
ID AAA68102 standard; DNA; 296 BP.
DE E. grandis caffeoyl CoA methyl transferase DNA sequence SEQ ID NO:195.
PN WO200022099-A1.
PD 20-APR-2000.
PA (GENE-) GENESIS RES & DEV CORP LTD.
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.
Percent Similarity: 62.89% Conservative: 23
Best Local Similarity: 39.18% Mismatches: 32
Indels: 4
Query Match:
RESULT 222
ID ADD41852 standard; DNA; 296 BP.
DE Caffeoyl CoA methyl transferase DNA #3.
PN US200313173-A1.
PD 10-JUL-2003.
PA (BLOK/) BLOKSBERG L N.
PA (HAVU/) HAVUKKALA I.
Percent Similarity: 62.89% Conservative: 23
Best Local Similarity: 39.18% Mismatches: 32
Indels: 4
Query Match:
RESULT 223
ID ABQ81846 standard; DNA; 349980 BP.
DE Bifidobacterium longum NCC2705 related nucleotide sequence SEQ ID:1102.
PN US200313173-A1.
PD 31-JUL-2002.
PA (NEST) SOC PROD NESTLE SA.
Percent Similarity: 42.31% Conservative: 39
Best Local Similarity: 27.31% Mismatches: 137
Indels: 13
Query Match:
RESULT 224
ID AAV23873 standard; DNA; 562 BP.
DE Plant OMT enzyme DNA sequence.
PN WO9811205-A2.
PD 19-MAR-1998.
PA (GENE-) GENESIS RES & DEV CORP LTD.
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.
Percent Similarity: 58.26% Conservative: 29
Best Local Similarity: 33.04% Mismatches: 42
Indels: 6
Query Match:
RESULT 225
ID AAZ06876 standard; cDNA; 562 BP.
DE Fine O-methyl transferase (OMT) partial cDNA 2.
PN US5952486-A.

PD 14-SEP-1999.
PA (GENE-) GENESIS RES & DEV CORP LTD.
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.
Percent Similarity: 58.26% Conservative: 29
Best Local Similarity: 33.04% Mismatches: 42
Query Match: 12.77% Indels: 6
RESULT 226
ID AAA69580 standard; cDNA; 562 BP.
DE Pinus radiata O-methyltransferase cDNA SEQ ID NO:54.
PN WO200036091-A2.
PD 22-JUN-2000.
PA (GENE-) GENESIS RES & DEV CORP LTD.
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.
Percent Similarity: 58.26% Conservative: 29
Best Local Similarity: 33.04% Mismatches: 42
Query Match: 12.77% Indels: 6
RESULT 227
ID AAA67960 standard; DNA; 562 BP.
DE Pinus radiata OMT nucleotide sequence SEQ ID NO:53.
PN WO200022099-A1.
PD 20-APR-2000.
PA (GENE-) GENESIS RES & DEV CORP LTD.
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.
Percent Similarity: 58.26% Conservative: 29
Best Local Similarity: 33.04% Mismatches: 42
Query Match: 12.77% Indels: 6
RESULT 228
ID ADA41710 standard; DNA; 562 BP.
DE O-methyl transferase DNA #6.
PN US2003131373-A1.
PD 10-JUL-2003.
PA (BLOK/) BLOKSBERG L N.
PA (HAVU/) HAVUKKALA I.
Percent Similarity: 58.26% Conservative: 29
Best Local Similarity: 33.04% Mismatches: 42
Query Match: 12.77% Indels: 6
RESULT 229
ID ADP95323 standard; cDNA; 447 BP.
DE Cotton expressed sequence tag, EST, #4334.
PN US2004123338-A1.
PD 24-JUN-2004.
PA (FINC/) FINCHER K L.
Percent Similarity: 60.42% Conservative: 22
Best Local Similarity: 37.50% Mismatches: 36
Query Match: 12.66% Indels: 2
RESULT 230
ID ABX09141 standard; DNA; 75216 BP.
DE Mycobacterium tuberculosis H37Rv BAC clone BAC-RV230.
PN WO200274903-A2.
PD 26-SEP-2002.
PA (INSP) INST PASTEUR.
Percent Similarity: 41.32% Conservative: 33
Best Local Similarity: 29.86% Mismatches: 134
Query Match: 12.66% Indels: 37
RESULT 231
Percent Similarity: 41.32% Conservative: 33
Best Local Similarity: 29.86% Mismatches: 134
Query Match: 12.66% Indels: 37
RESULT 232
Percent Similarity: 41.32% Conservative: 33
Best Local Similarity: 29.86% Mismatches: 134
Query Match: 12.66% Indels: 37
RESULT 233
ID ABO68900 standard; DNA; 1289 BP.
DE Listeria monocytogenes 4b contig DNA sequence #1666.
PN WO200228891-A2.
PD 11-APR-2002.
PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
Percent Similarity: 43.93% Conservative: 36
Best Local Similarity: 27.10% Mismatches: 96
Query Match: 12.58% Indels: 24
RESULT 234

Percent Similarity: 44.95% Conservative: 37
Best Local Similarity: 27.98% Mismatches: 88
Query Match: 12.58% Indels: 32
RESULT 235
ID ABO70732 standard; DNA; 2233 BP.
DE Listeria monocytogenes 4b contig DNA sequence #674.
PN WO200228891-A2.
PD 11-APR-2002.
PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
Percent Similarity: 43.93% Conservative: 36
Best Local Similarity: 27.10% Mismatches: 96
Query Match: 12.51% Indels: 24
RESULT 236
ID AAA68100 standard; DNA; 399 BP.
DE E. grandis caffeoyl CoA methyl transferase DNA sequence SEQ ID NO:193.
PN WO200022099-A1.
PD 20-APR-2000.
PA (GENE-) GENESIS RES & DEV CORP LTD.
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.
Percent Similarity: 61.86% Conservative: 21
Best Local Similarity: 40.21% Mismatches: 27
Query Match: 12.21% Indels: 11
RESULT 237
ID ADA41850 standard; DNA; 399 BP.
DE Caffeoyl CoA methyl transferase DNA #1.
PN US2003131373-A1.
PD 10-JUL-2003.
PA (BLOK/) BLOKSBERG L N.
PA (HAVU/) HAVUKKALA I.
Percent Similarity: 61.86% Conservative: 21
Best Local Similarity: 40.21% Mismatches: 27
Query Match: 12.21% Indels: 11
RESULT 238
Percent Similarity: 41.84% Conservative: 37
Best Local Similarity: 26.36% Mismatches: 93
Query Match: 12.21% Indels: 46
RESULT 239
Percent Similarity: 41.84% Conservative: 37
Best Local Similarity: 26.36% Mismatches: 93
Query Match: 12.21% Indels: 46
RESULT 240
ID ADA31376 standard; DNA; 702 BP.
DE DNA encoding Acinetobacter baumannii protein #2663.
PN US6562958-B1.
PD 13-MAY-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Percent Similarity: 42.92% Conservative: 37
Best Local Similarity: 26.03% Mismatches: 104
Query Match: 12.10% Indels: 21
RESULT 241
Percent Similarity: 51.18% Conservative: 38
Best Local Similarity: 28.82% Mismatches: 72
Query Match: 12.10% Indels: 11
RESULT 242
ID ABX62366 standard; DNA; 415 BP.
DE Arabidopsis thaliana expressed sequence related polynucleotide #481.
PN US2002040490-A1.
PD 04-APR-2002.
PA (GORL/) GORLACH J.
PA (ANY/) AN Y.
PA (HAMI/) HAMILTON C M.
PA (PRIC/) PRICE J L.
PA (RAIN/) RAINES T M.
PA (YUY/) YU Y.
PA (RAME/) RAMEKA J G.
PA (PAGE/) PAGE A.
PA (MATH/) MATHAW A V.
PA (LEDF/) LEDFORD B L.
PA (WOES/) WOESSNER J P.
PA (HAAS/) HAAS W D.
PA (GARC/) GARCIA C A.
PA (KRIC/) KRICKER M.

PA (SLAT/) SLATER T. Conservative: 26
 PA (DAVI/) DAVIS K R. Mismatches: 45
 PA (ALLE/) ALLEN K. Indels: 11
 PA (HOFF/) HOFFMAN N. Conservative: 26
 PA (HURB/) HURBAN P. Mismatches: 45
 Percent Similarity: 54.10% Indels: 11
 Best Local Similarity: 32.79%
 Query Match: 11.88%
 RESULT 243
 ID ADE74386 standard; DNA; 38675 BP.
 DE Mycobacterium leprae DNA #20.
 PN US583266-B1.
 PD 24-JUN-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Percent Similarity: 40.42% Conservative: 43
 Best Local Similarity: 25.44% Mismatches: 128
 Indels: 44
 Query Match: 11.76%
 RESULT 244
 ID ADH82166 standard; DNA; 801 BP.
 DE Enterococcus faecalis polynucleotide #51.
 PN US6617156-B1.
 PD 09-SEP-2003.
 PA (DOUC/) DOUCETTE-STAMM L A.
 PA (BUSH/) BUSH D. Conservative: 37
 Percent Similarity: 41.38% Mismatches: 112
 Best Local Similarity: 25.43% Indels: 24
 Query Match: 11.69%
 RESULT 245
 ID RAX13116 standard; DNA; 19024 BP.
 DE Enterococcus faecalis genome contig SEQ ID NO:179.
 PN WO9850555-A2.
 PD 12-NOV-1998.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Percent Similarity: 41.38% Conservative: 37
 Best Local Similarity: 25.43% Mismatches: 112
 Indels: 24
 Query Match: 11.62%
 RESULT 246
 ID ABS98911 standard; DNA; 19024 BP.
 DE Enterococcus faecalis contig sequence #179.
 PN US2002120116-A1.
 PD 29-AUG-2002.
 PA (KUNS/) KUNSCH C A. Conservative: 37
 PA (DILL/) DILLON P J. Mismatches: 112
 PA (BARA/) BARASH S. Indels: 24
 Percent Similarity: 41.38%
 Best Local Similarity: 25.43%
 Query Match: 11.62%
 RESULT 247
 ID ABS63414 standard; cDNA; 508 BP.
 DE DNA encoding rice caffeoyl-CoA O-methyltransferase (CCOMT).
 PN US2002081693-A1.
 PD 27-JUN-2002.
 PA (CAHO/) CAHOON R E. Conservative: 16
 PA (FADE/) FADER G M. Mismatches: 39
 PA (RAFA/) RAFALSKI J A. Indels: 19
 Percent Similarity: 51.28%
 Best Local Similarity: 37.61%
 Query Match: 11.13%
 RESULT 248
 ID ACL23251 standard; DNA; 422 BP.
 DE DNA clone originating in barley containing SNP encoding sequence #13242.
 PN WO2003057877-A1.
 PD 17-JUL-2003.
 PA (UTNI-) UNIV JAPAN OKAYAMA. Conservative: 15
 Percent Similarity: 58.02% Mismatches: 28
 Best Local Similarity: 39.51% Indels: 6
 Query Match: 10.87%
 RESULT 249
 ID AAF08409 standard; cDNA; 645 BP.
 DE Fusarium venenatum EST SEQ ID NO:932.
 PN WO200056762-A2.
 PD 28-SEP-2000.
 PA (NOVO) NOVO NORDISK BIOTECH INC. Conservative: 25
 Mismatches: 80
 Indels: 65

PA (NOVO) NOVO NORDISK AS. Conservative: 39
 Percent Similarity: 48.35% Mismatches: 79
 Best Local Similarity: 26.92% Indels: 16
 Query Match: 10.46%
 RESULT 250
 ID ABN69362 standard; DNA; 705 BP.
 DE Streptococcus polynucleotide SEQ ID NO 6637.
 PN WO200234771-A2.
 PD 02-MAY-2002.
 PA (CHIR-) CHIRON SPA. Conservative: 38
 PA (GENO-) INST GENOMICS RES. Mismatches: 87
 Percent Similarity: 44.06% Indels: 26
 Best Local Similarity: 25.25%
 Query Match: 10.13%
 RESULT 251
 ID ABX72177 standard; cDNA; 894 BP.
 DE Human NOVX polynucleotide #8.
 PN WO200281498-A2.
 PD 17-OCT-2002.
 PA (CURA-) CURAGEN CORP. Conservative: 26
 Percent Similarity: 40.00% Mismatches: 79
 Best Local Similarity: 29.17% Indels: 65
 Query Match: 9.53%
 RESULT 252
 ID AAD13478 standard; DNA; 2316 BP.
 DE Catechol-O-methyltransferase-like human enzyme encoding DNA.
 PN WO200157220-A2.
 PD 09-AUG-2001.
 PA (LEXI-) LEXICON GENETICS INC. Conservative: 21
 Percent Similarity: 39.54% Mismatches: 100
 Best Local Similarity: 31.56% Indels: 61
 Query Match: 9.53%
 RESULT 253
 ID ABK74977 standard; DNA; 534 BP.
 DE Bacillus licheniformis genomic sequence tag (GST) #2268.
 PN WO200229113-A2.
 PD 11-APR-2002.
 PA (NOVO) NOVOZYMES BIOTECH INC. Conservative: 35
 PA (NOVO) NOVOZYMES AS. Mismatches: 88
 Percent Similarity: 44.81% Indels: 13
 Best Local Similarity: 25.68%
 Query Match: 9.42%
 RESULT 254
 ID AAD13476 standard; cDNA; 777 BP.
 DE Catechol-O-methyltransferase-like human enzyme encoding cDNA #1.
 PN WO200157220-A2.
 PD 09-AUG-2001.
 PA (LEXI-) LEXICON GENETICS INC. Conservative: 25
 Percent Similarity: 39.58% Mismatches: 80
 Best Local Similarity: 29.17% Indels: 65
 Query Match: 9.38%
 RESULT 255
 ID AAD33497 standard; cDNA; 777 BP.
 DE Human drug metabolising enzyme (DME-18) cDNA.
 PN WO200212467-A2.
 PD 14-FEB-2002.
 PA (INCY-) INCYTE GENOMICS INC. Conservative: 25
 Percent Similarity: 39.58% Mismatches: 80
 Best Local Similarity: 29.17% Indels: 65
 Query Match: 9.38%
 RESULT 256
 ID ABX72178 standard; cDNA; 897 BP.
 DE Human NOVX polynucleotide #9.
 PN WO200281498-A2.
 PD 17-OCT-2002.
 PA (CURA-) CURAGEN CORP. Conservative: 25
 Percent Similarity: 39.58% Mismatches: 80
 Best Local Similarity: 29.17% Indels: 65
 Query Match: 9.38%
 RESULT 257
 ID ABN69361 standard; DNA; 705 BP.
 DE Streptococcus polynucleotide SEQ ID NO 6635.
 PN WO200234771-A2.

Query Match: 8.56% Indels: 38
 RESULT 274
 ID ACA00413 standard; DNA: 639 BP.
 DE C. glutamicum derived ORF SEQ ID 404.
 PN DE10128510-A1.
 PD 19-DEC-2002.
 PA (DEGS) DEGUSSA AG.
 Percent Similarity: 39.70%
 Best Local Similarity: 25.63%
 Mismatches: 82
 Indels: 38
 Query Match:
 RESULT 275
 ID ADD13690 standard; DNA: 769 BP.
 DE C. glutamicum homeostasis and adaptation associated DNA SEQ ID 91.
 PN WO2003040290-A2.
 PD 15-MAY-2003.
 PA (BADI) BASF AG.
 Percent Similarity: 39.70%
 Best Local Similarity: 25.63%
 Mismatches: 82
 Indels: 38
 Query Match:
 RESULT 276
 ID AAH68527 standard; DNA: 349980 BP.
 DE C. glutamicum coding sequence fragment SEQ ID NO: 7062.
 PN EP1108790-A2.
 PD 20-JUN-2001.
 PA (KYOW) KYOWA HAKKO KOGYO KK.
 Percent Similarity: 39.70%
 Best Local Similarity: 25.63%
 Mismatches: 82
 Indels: 38
 Query Match:
 RESULT 277
 ID ACF72506 standard; DNA: 636 BP.
 DE Staphylococcus aureus DNA #186.
 PN WO200294868-A2.
 PD 28-NOV-2002.
 PA (CHIR-) CHIRON SPA.
 Percent Similarity: 42.01%
 Best Local Similarity: 21.92%
 Mismatches: 99
 Indels: 28
 Query Match:
 RESULT 278
 ID ABL12193 standard; cDNA: 5514 BP.
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 31061.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE-) PE CORP NY.
 Percent Similarity: 36.09%
 Best Local Similarity: 25.19%
 Mismatches: 70
 Indels: 100
 Query Match:
 RESULT 281
 ID AAC89765 standard; cDNA: 178 BP.
 DE Human gastrointestinal inflammation-related cDNA, SEQ ID NO: 34.
 PN WO200007334-A2.
 PD 07-DEC-2000.
 PA (DIGI-) DIGITAL GENE TECHNOLOGIES INC.
 Percent Similarity: 100.00%
 Best Local Similarity: 100.00%
 Mismatches: 0
 Indels: 0
 Query Match:
 RESULT 282
 ID ABN87116 standard; cDNA: 457 BP.
 DE Lolium perenne lpCCoAMia partial nucleotide sequence SEQ ID NO:10.
 PN WO200226994-A1.
 PD 04-APR-2002.
 PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.
 Percent Similarity: 54.93%
 Best Local Similarity: 35.21%
 Mismatches: 26
 Indels: 6
 Query Match:

RESULT 283
 ID AAD35115 standard; DNA: 2086 BP.
 DE Corynebacterium glutamicum sigE gene.
 PN WO200218428-A2.
 PD 07-MAR-2002.
 PA (DEGS) DEGUSSA AG.
 Percent Similarity: 39.80%
 Best Local Similarity: 25.51%
 Mismatches: 80
 Indels: 38
 Query Match:
 RESULT 284
 ID ABQ90300 standard; DNA: 4029 BP.
 DE M. capsulatus gene #285 for DNA array.
 PN WO200255655-A2.
 PD 18-JUL-2002.
 PA (UNIF-) UNIFOB STIFTTELSEN UNIV BERGEN.
 Percent Similarity: 37.63%
 Best Local Similarity: 25.44%
 Mismatches: 98
 Indels: 83
 Query Match:
 RESULT 285
 ID AAH53823 standard; DNA: 495 BP.
 DE S. epidermidis open reading frame nucleotide sequence SEQ ID NO:3039.
 PN WO200134809-A2.
 PD 17-MAY-2001.
 PA (GLAX) GLAXO GROUP LTD.
 Percent Similarity: 44.24%
 Best Local Similarity: 22.42%
 Mismatches: 82
 Indels: 10
 Query Match:
 RESULT 286
 ID ADB74275 standard; DNA: 38494 BP.
 DE Mycobacterium leprae DNA #2.
 PN US6583266-B1.
 PD 24-JUN-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Percent Similarity: 50.00%
 Best Local Similarity: 33.33%
 Mismatches: 42
 Indels: 0
 Query Match:
 RESULT 287
 ID AAA68082 standard; DNA: 236 BP.
 DE Pinus radiata OMT nucleotide sequence SEQ ID NO:175.
 PN WO200022099-A1.
 PD 20-APR-2000.
 PA (GENE-) GENESIS RES & DEV CORP LTD.
 Percent Similarity: 54.55%
 Best Local Similarity: 29.87%
 Mismatches: 27
 Indels: 8
 Query Match:
 RESULT 288
 ID ADD41832 standard; DNA: 236 BP.
 DE O-methyl transferase DNA #16.
 PN US200313173-A1.
 PD 10-JUL-2003.
 PA (BLOK-) BLOKBERG L N.
 Percent Similarity: 54.55%
 Best Local Similarity: 29.87%
 Mismatches: 27
 Indels: 8
 Query Match:
 RESULT 289
 ID AAQ13306 standard; DNA: 1107 BP.
 DE Human catechol-O-methyltransferase gene.
 PN WO9111513-A.
 PD 08-AUG-1991.
 PA (ORIN) ORION YHTVMAE OY.
 Percent Similarity: 38.72%
 Best Local Similarity: 23.31%
 Mismatches: 118
 Indels: 45
 Query Match:
 RESULT 290
 ID ADP45594 standard; DNA: 133100 BP.
 DE Human NUMA1/FLJ20625/LOC220074 region gDNA.
 PN WO200226994-A1.
 PD 04-APR-2002.
 PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.
 Percent Similarity: 41.83%
 Best Local Similarity: 28.37%
 Mismatches: 81
 Indels: 41
 Query Match:
 RESULT 291

ID ABZ83278 standard; cDNA; 1024 BP.
DE Toxicologically relevant human nucleotide sequence #437.
PN WO2003016500-A2.
PD 27-FEB-2003.
PA (PHAS-) PHASE-1 MOLECULAR TOXICOLOGY INC.
Percent Similarity: 38.72% Conservative: 41
Best Local Similarity: 23.31% Mismatches: 118
Indels: 45
Query Match: 8.00%
RESULT 292
ID ADE84973 standard; DNA; 1206 BP.
DE Farnesyl transferase inhibitor modulated leukemia associated gene #192.
PN WO2003038129-A2.
PD 08-MAY-2003.
PA (ORTH) ORTHO CLINICAL DIAGNOSTICS INC.
Percent Similarity: 38.72% Conservative: 41
Best Local Similarity: 23.31% Mismatches: 118
Indels: 45
Query Match: 8.00%
RESULT 293
ID ABX63642 standard; cDNA; 1327 BP.
DE Human cDNA #642 differentially expressed in activated vascular tissue.
PN US2002137081-A1.
PD 26-SEP-2002.
PA (BAND/) BANDMAN O.
Percent Similarity: 38.72% Conservative: 41
Best Local Similarity: 23.31% Mismatches: 118
Indels: 45
Query Match: 8.00%
RESULT 294
ID ABZ51068 standard; cDNA; 836 BP.
DE Aspergillus oryzae polynucleotide SEQ ID NO 181.
PN WO200279476-A1.
PD 10-OCT-2002.
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (NARE-) NAT RES INST BREWING.
PA (NORQ) NAT FOOD RES INST MIN AGRIC.
Percent Similarity: 40.96% Conservative: 21
Best Local Similarity: 28.31% Mismatches: 57
Indels: 41
Query Match: 7.97%
RESULT 295
ID AAC77872 standard; cDNA; 1350 BP.
DE Human cancer associated gene sequence SEQ ID NO:266.
PN WO200055350-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 39.84% Conservative: 38
Best Local Similarity: 24.70% Mismatches: 116
Indels: 35
Query Match: 7.89%
RESULT 296
ID AAA31195 standard; DNA; 356 BP.
DE Plant microsatellite marker #156.
PN WO9967421-A1.
PD 29-DEC-1999.
PA (GENE-) GENESIS RES & DEV CORP LTD.
PA (FLET-) FLETCHER CHALLENGE FOREST LTD.
Percent Similarity: 52.87% Conservative: 16
Best Local Similarity: 34.48% Mismatches: 33
Indels: 9
Query Match: 7.82%
RESULT 297
ID AAB35116 standard; DNA; 457 BP.
DE Corynebacterium glutamicum sigE gene upstream region DNA.
PN WO200218428-A2.
PD 07-MAR-2002.
PA (DEGS) DEGUSA AG.
Percent Similarity: 44.37% Conservative: 26
Best Local Similarity: 26.06% Mismatches: 59
Indels: 20
Query Match: 7.82%
RESULT 298
ID ACA51621 standard; DNA; 834 BP.
DE Prokaryotic essential gene #33278.
PN WO20027183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Percent Similarity: 38.11% Conservative: 33
Best Local Similarity: 26.57% Mismatches: 95

Query Match: 7.71% Indels: 82
RESULT 299
ID ADB58045 standard; DNA; 1531 BP.
DE Toxicity-related gene, SEQ ID 3071.
PN WO2003064624-A2.
PD 07-AUG-2003.
PA (GENE-) GENE LOGIC INC.
Percent Similarity: 43.19% Conservative: 41
Best Local Similarity: 23.94% Mismatches: 92
Indels: 31
Query Match: 7.71%
RESULT 300
ID ADB52519 standard; DNA; 1531 BP.
DE Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:3061.
PN WO2003065993-A2.
PD 14-AUG-2003.
PA (GENE-) GENE LOGIC INC.
Percent Similarity: 43.19% Conservative: 41
Best Local Similarity: 23.94% Mismatches: 92
Indels: 31
Query Match: 7.71%
RESULT 301
ID ADK16023 standard; DNA; 64492 BP.
DE Streptomyces halstedii vincenistatin gene cluster seq id 1.
PN US2004053274-A1.
PD 18-MAR-2004.
PA (TOKD) TOKYO INST TECHNOLOGY.
Percent Similarity: 30.15% Conservative: 24
Best Local Similarity: 22.77% Mismatches: 85
Indels: 142
Query Match: 7.67%
RESULT 302
ID AAQ13305 standard; DNA; 1591 BP.
DE Rat catechol-O-methyltransferase gene.
PN WO9111513-A.
PD 08-AUG-1991.
PA (ORIN) ORION YHTYMAE OY.
Percent Similarity: 43.19% Conservative: 41
Best Local Similarity: 23.94% Mismatches: 92
Indels: 31
Query Match: 7.63%
RESULT 303
ID AAS83954 standard; cDNA; 4083 BP.
DE DNA encoding novel human diagnostic protein #19758.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 37.29% Conservative: 18
Best Local Similarity: 27.12% Mismatches: 66
Indels: 45
Query Match: 7.63%
RESULT 304
ID AAQ88760 standard; DNA; 1813 BP.
DE Human ubiquitous nuclear receptor protein DNA.
PN WO9513373-A1.
PD 18-MAY-1995.
PA (ARCH-) ARCH DEV CORP.
Percent Similarity: 34.41% Conservative: 30
Best Local Similarity: 25.59% Mismatches: 122
Indels: 101
Query Match: 7.59%
RESULT 305
ID AAT79634 standard; DNA; 1898 BP.
DE DNA encoding human ubiquitous nuclear receptor polypeptide.
PN US5639616-A.
PD 17-JUN-1997.
PA (ARCH-) ARCH DEV CORP.
Percent Similarity: 34.21% Conservative: 29
Best Local Similarity: 25.73% Mismatches: 120
Indels: 105
Query Match: 7.59%
RESULT 306
ID AAT27617 standard; cDNA to mRNA; 1688 BP.
DE Steroid hormone receptor analogue ECDN small mol. variant cDNA.
PN WO9609324-A1.
PD 28-MAR-1996.
PA (CANC-) CANCER INST.
PA (EISA) EISAI CO LTD.
Percent Similarity: 37.41% Conservative: 32
Best Local Similarity: 25.90% Mismatches: 106

Query Match: 7.56% Indels: 68

RESULT 307

ID ACC85541 standard; DNA; 2505 BP.

DE T thermophilus strain GK24 DNA polymerase gene SEQ ID NO: 1.

PN WO2003048309-A2.

PD 12-JUN-2003.

PA (APPL-) APPLERA CORP.

Percent Similarity: 36.73%

Best Local Similarity: 26.19%

Query Match: 7.56%

RESULT 308

ID ACC85544 standard; DNA; 2505 BP.

DE T thermophilus strain GK24 variant DNA polymerase gene SEQ ID NO: 4.

PN WO2003048309-A2.

PD 12-JUN-2003.

PA (APPL-) APPLERA CORP.

Percent Similarity: 36.73%

Best Local Similarity: 26.19%

Query Match: 7.56%

RESULT 309

ID ABZ11775 standard; cDNA; 1564 BP.

DE Human polynucleotide SEQ ID NO 657.

PN WO200270539-A2.

PD 12-SEP-2002.

PA (HYSE-) HYSEQ INC.

Percent Similarity: 31.96%

Best Local Similarity: 24.63%

Query Match: 7.52%

RESULT 310

ID ADM44293 standard; cDNA; 1786 BP.

DE Novel human arginine-rich protein cDNA #657.

PN US2004053250-A1.

PD 18-MAR-2004.

PA (TANG/) TANG Y T.

PA (XUE/) XUE A.

PA (DRMA/) DRMANAC R T.

Percent Similarity: 31.96%

Best Local Similarity: 24.63%

Query Match: 7.52%

RESULT 311

ID ADC30127 standard; cDNA; 3298 BP.

DE Human novel cDNA sequence, SEQ ID NO:209.

PN WO2003029271-A2.

PD 10-APR-2003.

PA (HYSE-) HYSEQ INC.

Percent Similarity: 37.09%

Best Local Similarity: 28.17%

Query Match: 7.52%

RESULT 312

ID ACF36088 standard; DNA; 1815 BP.

DE Human LXR beta polypeptide encoding DNA.

PN WO2003059884-A1.

PD 24-JUL-2003.

PA (XCEP-) X-CEPTOR THERAPEUTICS INC.

Percent Similarity: 37.68%

Best Local Similarity: 27.90%

Query Match: 7.48%

RESULT 313

ID ACF04414 standard; DNA; 1815 BP.

DE Human liver X receptor LXR beta coding sequence.

PN WO2003060078-A2.

PD 24-JUL-2003.

PA (XCEP-) X-CEPTOR THERAPEUTICS INC.

Percent Similarity: 37.68%

Best Local Similarity: 27.90%

Query Match: 7.48%

RESULT 314

ID ADL12925 standard; cDNA; 1987 BP.

DE Human steroid-induced C3A liver cell cDNA #654.

PN US6673549-B1.

PD 06-JAN-2004.

PA (INCY-) INCYTE CORP.

Percent Similarity: 37.68%

Conservative: 27

Mismatches: 108

Indels: 64

Best Local Similarity: 27.90%

Query Match: 7.48%

Indels: 64

RESULT 315

ID AAT88206 standard; cDNA; 8460 BP.

DE cDNA for protein (OA-519) cross-reactive with hpr gene product.

PN US5665874-A.

PD 09-SEP-1997.

PA (UYJO) UNIV JOHNS HOPKINS.

Percent Similarity: 33.23%

Best Local Similarity: 24.70%

Query Match: 7.45%

RESULT 316

ID ACC49471 standard; cDNA; 8460 BP.

DE Human fatty acid synthase encoding cDNA.

PN WO2003023355-A2.

PD 20-MAR-2003.

PA (BURN-) BURNHAM INST.

Percent Similarity: 33.23%

Best Local Similarity: 24.70%

Query Match: 7.45%

RESULT 317

ID ACA64923 standard; DNA; 8460 BP.

DE Human breast carcinoma fatty acid synthase DNA corresponding to U29344.

PN DE10127572-A1.

PD 05-DEC-2002.

PA (PATH-) PATHOARRAY GMBH.

Percent Similarity: 33.23%

Best Local Similarity: 24.70%

Query Match: 7.45%

RESULT 318

ID ACF63393 standard; DNA; 8460 BP.

DE Human fatty acid synthase gene SEQ ID NO:115.

PN WO2003006478-A1.

PD 23-JAN-2003.

PA (OLIG-) OLIGOS ETC INC.

Percent Similarity: 33.23%

Best Local Similarity: 24.70%

Query Match: 7.45%

RESULT 319

ID ADO21281 standard; cDNA; 8460 BP.

DE DNA encoding human fatty acid synthase.

PN US2004077570-A1.

PD 22-APR-2004.

PA (FREI/) FREIER S M.

PA (DOBI/) DOBIE K W.

PA (BHAN/) BHANOT S.

Percent Similarity: 33.23%

Best Local Similarity: 24.70%

Query Match: 7.45%

RESULT 320

ID ADP13456 standard; DNA; 8460 BP.

DE Renal cell carcinoma differentially expressed gene #192.

PN WO2004048933-A2.

PD 10-JUN-2004.

PA (AMHP) WYETH.

PA (TWIN/) TWINE N C.

PA (BURC/) BURCZYNSKI M E.

PA (TREP/) TREPICCHIO W L.

PA (DORN/) DORNER A.

PA (STOV/) STOVER J A.

PA (SLON/) SLONI D K.

Percent Similarity: 33.23%

Best Local Similarity: 24.70%

Query Match: 7.45%

RESULT 321

ID AAV74506 standard; DNA; 13715 BP.

DE Staphylococcus aureus contig SEQ ID #195.

PN EP786519-A2.

PD 30-JUL-1997.

PA (HUNA-) HUMAN GENOME SCI INC.

Percent Similarity: 39.27%

Best Local Similarity: 21.46%

Query Match: 7.45%

Conservative: 39

Mismatches: 105

Indels: 28

RESULT 322
 ID ABD07304 standard; DNA; 2469 BP.
 DE Pseudomonas aeruginosa polynucleotide #5908.
 PN US6551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Percent Similarity: 37.3%
 Best Local Similarity: 27.4%
 Query Match: 7.41%
 Indels: 69
 Conservative: 28
 Mismatches: 107
 RESULT 323
 ID ABD11218 standard; DNA; 636 BP.
 DE Pseudomonas aeruginosa polynucleotide #9822.
 PN US6551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Percent Similarity: 43.8%
 Best Local Similarity: 28.7%
 Query Match: 7.37%
 Indels: 20
 Conservative: 21
 Mismatches: 58
 RESULT 324
 ID ABD1311 standard; DNA; 1275 BP.
 DE Pseudomonas aeruginosa polynucleotide #9915.
 PN US6551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Percent Similarity: 43.8%
 Best Local Similarity: 28.7%
 Query Match: 7.37%
 Indels: 20
 Conservative: 21
 Mismatches: 58
 RESULT 325
 ID ABD11556 standard; DNA; 1443 BP.
 DE Pseudomonas aeruginosa polynucleotide #10160.
 PN US6551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Percent Similarity: 43.8%
 Best Local Similarity: 28.7%
 Query Match: 7.37%
 Indels: 20
 Conservative: 21
 Mismatches: 58
 RESULT 326
 ID AAQ24322 standard; DNA; 1635 BP.
 DE Mutant thermostable DNA polymerase p205A292.
 PN WO9206200-A.
 PD 16-APR-1992.
 PA (CETU) CETUS CORP.
 Percent Similarity: 37.9%
 Best Local Similarity: 25.0%
 Query Match: 7.37%
 Indels: 67
 Conservative: 37
 Mismatches: 112
 RESULT 327
 ID AAQ24321 standard; DNA; 1899 BP.
 DE Mutant thermostable DNA polymerase p205d2-203.
 PN WO9206200-A.
 PD 16-APR-1992.
 PA (CETU) CETUS CORP.
 Percent Similarity: 37.9%
 Best Local Similarity: 25.0%
 Query Match: 7.37%
 Indels: 67
 Conservative: 37
 Mismatches: 112
 RESULT 328
 ID ABX84201 standard; cDNA; 2010 BP.
 DE Human cDNA differentially expressed in granulocytic cells #772.
 PN WO200228999-A2.
 PD 11-APR-2002.
 PA (GENE-) GENE LOGIC INC.
 Percent Similarity: 37.7%
 Best Local Similarity: 27.6%
 Query Match: 7.37%
 Indels: 67
 Conservative: 29
 Mismatches: 111
 RESULT 329
 ID ADJ14181 standard; DNA; 2010 BP.
 DE DNA encoding human liver X receptor LXR beta.
 PN US2004018560-A1.
 PD 29-JAN-2004.
 PA (BLED/) BLED SOE R K.
 PA (MILL/) MILLER A.
 PA (MOOR/) MOORE J T.
 PA (WILL/) WILLIAMS S P.

PA (WISE/) WISELY G B.
 Percent Similarity: 37.7%
 Best Local Similarity: 27.6%
 Query Match: 7.37%
 Indels: 67
 Conservative: 29
 Mismatches: 111
 RESULT 330
 ID ADM41245 standard; DNA; 2010 BP.
 DE Human liver X receptor beta gene.
 PN EPI398032-A1.
 PD 17-MAR-2004.
 PA (PHEN-) PHENEX PHARM AG.
 Percent Similarity: 37.7%
 Best Local Similarity: 27.6%
 Query Match: 7.37%
 Indels: 67
 Conservative: 29
 Mismatches: 111
 RESULT 331
 ID AAQ63134 standard; cDNA; 2030 BP.
 DE Human recombinant steroid hormone receptor NERI cDNA.
 PN WO9407916-A1.
 PD 14-APR-1994.
 PA (MERI) MERCK & CO INC.
 Percent Similarity: 37.7%
 Best Local Similarity: 27.6%
 Query Match: 7.37%
 Indels: 67
 Conservative: 29
 Mismatches: 111
 RESULT 332
 ID AAT18996 standard; DNA; 2030 BP.
 DE Human steroid receptor NER gene.
 PN WO9613519-A1.
 PD 09-MAY-1996.
 PA (MERI) MERCK & CO INC.
 Percent Similarity: 37.7%
 Best Local Similarity: 27.6%
 Query Match: 7.37%
 Indels: 67
 Conservative: 29
 Mismatches: 111
 RESULT 333
 ID AAT30031 standard; DNA; 2030 BP.
 DE NER receptor potentiator DNA.
 PN WO9613257-A1.
 PD 09-MAY-1996.
 PA (MERI) MEDICAL COLLEGE PENNSYLVANIA.
 Percent Similarity: 37.7%
 Best Local Similarity: 27.6%
 Query Match: 7.37%
 Indels: 67
 Conservative: 29
 Mismatches: 111
 RESULT 334
 ID AAQ24320 standard; DNA; 2043 BP.
 DE Mutant thermostable DNA polymerase p205d2-155.
 PN WO9206200-A.
 PD 16-APR-1992.
 PA (CETU) CETUS CORP.
 Percent Similarity: 37.9%
 Best Local Similarity: 25.0%
 Query Match: 7.37%
 Indels: 67
 Conservative: 37
 Mismatches: 112
 RESULT 335
 ID AAQ24013 standard; DNA; 2277 BP.
 DE Mutant thermostable DNA polymerase p205d2-77.
 PN WO9206200-A.
 PD 16-APR-1992.
 PA (CETU) CETUS CORP.
 Percent Similarity: 37.9%
 Best Local Similarity: 25.0%
 Query Match: 7.37%
 Indels: 67
 Conservative: 37
 Mismatches: 112
 RESULT 336
 ID AAQ24012 standard; DNA; 2370 BP.
 DE Mutant thermostable DNA polymerase p205d2-46.
 PN WO9206200-A.
 PD 16-APR-1992.
 PA (CETU) CETUS CORP.
 Percent Similarity: 37.9%
 Best Local Similarity: 25.0%
 Query Match: 7.37%
 Indels: 67
 Conservative: 37
 Mismatches: 112
 RESULT 337
 ID AAQ24011 standard; DNA; 2505 BP.
 DE Mutant thermostable DNA polymerase from Thermus species Z05.
 PN WO9206200-A.

Query Match:	7.33%	Indels:	58
PD 16-APR-1992.			
PA (CETU) CETUS CORP.			
Conservative: 37			
Mismatches: 112			
Indels: 67			
PERCENT SIMILARITY: 25.09%			
Best Local Similarity: 7.37%			
Query Match:			
RESULT 338			
ID ADG64486 standard; DNA; 2685 BP.			
DE Chimeric thermostable DNA polymerase CS8 encoding DNA SEQ ID NO:171.			
PD 08-OCT-2003.			
PA (HOFF) ROCHE DIAGNOSTICS GMBH.			
Conservative: 37			
Mismatches: 112			
Indels: 67			
PERCENT SIMILARITY: 25.09%			
Best Local Similarity: 7.37%			
Query Match:			
RESULT 339			
ID ADG64462 standard; DNA; 2685 BP.			
DE Chimeric thermostable DNA polymerase CS7 encoding DNA SEQ ID NO:147.			
PD 08-OCT-2003.			
PA (HOFF) ROCHE DIAGNOSTICS GMBH.			
Conservative: 37			
Mismatches: 112			
Indels: 67			
PERCENT SIMILARITY: 25.09%			
Best Local Similarity: 7.37%			
Query Match:			
RESULT 340			
ID ADA13364 standard; cDNA; 2877 BP.			
DE Human intracellular signalling molecule INTS1G-1 cDNA, SEQ ID NO:46.			
PD 17-APR-2003.			
PA (INCY) INCYTE GENOMICS INC.			
Conservative: 26			
Mismatches: 111			
Indels: 60			
PERCENT SIMILARITY: 36.80%			
Best Local Similarity: 7.37%			
Query Match:			
RESULT 341			
ID ADMA1248 standard; DNA; 8461 BP.			
DE Human fatty acid synthase gene.			
PD 17-MAR-2004.			
PA (PHEN) PHENEX PHARM AG.			
Conservative: 30			
Mismatches: 91			
Indels: 120			
PERCENT SIMILARITY: 34.27%			
Best Local Similarity: 7.37%			
Query Match:			
RESULT 342			
ID AAA37760 standard; DNA; 8519 BP.			
DE Human fatty acid synthase (FAS) coding sequence.			
PD 08-SEP-2000.			
PA (SMIK) SMITHKLINE BEECHAM CORP.			
Conservative: 30			
Mismatches: 91			
Indels: 120			
PERCENT SIMILARITY: 34.27%			
Best Local Similarity: 7.37%			
Query Match:			
RESULT 343			
ID AAK73222 standard; DNA; 15914 BP.			
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:28034.			
PD 09-AUG-2001.			
PA (HUMA-) HUMAN GENOME SCI INC.			
Conservative: 22			
Mismatches: 73			
Indels: 70			
PERCENT SIMILARITY: 34.70%			
Best Local Similarity: 7.37%			
Query Match:			
RESULT 344			
ID AAG73222 standard; DNA; 15914 BP.			
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:28034.			
PD 09-AUG-2001.			
PA (HUMA-) HUMAN GENOME SCI INC.			
Conservative: 22			
Mismatches: 73			
Indels: 70			
PERCENT SIMILARITY: 34.70%			
Best Local Similarity: 7.37%			
Query Match:			
RESULT 345			
ID ABD10818 standard; DNA; 855 BP.			
DE Pseudomonas aeruginosa polynucleotide #9422.			
PD 22-APR-2003.			
PA (GENO-) GENOME THERAPEUTICS CORP.			
Conservative: 24			
Mismatches: 38.56%			
Indels: 28.39%			
PERCENT SIMILARITY: 28.39%			
Best Local Similarity: 7.37%			
Query Match:			
RESULT 346			
ID ABD10851 standard; DNA; 1101 BP.			
DE Pseudomonas aeruginosa polynucleotide #9455.			
PD 22-APR-2003.			
PA (GENO-) GENOME THERAPEUTICS CORP.			
Conservative: 24			
Mismatches: 38.56%			
Indels: 28.39%			
PERCENT SIMILARITY: 28.39%			
Best Local Similarity: 7.33%			
Query Match:			

DE Pseudomonas aeruginosa polynucleotide #109.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Percent Similarity: 36.16%
Best Local Similarity: 26.57%
Query Match: 7.30%
Indels: 101
RESULT 355
ID AAI16078 standard; cDNA; 1782 BP.
DE Human cDNA sequence SEQ ID NO:14776.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Percent Similarity: 31.67%
Best Local Similarity: 24.63%
Query Match: 7.30%
Indels: 108
RESULT 356
ID ACC78000 standard; DNA; 3221 BP.
DE Thermus thermophilus mutant DNA polymerase encoding DNA.
PN WO2003025132-A2.
PD 27-MAR-2003.
PA (INVI-) INVITROGEN CORP.
Percent Similarity: 37.37%
Best Local Similarity: 25.61%
Query Match: 7.30%
Indels: 68
RESULT 357
ID ADP64454 standard; DNA; 76994 BP.
DE Sorangium cellulosum disorazole polyketide synthase gene cluster DNA.
PN WO2004053065-A2.
PD 24-JUN-2004.
PA (KOSA-) KOSAN BIOSCIENCES INC.
Percent Similarity: 32.34%
Best Local Similarity: 21.66%
Query Match: 7.30%
Indels: 149
RESULT 358
ID ABD10747 standard; DNA; 657 BP.
DE Pseudomonas aeruginosa polynucleotide #9351.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Percent Similarity: 38.50%
Best Local Similarity: 28.32%
Query Match: 7.26%
Indels: 56
RESULT 359
ID AA291260 standard; DNA; 1632 BP.
DE Acetohydroxyacid synthase nucleotide sequence SEQ ID NO:14.
PN WO200004158-A2.
PD 27-JAN-2000.
PA (PION-) PIONEER HI-BRED INT INC.
Percent Similarity: 38.33%
Best Local Similarity: 26.48%
Query Match: 7.26%
Indels: 53
RESULT 360
ID AA127616 standard; cDNA to mRNA; 1979 BP.
DE Human foetal lung steroid hormone receptor analogue ECDN cDNA.
PN WO9609324-A1.
PD 28-MAR-1996.
PA (CANC-) CANCER INST.
PA (EISA) EISAI CO LTD.
Percent Similarity: 37.77%
Best Local Similarity: 28.42%
Query Match: 7.26%
Indels: 68
RESULT 361
ID ABD13152 standard; DNA; 2232 BP.
DE Pseudomonas aeruginosa polynucleotide #11756.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Percent Similarity: 38.11%
Best Local Similarity: 28.32%
Query Match: 7.26%
Indels: 67
RESULT 362
ID ABD13005 standard; DNA; 2274 BP.

DE Pseudomonas aeruginosa polynucleotide #11609.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Percent Similarity: 38.11%
Best Local Similarity: 28.32%
Query Match: 7.26%
Indels: 67
RESULT 363
ID ACC85543 standard; DNA; 2505 BP.
DE T thermophilus strain 1b21 DNA polymerase gene SEQ ID NO: 3.
PN WO2003048309-A2.
PD 12-JUN-2003.
PA (APPL-) APPLERA CORP.
Percent Similarity: 37.33%
Best Local Similarity: 25.68%
Query Match: 7.26%
Indels: 74
RESULT 364
ID ACC85542 standard; DNA; 2505 BP.
DE T thermophilus strain RQ-1 DNA polymerase gene SEQ ID NO: 2.
PN WO2003048309-A2.
PD 12-JUN-2003.
PA (APPL-) APPLERA CORP.
Percent Similarity: 36.64%
Best Local Similarity: 25.68%
Query Match: 7.26%
Indels: 74
RESULT 365
ID ACC85547 standard; DNA; 2505 BP.
DE T thermophilus strain GK24 variant DNA polymerase gene SEQ ID NO: 7.
PN WO2003048309-A2.
PD 12-JUN-2003.
PA (APPL-) APPLERA CORP.
Percent Similarity: 36.39%
Best Local Similarity: 26.19%
Query Match: 7.26%
Indels: 78
RESULT 366
ID ACC85545 standard; DNA; 2505 BP.
DE T thermophilus strain RQ-1 variant DNA polymerase gene SEQ ID NO: 5.
PN WO2003048309-A2.
PD 12-JUN-2003.
PA (APPL-) APPLERA CORP.
Percent Similarity: 36.64%
Best Local Similarity: 25.68%
Query Match: 7.26%
Indels: 74
RESULT 367
ID ACC85550 standard; DNA; 2505 BP.
DE T thermophilus strain GK24 variant DNA polymerase gene SEQ ID NO: 10.
PN WO2003048309-A2.
PD 12-JUN-2003.
PA (APPL-) APPLERA CORP.
Percent Similarity: 36.39%
Best Local Similarity: 26.19%
Query Match: 7.26%
Indels: 78
RESULT 368
ID ACC85546 standard; DNA; 2505 BP.
DE T thermophilus strain 1b21 variant DNA polymerase gene SEQ ID NO: 6.
PN WO2003048309-A2.
PD 12-JUN-2003.
PA (APPL-) APPLERA CORP.
Percent Similarity: 37.33%
Best Local Similarity: 25.68%
Query Match: 7.26%
Indels: 74
RESULT 369
ID ABD13232 standard; DNA; 2613 BP.
DE Pseudomonas aeruginosa polynucleotide #11836.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Percent Similarity: 38.11%
Best Local Similarity: 28.32%
Query Match: 7.26%
Indels: 67
RESULT 370
ID ACC77974 standard; DNA; 3221 BP.
DE Thermus thermophilus mutant DNA polymerase encoding DNA.

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PN WO2003025132-A2.
PD 27-MAR-2003.
PA (INVI-) INVITROGEN CORP.
Percent Similarity: 36.64%
Best Local Similarity: 25.34%
Query Match: 7.26%
Conservative: 33
Mismatch: 113
Indels: 74
RESULT 371
ID ACC77971 standard; DNA; 3221 BP.
DE Thermus thermophilus mutant DNA polymerase encoding DNA.
PN WO2003025132-A2.
PD 27-MAR-2003.
PA (INVI-) INVITROGEN CORP.
Percent Similarity: 36.99%
Best Local Similarity: 25.34%
Query Match: 7.26%
Conservative: 34
Mismatch: 112
Indels: 74
RESULT 372
ID AA231253 standard; DNA; 24494 BP.
DE Bacterium 2412.1 fumonis-catabolising gene cluster.
PN WO200004158-A2.
PD 27-JAN-2000.
PA (PION-) PIONEER HI-BRED INT INC.
Percent Similarity: 38.33%
Best Local Similarity: 26.48%
Query Match: 7.26%
Conservative: 34
Mismatch: 124
Indels: 53
RESULT 373
ID AAQ46806 standard; DNA; 29879 BP.
DE eryA region of S. erythraea chromosome.
PN WO9313663-A1.
PD 22-JUL-1993.
PA (ABBO-) ABBOTT LAB.
Percent Similarity: 33.03%
Best Local Similarity: 24.62%
Query Match: 7.26%
Conservative: 28
Mismatch: 93
Indels: 130
RESULT 374
ID ABD11655 standard; DNA; 1086 BP.
DE Pseudomonas aeruginosa polynucleotide #10259.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Percent Similarity: 40.35%
Best Local Similarity: 26.32%
Query Match: 7.22%
Conservative: 40
Mismatch: 122
Indels: 49
RESULT 375
ID ABD11993 standard; DNA; 1101 BP.
DE Pseudomonas aeruginosa polynucleotide #10597.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Percent Similarity: 40.35%
Best Local Similarity: 26.32%
Query Match: 7.22%
Conservative: 40
Mismatch: 122
Indels: 49
RESULT 376
ID ACA45703 standard; DNA; 1104 BP.
DE Prokaryotic essential gene #27360.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Percent Similarity: 44.22%
Best Local Similarity: 26.63%
Query Match: 7.22%
Conservative: 35
Mismatch: 72
Indels: 39
RESULT 377
ID AA81453 standard; DNA; 36471 BP.
DE N. meningitidis partial DNA sequence gnm_1 SEQ ID NO:1.
PN WO200022430-A2.
PD 20-APR-2000.
PA (CHIR-) CHIRON CORP.
Percent Similarity: 35.76%
Best Local Similarity: 23.84%
Query Match: 7.22%
Conservative: 36
Mismatch: 103
Indels: 92
RESULT 378
ID ACC77971 standard; DNA; 3221 BP.
DE Thermus thermophilus mutant DNA polymerase encoding DNA.
PN WO2003025132-A2.
PD 27-MAR-2003.
PA (INVI-) INVITROGEN CORP.
Percent Similarity: 36.64%
Best Local Similarity: 25.34%
Query Match: 7.26%
Conservative: 33
Mismatch: 113
Indels: 74
RESULT 379
ID AAF21611 standard; DNA; 349980 BP.
DE Neisseria meningitidis B nucleotide sequence SEQ ID NO:112.
PN WO200066791-A1.
PD 09-NOV-2000.
PA (CHIR-) CHIRON CORP.
Percent Similarity: 35.76%
Best Local Similarity: 23.84%
Query Match: 7.22%
Conservative: 36
Mismatch: 103
Indels: 92
RESULT 380
ID ABD13494 standard; DNA; 783 BP.
DE Pseudomonas aeruginosa polynucleotide #12098.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Percent Similarity: 35.43%
Best Local Similarity: 25.98%
Query Match: 7.19%
Conservative: 24
Mismatch: 93
Indels: 71
RESULT 381
ID ABD13569 standard; DNA; 984 BP.
DE Pseudomonas aeruginosa polynucleotide #12173.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Percent Similarity: 35.43%
Best Local Similarity: 25.98%
Query Match: 7.19%
Conservative: 24
Mismatch: 93
Indels: 71
RESULT 382
ID ABD13816 standard; DNA; 1254 BP.
DE Pseudomonas aeruginosa polynucleotide #12420.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Percent Similarity: 36.03%
Best Local Similarity: 27.57%
Query Match: 7.19%
Conservative: 23
Mismatch: 125
Indels: 50
RESULT 383
ID ACC77992 standard; DNA; 3221 BP.
DE Thermus thermophilus mutant DNA polymerase encoding DNA.
PN WO2003025132-A2.
PD 27-MAR-2003.
PA (INVI-) INVITROGEN CORP.
Percent Similarity: 36.64%
Best Local Similarity: 25.34%
Query Match: 7.19%
Conservative: 33
Mismatch: 113
Indels: 74
RESULT 384
ID ABD07318 standard; DNA; 3135 BP.
DE Pseudomonas aeruginosa polynucleotide #5922.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Percent Similarity: 37.17%
Best Local Similarity: 27.14%
Query Match: 7.15%
Conservative: 27
Mismatch: 101
Indels: 68
RESULT 385
ID ADC59447 standard; cDNA; 15534 BP.
DE Human epiplakin-encoding cDNA.
PN JP2003047469-A.
PD 18-FEB-2003.
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
Percent Similarity: 34.68%
Best Local Similarity: 25.25%
Query Match: 7.15%
Conservative: 28
Mismatch: 101
Indels: 93
RESULT 386
ID ADJ75047 standard; DNA; 15534 BP.
DE Marker gene SEQ ID NO:299.
PN EP1394274-A2.
PD 03-MAR-2004.
PA (GENO-) GENOX RES INC.
Percent Similarity: 34.68%
Best Local Similarity: 25.25%
Query Match: 7.15%
Conservative: 28
Mismatch: 101
Indels: 93

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RESULT 387
 ID ACPI2853 standard; cDNA; 15952 BP.
 DE Human cervical cancer cell marker encoding cDNA SEQ ID NO:51.
 FN WO2002101075-A2.
 PD 19-DEC-2002.
 PA (MILL-) MILLENNIUM PHARM INC.
 Percent Similarity: 34.68%
 Best Local Similarity: 25.25%
 Query Match: 7.15%
 RESULT 388
 ID ABD09003 standard; DNA; 852 BP.
 DE Pseudomonas aeruginosa polynucleotide #7607.
 FN US5551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Percent Similarity: 39.39%
 Best Local Similarity: 27.27%
 Query Match: 7.11%
 RESULT 389
 ID ABD09003 standard; DNA; 852 BP.
 DE Pseudomonas aeruginosa polynucleotide #7607.
 FN US5551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Percent Similarity: 38.89%
 Best Local Similarity: 26.30%
 Query Match: 7.11%
 RESULT 390
 ID AAT27255 standard; DNA; 1794 BP.
 DE DNA polymerase I exonuclease-free fragment.
 FN WO9614405-A2.
 PD 17-MAY-1996.
 PA (MOLE-) MOLECULAR BIOLOGY RESOURCES INC.
 Percent Similarity: 36.99%
 Best Local Similarity: 25.68%
 Query Match: 7.11%
 RESULT 391
 ID AAT732327 standard; DNA; 1794 BP.
 DE Thermus flavus DNA polymerase I exonuclease free fragment.
 FN WO9614417-A1.
 PD 17-MAY-1996.
 PA (MOLE-) MOLECULAR BIOLOGY RESOURCES INC.
 Percent Similarity: 36.99%
 Best Local Similarity: 25.68%
 Query Match: 7.11%
 RESULT 392
 ID ADN96193 standard; cDNA; 1837 BP.
 DE Human NOVX polynucleotide #124.
 FN US2004067490-A1.
 PD 08-APR-2004.
 PA (ZHON/) ZHONG M.
 PA (LILL/) LI L.
 PA (GORM/) GORMAN L.
 PA (SPIT/) SPYTEK K A.
 PA (KEKU/) KEKUDA R.
 PA (TAUP/) TAUPIER R J.
 PA (ANDE/) ANDERSON D W.
 PA (VERN/) VERNET C A M.
 PA (CATT/) CATTERTON E.
 PA (MILL/) MILLER C E.
 PA (SHEN/) SHENOY S G.
 PA (PATT/) PATTURAJAN M.
 PA (PENA/) PENA C E A.
 PA (TCHE/) TCHERNEV V T.
 PA (PADI/) PADIGARU M.
 PA (GUSE/) GUSEV V Y.
 PA (MALY/) MALYANKAR U M.
 PA (BURG/) BURGESS C E.
 PA (GERL/) GERLACH V.
 PA (CASM/) CASMAN S J.
 PA (RIEG/) RIEGER D K.
 PA (GROS/) GROSSE W M.
 PA (SMIT/) SMITHSON G.

PA (PEYM/) PEYMAN J A.
 PA (STAR/) STARLING G.
 PA (ROTH/) ROTHENBERG M E.
 PA (LARO/) LAROCHELLE W J.
 PA (SHIM/) SHIMKETS R A.
 PA (CRAB/) CRABTREE J.
 PA (RAST/) RASTELLI L.
 PA (VOSS/) VOSS E Z.
 PA (BOLD/) BOLDOG F L.
 PA (EDIN/) EDINGER S R.
 PA (MILL/) MILLET I.
 PA (MACD/) MACDOUGALL J R.
 PA (ELLE/) ELLERMAN K.
 PA (CHAP/) CHAPOVAL A.
 Percent Similarity: 32.99%
 Best Local Similarity: 24.40%
 Query Match: 7.11%
 RESULT 393
 ID AAS4053 standard; DNA; 2553 BP.
 DE Pseudomonas aeruginosa DNA for cellular proliferation protein #184.
 FN WO200170955-A2.
 PD 27-SEP-2001.
 PA (ELIT-) ELITRA PHARM INC.
 Percent Similarity: 36.26%
 Best Local Similarity: 27.47%
 Query Match: 7.11%
 RESULT 394
 ID ACA42124 standard; DNA; 2553 BP.
 DE Prokaryotic essential gene #23781.
 FN WO200277183-A2.
 PD 03-OCT-2002.
 PA (ELIT-) ELITRA PHARM INC.
 Percent Similarity: 36.26%
 Best Local Similarity: 27.47%
 Query Match: 7.11%
 RESULT 395
 ID AAZ48661 standard; DNA; 2942 BP.
 DE L. mycophilus chitinase gene, N4-7 chia.
 FN WO9955833-A2.
 PD 04-NOV-1999.
 PA (RUTP/) UNIV RUTGERS STATE NEW JERSEY.
 Percent Similarity: 35.89%
 Best Local Similarity: 27.42%
 Query Match: 7.11%
 RESULT 396
 ID AAT27254 standard; DNA; 3048 BP.
 DE DNA polymerase I holoenzyme coding sequence.
 FN WO9614405-A2.
 PD 17-MAY-1996.
 PA (MOLE-) MOLECULAR BIOLOGY RESOURCES INC.
 Percent Similarity: 36.99%
 Best Local Similarity: 25.68%
 Query Match: 7.11%
 RESULT 397
 ID ACC78014 standard; DNA; 3221 BP.
 DE Thermus thermophilus mutant DNA polymerase encoding DNA.
 FN WO2003025132-A2.
 PD 27-MAR-2003.
 PA (INVI-) INVITROGEN CORP.
 Percent Similarity: 36.64%
 Best Local Similarity: 25.34%
 Query Match: 7.11%
 RESULT 398
 ID ACC78011 standard; DNA; 3221 BP.
 DE Thermus thermophilus mutant DNA polymerase encoding DNA.
 FN WO2003025132-A2.
 PD 27-MAR-2003.
 PA (INVI-) INVITROGEN CORP.
 Percent Similarity: 36.64%
 Best Local Similarity: 25.34%
 Query Match: 7.11%
 RESULT 399
 ID ACC77998 standard; DNA; 3221 BP.

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DE Thermus thermophilus mutant DNA polymerase encoding DNA.
PN WO2003025132-A2.
PD 27-MAR-2003.
PA (INVI-) INVITROGEN CORP.
Percent Similarity: 36.99%
Best Local Similarity: 25.68%
Query Match: 7.11%
Conservative: 33
Mismatch: 112
Indels: 74
RESULT 400
ID ABD05402 standard; DNA; 4284 BP.
DE Pseudomonas aeruginosa polynucleotide #4006.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Percent Similarity: 38.89%
Best Local Similarity: 26.30%
Query Match: 7.11%
Conservative: 34
Mismatch: 95
Indels: 70
RESULT 401
ID ABO55289 standard; cDNA; 553 BP.
DE Human ovarian antigen HCOQX38 cDNA, SEQ ID NO:1169.
PN WO200200677-A1.
PD 03-JAN-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 45.66%
Best Local Similarity: 25.00%
Query Match: 7.07%
Conservative: 24
Mismatch: 59
Indels: 4
RESULT 402
ID AAH13983 standard; cDNA; 1416 BP.
DE Human cDNA sequence SEQ ID NO:11048.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Percent Similarity: 37.13%
Best Local Similarity: 24.89%
Query Match: 7.07%
Conservative: 29
Mismatch: 94
Indels: 55
RESULT 403
ID ACA27231 standard; DNA; 1948 BP.
DE Prokaryotic essential gene #8888.
PN WO20027183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Percent Similarity: 29.66%
Best Local Similarity: 22.57%
Query Match: 7.07%
Conservative: 27
Mismatch: 96
Indels: 172
RESULT 404
ID ADA52678 standard; cDNA; 2597 BP.
DE Human coding sequence, SEQ ID 246.
PN EP1293569-A2.
PD 19-MAR-2003.
PA (HELI-) HELIX RES INST.
Percent Similarity: 37.13%
Best Local Similarity: 24.89%
Query Match: 7.07%
Conservative: 29
Mismatch: 94
Indels: 55
RESULT 405
ID ADD69665 standard; cDNA; 3153 BP.
DE Human REMAP cDNA - SEQ ID 94.
PN WO2003048305-A2.
PD 12-JUN-2003.
PA (INCY-) INCYTE GENOMICS INC.
Percent Similarity: 39.81%
Best Local Similarity: 26.07%
Query Match: 7.07%
Conservative: 29
Mismatch: 72
Indels: 55
RESULT 406
ID ADD24914 standard; DNA; 4184 BP.
DE DNA encoding Escherichia coli intracellular protease #6.
PN US2003036176-A1.
PD 20-FEB-2003.
PA (BOWE/) BOWEN S G.
Percent Similarity: 36.84%
Best Local Similarity: 25.39%
Query Match: 7.07%
Conservative: 37
Mismatch: 109
Indels: 97
RESULT 407
ID AAF86431 standard; DNA; 349980 BP.
DE Pyrococcus abyssi genomic fragment #1.
PN FR2792851-A1.
PD 27-OCT-2000.
PA (CNRS) CNRS CENT NAT RECH SCI.
PA (IFRE-) IFREMER INST FR RECH EXPL MER.
Percent Similarity: 36.00%
Best Local Similarity: 20.36%
Query Match: 7.07%
Conservative: 43
Mismatch: 100
Indels: 76
RESULT 408
ID AAQ14176 standard; cDNA; 2304 BP.
DE Clone pXR2C8 encoding insect steroid receptor XR2C.
PN WO9114695-A.
PD 03-OCT-1991.
PA (SALK) SALK INST BIOLOGICAL STUDIES.
Percent Similarity: 34.46%
Best Local Similarity: 25.00%
Query Match: 7.04%
Conservative: 28
Mismatch: 109
Indels: 85
RESULT 409
ID AAQ55374 standard; DNA; 2304 BP.
DE pXR2C8 DNA.
PN WO9401558-A2.
PD 20-JAN-1994.
PA (SALK) SALK INST BIOLOGICAL STUDIES.
Percent Similarity: 34.46%
Best Local Similarity: 25.00%
Query Match: 7.04%
Conservative: 28
Mismatch: 109
Indels: 85
RESULT 410
ID AAT76787 standard; DNA; 2304 BP.
DE Insect XR2C receptor coding sequence.
PN US5641652-A.
PD 24-JUN-1997.
PA (SALK) SALK INST BIOLOGICAL STUDIES.
Percent Similarity: 34.46%
Best Local Similarity: 25.00%
Query Match: 7.04%
Conservative: 28
Mismatch: 109
Indels: 85
RESULT 411
ID AAT89959 standard; DNA; 2304 BP.
DE D. melanogaster XR2C retinoid-like receptor DNA.
PN US5688691-A.
PD 18-NOV-1997.
PA (SALK) SALK INST BIOLOGICAL STUDIES.
Percent Similarity: 34.46%
Best Local Similarity: 25.00%
Query Match: 7.04%
Conservative: 28
Mismatch: 109
Indels: 85
RESULT 412
ID ABL07559 standard; cDNA; 2483 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 17159.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Percent Similarity: 34.46%
Best Local Similarity: 25.00%
Query Match: 7.04%
Conservative: 28
Mismatch: 109
Indels: 85
RESULT 413
ID ACC77970 standard; DNA; 3221 BP.
DE Thermus thermophilus mutant DNA polymerase encoding DNA.
PN WO2003025132-A2.
PD 27-MAR-2003.
PA (INVI-) INVITROGEN CORP.
Percent Similarity: 36.64%
Best Local Similarity: 25.34%
Query Match: 7.04%
Conservative: 33
Mismatch: 113
Indels: 74
RESULT 414
ID ACC77978 standard; DNA; 3221 BP.
DE Thermus thermophilus mutant DNA polymerase encoding DNA.
PN WO2003025132-A2.
PD 27-MAR-2003.
PA (INVI-) INVITROGEN CORP.
Percent Similarity: 36.64%
Best Local Similarity: 25.34%
Query Match: 7.04%
Conservative: 33
Mismatch: 113
Indels: 74
RESULT 415

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ID ACC77991 standard; DNA; 3221 BP.
DE Thermus thermophilus mutant DNA polymerase encoding DNA.
PN WO20030325132-A2.
PD 27-MAR-2003.
PA (INVI-) INVITROGEN CORP.
Percent Similarity: 36.64% Conservative: 33
Best Local Similarity: 25.34% Mismatches: 113
Query Match: 7.04% Indels: 74
RESULT 416
ID ACC77984 standard; DNA; 3221 BP.
DE Thermus thermophilus mutant DNA polymerase encoding DNA.
PN WO20030325132-A2.
PD 27-MAR-2003.
PA (INVI-) INVITROGEN CORP.
Percent Similarity: 36.64% Conservative: 33
Best Local Similarity: 25.34% Mismatches: 113
Query Match: 7.04% Indels: 74
RESULT 417
ID ABL07558 standard; CDNA; 4483 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 17156.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Percent Similarity: 34.46% Conservative: 28
Best Local Similarity: 25.00% Mismatches: 109
Query Match: 7.04% Indels: 85
RESULT 418
ID ABL07492 standard; CDNA; 18737 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 16958.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Percent Similarity: 34.46% Conservative: 28
Best Local Similarity: 25.00% Mismatches: 109
Query Match: 7.04% Indels: 85
RESULT 419
ID ABL07530 standard; CDNA; 18737 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 17072.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Percent Similarity: 34.46% Conservative: 28
Best Local Similarity: 25.00% Mismatches: 109
Query Match: 7.04% Indels: 85
RESULT 420
ID ACA43915 standard; DNA; 717 BP.
DE Prokaryotic essential gene #25572.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Percent Similarity: 34.08% Conservative: 22
Best Local Similarity: 25.84% Mismatches: 84
Query Match: 7.00% Indels: 93
RESULT 421
ID AAS65542 standard; CDNA; 825 BP.
DE DNA encoding novel human diagnostic protein #1346.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 44.79% Conservative: 11
Best Local Similarity: 33.33% Mismatches: 33
Query Match: 7.00% Indels: 20
RESULT 422
ID AAO80524 standard; DNA; 1410 BP.
DE Oxidoreducing avermectin DNA from S. avermetilis ATCC31271.
PN JP06189774-A.
PD 12-JUL-1994.
PA (KITA) KITASATO KENKYUSHO SH.
Percent Similarity: 35.48% Conservative: 32
Best Local Similarity: 24.01% Mismatches: 104
Query Match: 7.00% Indels: 76
RESULT 423
ID ABD13438 standard; DNA; 1527 BP.

DE Pseudomonas aeruginosa polynucleotide #12042.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Percent Similarity: 37.62% Conservative: 23
Best Local Similarity: 26.67% Mismatches: 78
Query Match: 7.00% Indels: 53
RESULT 424
ID ABD01627 standard; DNA; 1962 BP.
DE Pseudomonas aeruginosa polynucleotide #231.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Percent Similarity: 36.64% Conservative: 24
Best Local Similarity: 28.42% Mismatches: 118
Query Match: 7.00% Indels: 67
RESULT 425
ID ABD13335 standard; DNA; 2313 BP.
DE Pseudomonas aeruginosa polynucleotide #11939.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Percent Similarity: 37.62% Conservative: 23
Best Local Similarity: 26.67% Mismatches: 78
Query Match: 7.00% Indels: 53
RESULT 426
ID ADQ22115 standard; DNA; 4618 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 4935.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Percent Similarity: 37.33% Conservative: 22
Best Local Similarity: 27.19% Mismatches: 79
Query Match: 7.00% Indels: 57
RESULT 427
ID ABD10637 standard; DNA; 1233 BP.
DE Pseudomonas aeruginosa polynucleotide #9241.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Percent Similarity: 31.86% Conservative: 26
Best Local Similarity: 24.65% Mismatches: 100
Query Match: 6.96% Indels: 147
RESULT 428
ID ABD10108 standard; DNA; 1980 BP.
DE Pseudomonas aeruginosa polynucleotide #8712.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Percent Similarity: 30.93% Conservative: 17
Best Local Similarity: 25.09% Mismatches: 78
Query Match: 6.96% Indels: 123
RESULT 429
ID ACC85548 standard; DNA; 2505 BP.
DE T thermophilus strain RQ-1 variant DNA polymerase gene SEQ ID NO: 8.
PN WO2003048309-A2.
PD 12-JUN-2003.
PA (APPL-) APPLERA CORP.
Percent Similarity: 36.30% Conservative: 31
Best Local Similarity: 25.68% Mismatches: 114
Query Match: 6.96% Indels: 74
RESULT 430
ID ACC85552 standard; DNA; 2505 BP.
DE T thermophilus strain lb21 variant DNA polymerase gene SEQ ID NO: 12.
PN WO2003048309-A2.
PD 12-JUN-2003.
PA (APPL-) APPLERA CORP.
Percent Similarity: 36.99% Conservative: 33
Best Local Similarity: 25.68% Mismatches: 112
Query Match: 6.96% Indels: 74
RESULT 431
ID ACC85549 standard; DNA; 2505 BP.
DE T thermophilus strain lb21 variant DNA polymerase gene SEQ ID NO: 9.

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Percent Similarity: 37.13% Conservative: 36
Best Local Similarity: 25.41% Mismatches: 119
Query Match: 6.92% Indels: 75
RESULT 448
ID AAQ53954 standard; DNA; 3221 BP.
DE Heat stable DNA polymerase coding sequence.
PN JP05317058-A.
PD 03-DEC-1993.
PA (TOYO) TOYOBO KK.
Percent Similarity: 35.64% Conservative: 34
Best Local Similarity: 23.27% Mismatches: 101
Query Match: 6.92% Indels: 77
RESULT 449
ID ACCT7985 standard; DNA; 3221 BP.
DE Thermus thermophilus mutant DNA polymerase encoding DNA.
PN WO2003025132-A2.
PD 27-MAR-2003.
PA (INVI-) INVITROGEN CORP.
Percent Similarity: 36.99% Conservative: 34
Best Local Similarity: 25.34% Mismatches: 112
Query Match: 6.92% Indels: 74
RESULT 450
ID ACCT7994 standard; DNA; 3221 BP.
DE Thermus thermophilus mutant DNA polymerase encoding DNA.
PN WO2003025132-A2.
PD 27-MAR-2003.
PA (INVI-) INVITROGEN CORP.
Percent Similarity: 36.99% Conservative: 34
Best Local Similarity: 25.34% Mismatches: 112
Query Match: 6.92% Indels: 74
RESULT 451
ID ACCT7979 standard; DNA; 3221 BP.
DE Thermus thermophilus mutant DNA polymerase encoding DNA.
PN WO2003025132-A2.
PD 27-MAR-2003.
PA (INVI-) INVITROGEN CORP.
Percent Similarity: 36.64% Conservative: 33
Best Local Similarity: 25.34% Mismatches: 113
Query Match: 6.92% Indels: 74
RESULT 452
ID AB211703 standard; cDNA; 3744 BP.
DE Human polynucleotide SEQ ID NO 585.
PN WO200270539-A2.
PD 12-SEP-2002.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 40.00% Conservative: 16
Best Local Similarity: 30.00% Mismatches: 65
Query Match: 6.92% Indels: 31
RESULT 453
ID ADM44221 standard; cDNA; 3744 BP.
DE Novel human arginine-rich protein cDNA #585.
PN US2004053250-A1.
PD 18-MAR-2004.
PA (TANG/) TANG Y T.
PA (XUEA/) XUE A.
PA (DRMA/) DRMANAC R T.
Percent Similarity: 40.00% Conservative: 16
Best Local Similarity: 30.00% Mismatches: 65
Query Match: 6.92% Indels: 31
RESULT 454
ID ABQ83861 standard; DNA; 5032 BP.
DE Human MDDT-3 encoding cDNA SEQ ID NO:26.
PN WO200278420-A2.
PD 10-OCT-2002.
PA (INCY-) INCYTE GENOMICS INC.
Percent Similarity: 40.00% Conservative: 16
Best Local Similarity: 30.00% Mismatches: 65
Query Match: 6.92% Indels: 31
RESULT 455
ID ABV77879 standard; DNA; 5591 BP.
DE Hypoxia-induced protein coding sequence #7.
PN WO200246465-A2.
PD 13-JUN-2002.

PA (OXFO-) OXFORD BIOMEDICA UK LTD.
Percent Similarity: 40.00% Conservative: 16
Best Local Similarity: 30.00% Mismatches: 65
Query Match: 6.92% Indels: 31
RESULT 456
ID AD182477 standard; DNA; 5592 BP.
DE Human modifier of p21 (MP21) gene sequence SeqID43.
PN WO2004005486-A2.
PD 15-JAN-2004.
PA (EXEL-) EXELIXIS INC.
Percent Similarity: 40.00% Conservative: 16
Best Local Similarity: 30.00% Mismatches: 65
Query Match: 6.92% Indels: 31
RESULT 457
ID AD123894 standard; DNA; 7788 BP.
DE Streptomyces fradiae A541 locus ORF3.
PN US2003198981-A1.
PD 23-OCT-2003.
PA (ECOP-) ECOPIA BIOSCIENCES INC.
Percent Similarity: 36.24% Conservative: 33
Best Local Similarity: 24.74% Mismatches: 114
Query Match: 6.92% Indels: 70
RESULT 458
ID AD123892 standard; DNA; 37360 BP.
DE Streptomyces fradiae A541 locus contig 2.
PN US2003198981-A1.
PD 23-OCT-2003.
PA (ECOP-) ECOPIA BIOSCIENCES INC.
Percent Similarity: 36.24% Conservative: 33
Best Local Similarity: 24.74% Mismatches: 114
Query Match: 6.92% Indels: 70
RESULT 459
ID AD123892 standard; DNA; 1052 BP.
DE S. pristinaespiralis papM gene C658T mutant.
PN WO2004003012-A2.
PD 08-JAN-2004.
PA (AVET-) AVENTIS PHARMA SA.
Percent Similarity: 32.23% Conservative: 26
Best Local Similarity: 22.71% Mismatches: 120
Query Match: 6.89% Indels: 65
RESULT 460
ID AD122710 standard; DNA; 1052 BP.
DE S. pristinaespiralis papM gene C658T mutant.
PN WO2004003012-A2.
PD 08-JAN-2004.
PA (AVET-) AVENTIS PHARMA SA.
Percent Similarity: 32.23% Conservative: 26
Best Local Similarity: 22.71% Mismatches: 120
Query Match: 6.89% Indels: 65
RESULT 461
ID AD122712 standard; DNA; 1052 BP.
DE S. pristinaespiralis papM gene C658T mutant.
PN WO2004003012-A2.
PD 08-JAN-2004.
PA (AVET-) AVENTIS PHARMA SA.
Percent Similarity: 32.23% Conservative: 26
Best Local Similarity: 22.71% Mismatches: 120
Query Match: 6.89% Indels: 65
RESULT 462
ID AD122712 standard; DNA; 1052 BP.
DE S. pristinaespiralis papM gene C658T mutant.
PN WO2004003012-A2.
PD 08-JAN-2004.
PA (AVET-) AVENTIS PHARMA SA.
Percent Similarity: 32.23% Conservative: 26
Best Local Similarity: 22.71% Mismatches: 120
Query Match: 6.89% Indels: 65
RESULT 463
ID AD122712 standard; DNA; 1052 BP.
DE S. pristinaespiralis papM gene C658T mutant.
PN WO2004003012-A2.
PD 08-JAN-2004.
PA (AVET-) AVENTIS PHARMA SA.
Percent Similarity: 32.23% Conservative: 26
Best Local Similarity: 22.71% Mismatches: 120
Query Match: 6.89% Indels: 65
RESULT 464
ID AD122712 standard; DNA; 1052 BP.
DE S. pristinaespiralis papM gene C658T mutant.
PN WO2004003012-A2.
PD 08-JAN-2004.
PA (AVET-) AVENTIS PHARMA SA.
Percent Similarity: 32.23% Conservative: 26
Best Local Similarity: 22.71% Mismatches: 120
Query Match: 6.89% Indels: 65
RESULT 465
ID ABD01646 standard; DNA; 1200 BP.
DE Pseudomonas aeruginosa polynucleotide #250.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Percent Similarity: 36.17% Conservative: 23
Best Local Similarity: 28.01% Mismatches: 114

Query Match: 6.89% Indels: 66
 RESULT 466
 ID ABS05045 standard; DNA; 1311 BP.
 DE Pseudomonas aeruginosa polynucleotide #3649.
 PN US6551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Percent Similarity: 37.06% Conservative: 33
 Best Local Similarity: 25.52% Mismatches: 95
 Indels: 86
 Query Match: 6.89%
 RESULT 467
 ID ADS6578 standard; DNA; 1828 BP.
 DE Plant DNA sequence which confers altered metabolic characteristic #3961.
 PN WO2003020936-A1.
 PD 13-MAR-2003.
 PA (DMC) DOW CHEM CO.
 PA (DMC) DOW AGROSCIENCES LLC.
 Percent Similarity: 34.20% Conservative: 38
 Best Local Similarity: 21.82% Mismatches: 102
 Indels: 100
 Query Match: 6.89%
 RESULT 468
 ID AAV5395 standard; DNA; 2511 BP.
 DE Nucleotide sequence of the structure specific endonuclease 2.
 PN WO9823774-A1.
 PD 04-JUN-1998.
 PA (THIR-) THIRD WAVE TECHNOLOGIES INC.
 Percent Similarity: 36.64% Conservative: 33
 Best Local Similarity: 25.34% Mismatches: 113
 Indels: 74
 Query Match: 6.89%
 RESULT 469
 ID ABS68749 standard; DNA; 2511 BP.
 DE DNA encoding Thermus thermophilus mutant DNA polymerase #2.
 PN WO200263030-A2.
 PD 15-AUG-2002.
 PA (THIR-) THIRD WAVE TECHNOLOGIES INC.
 Percent Similarity: 36.64% Conservative: 33
 Best Local Similarity: 25.34% Mismatches: 113
 Indels: 74
 Query Match: 6.89%
 RESULT 470
 ID ADE53076 standard; DNA; 2511 BP.
 DE FEN-1 related DNA used within the scope of the invention, #231.
 PN WO200270755-A2.
 PD 12-SEP-2002.
 PA (THIR-) THIRD WAVE TECHNOLOGIES INC.
 Percent Similarity: 36.64% Conservative: 33
 Best Local Similarity: 25.34% Mismatches: 113
 Indels: 74
 Query Match: 6.89%
 RESULT 471
 ID ABS68757 standard; DNA; 2526 BP.
 DE DNA encoding Thermus thermophilus mutant DNA polymerase #4.
 PN WO200263030-A2.
 PD 15-AUG-2002.
 PA (THIR-) THIRD WAVE TECHNOLOGIES INC.
 Percent Similarity: 36.68% Conservative: 34
 Best Local Similarity: 24.91% Mismatches: 111
 Indels: 74
 Query Match: 6.89%
 RESULT 472
 ID ABS68759 standard; DNA; 2526 BP.
 DE DNA encoding Thermus thermophilus mutant DNA polymerase #5.
 PN WO200263030-A2.
 PD 15-AUG-2002.
 PA (THIR-) THIRD WAVE TECHNOLOGIES INC.
 Percent Similarity: 36.68% Conservative: 34
 Best Local Similarity: 24.91% Mismatches: 111
 Indels: 74
 Query Match: 6.89%
 RESULT 473
 ID ABS68751 standard; DNA; 2526 BP.
 DE DNA encoding Thermus thermophilus mutant DNA polymerase #3.
 PN WO200263030-A2.
 PD 15-AUG-2002.
 PA (THIR-) THIRD WAVE TECHNOLOGIES INC.
 Percent Similarity: 36.64% Conservative: 33
 Best Local Similarity: 25.34% Mismatches: 113
 Indels: 74

Query Match: 6.89% Indels: 74
 RESULT 474
 ID ABS68755 standard; DNA; 2526 BP.
 DE DNA encoding Thermus thermophilus mutant DNA polymerase #3.
 PN WO200263030-A2.
 PD 15-AUG-2002.
 PA (THIR-) THIRD WAVE TECHNOLOGIES INC.
 Percent Similarity: 36.64% Conservative: 33
 Best Local Similarity: 25.34% Mismatches: 113
 Indels: 74
 Query Match: 6.89%
 RESULT 475
 ID ACC77865 standard; DNA; 3221 BP.
 DE Thermus thermophilus mutant DNA polymerase encoding DNA.
 PN WO2003025132-A2.
 PD 27-MAR-2003.
 PA (INVI-) INVITROGEN CORP.
 Percent Similarity: 36.49% Conservative: 33
 Best Local Similarity: 25.34% Mismatches: 116
 Indels: 74
 Query Match: 6.89%
 RESULT 476
 ID ACC77880 standard; DNA; 3221 BP.
 DE Thermus thermophilus mutant DNA polymerase encoding DNA.
 PN WO2003025132-A2.
 PD 27-MAR-2003.
 PA (INVI-) INVITROGEN CORP.
 Percent Similarity: 36.49% Conservative: 33
 Best Local Similarity: 25.34% Mismatches: 116
 Indels: 74
 Query Match: 6.89%
 RESULT 477
 ID ACC77960 standard; DNA; 3221 BP.
 DE Thermus thermophilus mutant DNA polymerase encoding DNA.
 PN WO2003025132-A2.
 PD 27-MAR-2003.
 PA (INVI-) INVITROGEN CORP.
 Percent Similarity: 36.64% Conservative: 33
 Best Local Similarity: 25.34% Mismatches: 113
 Indels: 74
 Query Match: 6.89%
 RESULT 478
 ID ACC77936 standard; DNA; 3221 BP.
 DE Thermus thermophilus mutant DNA polymerase encoding DNA.
 PN WO2003025132-A2.
 PD 27-MAR-2003.
 PA (INVI-) INVITROGEN CORP.
 Percent Similarity: 37.89% Conservative: 36
 Best Local Similarity: 25.26% Mismatches: 119
 Indels: 60
 Query Match: 6.89%
 RESULT 479
 ID ACC77975 standard; DNA; 3221 BP.
 DE Thermus thermophilus mutant DNA polymerase encoding DNA.
 PN WO2003025132-A2.
 PD 27-MAR-2003.
 PA (INVI-) INVITROGEN CORP.
 Percent Similarity: 36.64% Conservative: 33
 Best Local Similarity: 25.34% Mismatches: 113
 Indels: 74
 Query Match: 6.89%
 RESULT 480
 ID ACC78006 standard; DNA; 3221 BP.
 DE Thermus thermophilus mutant DNA polymerase encoding DNA.
 PN WO2003025132-A2.
 PD 27-MAR-2003.
 PA (INVI-) INVITROGEN CORP.
 Percent Similarity: 36.64% Conservative: 33
 Best Local Similarity: 25.34% Mismatches: 113
 Indels: 74
 Query Match: 6.89%
 RESULT 481
 ID ACC77873 standard; DNA; 3221 BP.
 DE Thermus thermophilus mutant DNA polymerase encoding DNA.
 PN WO2003025132-A2.
 PD 27-MAR-2003.
 PA (INVI-) INVITROGEN CORP.
 Percent Similarity: 36.49% Conservative: 33
 Best Local Similarity: 25.34% Mismatches: 116
 Indels: 74
 Query Match: 6.89%

RESULT 482
ID ACC77961 standard; DNA; 3221 BP.
DE Thermus thermophilus mutant DNA polymerase encoding DNA.
PN WO2003025132-A2.
PD 27-MAR-2003.
PA (INVI-) INVITROGEN CORP.
Percent Similarity: 36.64%
Best Local Similarity: 25.34%
Query Match: 6.89%
Conservative: 33
Mismatches: 113
Indels: 74

RESULT 483
ID ACC77990 standard; DNA; 3221 BP.
DE Thermus thermophilus mutant DNA polymerase encoding DNA.
PN WO2003025132-A2.
PD 27-MAR-2003.
PA (INVI-) INVITROGEN CORP.
Percent Similarity: 36.64%
Best Local Similarity: 25.34%
Query Match: 6.89%
Conservative: 33
Mismatches: 113
Indels: 74

RESULT 484
ID ACC78009 standard; DNA; 3221 BP.
DE Thermus thermophilus mutant DNA polymerase encoding DNA.
PN WO2003025132-A2.
PD 27-MAR-2003.
PA (INVI-) INVITROGEN CORP.
Percent Similarity: 36.64%
Best Local Similarity: 25.34%
Query Match: 6.89%
Conservative: 33
Mismatches: 113
Indels: 74

RESULT 485
ID ACC77999 standard; DNA; 3221 BP.
DE Thermus thermophilus mutant DNA polymerase encoding DNA.
PN WO2003025132-A2.
PD 27-MAR-2003.
PA (INVI-) INVITROGEN CORP.
Percent Similarity: 36.64%
Best Local Similarity: 25.34%
Query Match: 6.89%
Conservative: 33
Mismatches: 113
Indels: 74

RESULT 486
ID ACC77993 standard; DNA; 3221 BP.
DE Thermus thermophilus mutant DNA polymerase encoding DNA.
PN WO2003025132-A2.
PD 27-MAR-2003.
PA (INVI-) INVITROGEN CORP.
Percent Similarity: 36.64%
Best Local Similarity: 25.34%
Query Match: 6.89%
Conservative: 33
Mismatches: 113
Indels: 74

RESULT 487
ID ACC78083 standard; DNA; 3221 BP.
DE Thermus thermophilus mutant DNA polymerase encoding DNA.
PN WO2003025132-A2.
PD 27-MAR-2003.
PA (INVI-) INVITROGEN CORP.
Percent Similarity: 36.64%
Best Local Similarity: 25.34%
Query Match: 6.89%
Conservative: 33
Mismatches: 116
Indels: 74

RESULT 488
ID ACC77966 standard; DNA; 3221 BP.
DE Thermus thermophilus mutant DNA polymerase encoding DNA.
PN WO2003025132-A2.
PD 27-MAR-2003.
PA (INVI-) INVITROGEN CORP.
Percent Similarity: 36.64%
Best Local Similarity: 25.34%
Query Match: 6.89%
Conservative: 33
Mismatches: 113
Indels: 74

RESULT 489
ID ACC78012 standard; DNA; 3221 BP.
DE Thermus thermophilus mutant DNA polymerase encoding DNA.
PN WO2003025132-A2.
PD 27-MAR-2003.
PA (INVI-) INVITROGEN CORP.
Percent Similarity: 36.64%
Best Local Similarity: 25.34%
Query Match: 6.89%
Conservative: 33
Mismatches: 113
Indels: 74

RESULT 490
ID ACC77935 standard; DNA; 3221 BP.
DE Thermus thermophilus mutant DNA polymerase encoding DNA.
PN WO2003025132-A2.
PD 27-MAR-2003.
PA (INVI-) INVITROGEN CORP.
Percent Similarity: 37.89%
Best Local Similarity: 25.26%
Query Match: 6.89%
Conservative: 36
Mismatches: 119
Indels: 60

RESULT 491
ID ACC78003 standard; DNA; 3221 BP.
DE Thermus thermophilus mutant DNA polymerase encoding DNA.
PN WO2003025132-A2.
PD 27-MAR-2003.
PA (INVI-) INVITROGEN CORP.
Percent Similarity: 36.64%
Best Local Similarity: 25.34%
Query Match: 6.89%
Conservative: 33
Mismatches: 113
Indels: 74

RESULT 492
ID ACC77976 standard; DNA; 3221 BP.
DE Thermus thermophilus mutant DNA polymerase encoding DNA.
PN WO2003025132-A2.
PD 27-MAR-2003.
PA (INVI-) INVITROGEN CORP.
Percent Similarity: 36.64%
Best Local Similarity: 25.34%
Query Match: 6.89%
Conservative: 33
Mismatches: 113
Indels: 74

RESULT 493
ID AAF26352 standard; DNA; 1035 BP.
DE P. putida oxygenase encoding DNA ORF04472.
PN WO200107629-A2.
PD 01-FEB-2001.
PA (TIGR-) TIGR INST GENOMIC RES.
PA (QUIA-) QUIAGEN GMBH.
PA (GBFB) GES BIOTECHNOLOGISCHE FORSCHUNG MBH.
PA (DKFZ-) DKFZ DEUT KREBSFORSCHUNGSZENTRUM.
PA (MEDI-) MEDIZINISCHE HOCHSCHULE HANNOVER.
Percent Similarity: 33.21%
Best Local Similarity: 24.91%
Query Match: 6.85%
Conservative: 22
Mismatches: 100
Indels: 77

RESULT 494
ID ACA31567 standard; DNA; 1130 BP.
DE Prokaryotic essential gene #13224.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Percent Similarity: 37.62%
Best Local Similarity: 24.76%
Query Match: 6.85%
Conservative: 27
Mismatches: 89
Indels: 42

RESULT 495
ID AAS72289 standard; cDNA; 1390 BP.
DE DNA encoding novel human diagnostic protein #8093.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 32.03%
Best Local Similarity: 23.83%
Query Match: 6.85%
Conservative: 21
Mismatches: 75
Indels: 100

RESULT 496
ID ABD14414 standard; DNA; 1407 BP.
DE Pseudomonas aeruginosa polynucleotide #13018.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Percent Similarity: 38.41%
Best Local Similarity: 28.15%
Query Match: 6.85%
Conservative: 31
Mismatches: 96
Indels: 90

RESULT 497
ID ADO07762 standard; cDNA; 1932 BP.
DE Fly polynucleotide #43.
PN US2004071700-A1.
PD 15-APR-2004.
PA (LIFE-) LIFE SCI DEV CORP.
Percent Similarity: 33.33%
Conservative: 29

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Best Local Similarity: 23.05%      Mismatches: 101
Query Match: 6.85%      Indels: 87
RESULT 498
ID AAS94512 standard; cDNA; 2305 BP.
DE DNA encoding novel human diagnostic protein #30316.
PN WO200175067-A2.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 31.54%      Conservative: 19
Mismatches: 94
Best Local Similarity: 23.65%      Indels: 71
Query Match: 6.85%
RESULT 499
ID ABL08195 standard; cDNA; 2396 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 19067.
PN WO200171042-A2.
PA (PEKE-) PE CORP NY.
Percent Similarity: 33.33%      Conservative: 29
Mismatches: 101
Best Local Similarity: 23.05%      Indels: 87
Query Match: 6.85%
RESULT 500
ID ABL20321 standard; DNA; 2590 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 12436.
PN WO200171042-A2.
PA (PEKE-) PE CORP NY.
Percent Similarity: 33.33%      Conservative: 29
Mismatches: 101
Best Local Similarity: 23.05%      Indels: 87
Query Match: 6.85%
RESULT 501
ID ABL20331 standard; DNA; 2894 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 12466.
PN WO200171042-A2.
PA (PEKE-) PE CORP NY.
Percent Similarity: 33.33%      Conservative: 29
Mismatches: 101
Best Local Similarity: 23.05%      Indels: 87
Query Match: 6.85%
RESULT 502
ID ACC77995 standard; DNA; 3221 BP.
DE Thermus thermophilus mutant DNA polymerase encoding DNA.
PN WO2003025132-A2.
PA (INVI-) INVITROGEN CORP.
Percent Similarity: 36.99%      Conservative: 34
Mismatches: 112
Best Local Similarity: 25.34%      Indels: 74
Query Match: 6.85%
RESULT 503
ID AAS84829 standard; cDNA; 3451 BP.
DE DNA encoding novel human diagnostic protein #20633.
PN WO200175067-A2.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 42.95%      Conservative: 25
Mismatches: 58
Best Local Similarity: 26.92%      Indels: 32
Query Match: 6.85%
RESULT 504
ID ACA44278 standard; DNA; 1116 BP.
DE Prokaryotic essential gene #25935.
PN WO200277183-A2.
PA (ELIT-) ELITRA PHARM INC.
Percent Similarity: 37.45%      Conservative: 31
Mismatches: 76
Best Local Similarity: 25.10%      Indels: 81
Query Match: 6.81%
RESULT 505
ID ABD08133 standard; DNA; 1197 BP.
DE Pseudomonas aeruginosa polynucleotide #6737.
PN US6551795-B1.
PA (GENO-) GENOME THERAPEUTICS CORP.
Percent Similarity: 38.19%      Conservative: 31
Mismatches: 107
Best Local Similarity: 25.98%      Indels: 51
Query Match: 6.81%

Query Match: 6.81%      Indels: 51
RESULT 506
ID ABD08348 standard; DNA; 1272 BP.
DE Pseudomonas aeruginosa polynucleotide #6952.
PN US6551795-B1.
PA (GENO-) GENOME THERAPEUTICS CORP.
Percent Similarity: 38.19%      Conservative: 31
Mismatches: 107
Best Local Similarity: 25.98%      Indels: 51
Query Match: 6.81%
RESULT 507
ID ABZ38701 standard; DNA; 1560 BP.
DE N. gonorrhoeae nucleotide sequence SEQ ID 1991.
PN WO200279243-A2.
PA (CHIR-) CHIRON SPA.
Percent Similarity: 38.21%      Conservative: 33
Mismatches: 91
Best Local Similarity: 24.80%      Indels: 61
Query Match: 6.81%
RESULT 508
ID AAQ24328 standard; DNA; 1635 BP.
DE Mutant thermostable DNA polymerase pTTHA292.
PN WO9206200-A.
PA (CETU) CETUS CORP.
Percent Similarity: 36.64%      Conservative: 33
Mismatches: 113
Best Local Similarity: 25.34%      Indels: 74
Query Match: 6.81%
RESULT 509
ID AAQ24327 standard; DNA; 1899 BP.
DE Mutant thermostable DNA polymerase pTTHd2-203.
PN WO9206200-A.
PA (CETU) CETUS CORP.
Percent Similarity: 36.64%      Conservative: 33
Mismatches: 113
Best Local Similarity: 25.34%      Indels: 74
Query Match: 6.81%
RESULT 510
ID AAQ24326 standard; DNA; 2043 BP.
DE Mutant thermostable DNA polymerase pTTHd2-155.
PN WO9206200-A.
PA (CETU) CETUS CORP.
Percent Similarity: 36.64%      Conservative: 33
Mismatches: 113
Best Local Similarity: 25.34%      Indels: 74
Query Match: 6.81%
RESULT 511
ID ACA2740 standard; DNA; 2253 BP.
DE Prokaryotic essential gene #24397.
PN WO200277183-A2.
PA (ELIT-) ELITRA PHARM INC.
Percent Similarity: 37.85%      Conservative: 27
Mismatches: 101
Best Local Similarity: 27.09%      Indels: 55
Query Match: 6.81%
RESULT 512
ID AAQ24325 standard; DNA; 2277 BP.
DE Mutant thermostable DNA polymerase pTTHd2-77.
PN WO9206200-A.
PA (CETU) CETUS CORP.
Percent Similarity: 36.64%      Conservative: 33
Mismatches: 113
Best Local Similarity: 25.34%      Indels: 74
Query Match: 6.81%
RESULT 513
ID ABD08178 standard; DNA; 2346 BP.
DE Pseudomonas aeruginosa polynucleotide #6782.
PN US6551795-B1.
PA (GENO-) GENOME THERAPEUTICS CORP.
Percent Similarity: 38.19%      Conservative: 31
Mismatches: 107
Best Local Similarity: 25.98%      Indels: 51
Query Match: 6.81%

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RESULT 514
ID AAQ4324 standard; DNA; 2370 BP.
DE Mutant thermostable DNA polymerase pTthd2-46.
PN WO206200-A.
PD 16-APR-1992.
PA (CETU) CETUS CORP.
Percent Similarity: 36.64%
Best Local Similarity: 25.34%
Query Match: 6.81%
Conservative: 33
Mismatches: 113
Indels: 74
RESULT 515
ID AAQ24323 standard; DNA; 2505 BP.
DE Mutant thermostable DNA polymerase from Thermus thermophilus.
PN WO206200-A.
PD 16-APR-1992.
PA (CETU) CETUS CORP.
Percent Similarity: 36.64%
Best Local Similarity: 25.34%
Query Match: 6.81%
Conservative: 33
Mismatches: 113
Indels: 74
RESULT 516
ID AAV5393 standard; DNA; 2505 BP.
DE Nucleotide sequence of the nucleic acid 6.
PN WO9823774-A1.
PD 04-JUN-1998.
PA (THIRD) THIRD WAVE TECHNOLOGIES INC.
Percent Similarity: 36.64%
Best Local Similarity: 25.34%
Query Match: 6.81%
Conservative: 33
Mismatches: 113
Indels: 74
RESULT 517
ID AAV5394 standard; DNA; 2511 BP.
DE Nucleotide sequence of the structure specific endonuclease 1.
PN WO9823774-A1.
PD 04-JUN-1998.
PA (THIRD) THIRD WAVE TECHNOLOGIES INC.
Percent Similarity: 36.64%
Best Local Similarity: 25.34%
Query Match: 6.81%
Conservative: 33
Mismatches: 113
Indels: 74
RESULT 518
ID ABS68747 standard; DNA; 2511 BP.
DE Thermus thermophilus DNA polymerase, PCR primer #4.
PN WO200263030-A2.
PD 15-AUG-2002.
PA (THIRD) THIRD WAVE TECHNOLOGIES INC.
Percent Similarity: 36.64%
Best Local Similarity: 25.34%
Query Match: 6.81%
Conservative: 33
Mismatches: 113
Indels: 74
RESULT 519
ID AAQ12748 standard; DNA; 2640 BP.
DE T. thermophilus DNA polymerase I.
PN WO9109950-A.
PD 11-JUL-1991.
PA (CETU) CETUS CORP.
Percent Similarity: 36.64%
Best Local Similarity: 25.34%
Query Match: 6.81%
Conservative: 33
Mismatches: 113
Indels: 74
RESULT 520
ID AAH14004 standard; cDNA; 2653 BP.
DE Human cDNA sequence SEQ ID NO:11090.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Percent Similarity: 33.23%
Best Local Similarity: 25.16%
Query Match: 6.81%
Conservative: 25
Mismatches: 98
Indels: 109
RESULT 521
ID AAD45690 standard; DNA; 2653 BP.
DE Human LBDS4 DNA.
PN WO200270560-A2.
PD 12-SEP-2002.
PA (INPH-) INPHARMATICA LTD.
Percent Similarity: 33.23%
Best Local Similarity: 25.16%
Query Match: 6.81%
Conservative: 25
Mismatches: 98
Indels: 109
RESULT 522

ID AAA30241 standard; DNA; 2943 BP.
DE Chimaeric Pfu/T. thermophilus DNA polymerase coding sequence.
PN GB2344591-A.
PD 14-JUN-2000.
PA (BIOL-) BIOLINE LTD.
Percent Similarity: 36.64%
Best Local Similarity: 25.34%
Query Match: 6.81%
Conservative: 33
Mismatches: 113
Indels: 74
RESULT 523
ID ABD11116 standard; DNA; 3006 BP.
DE Pseudomonas aeruginosa polynucleotide #9720.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Percent Similarity: 31.97%
Best Local Similarity: 22.45%
Query Match: 6.81%
Conservative: 28
Mismatches: 80
Indels: 120
RESULT 524
ID ACC78016 standard; DNA; 3210 BP.
DE Thermus thermophilus mutant DNA polymerase encoding DNA.
PN WO2003025132-A2.
PD 27-MAR-2003.
PA (INVI-) INVITROGEN CORP.
Percent Similarity: 36.64%
Best Local Similarity: 25.34%
Query Match: 6.81%
Conservative: 33
Mismatches: 113
Indels: 74
RESULT 525
ID AAO96261 standard; DNA; 3221 BP.
DE Thermus thermophilus thermostable DNA polymerase genomic DNA.
PN JP07163343-A.
PD 27-JUN-1995.
PA (TOYM) TOYOBO KK.
Percent Similarity: 36.64%
Best Local Similarity: 25.34%
Query Match: 6.81%
Conservative: 33
Mismatches: 113
Indels: 74
RESULT 526
ID ACC77892 standard; DNA; 3221 BP.
DE Thermus thermophilus mutant DNA polymerase encoding DNA.
PN WO2003025132-A2.
PD 27-MAR-2003.
PA (INVI-) INVITROGEN CORP.
Percent Similarity: 36.64%
Best Local Similarity: 25.34%
Query Match: 6.81%
Conservative: 33
Mismatches: 113
Indels: 74
RESULT 527
ID ACC77919 standard; DNA; 3221 BP.
DE Thermus thermophilus mutant DNA polymerase encoding DNA.
PN WO2003025132-A2.
PD 27-MAR-2003.
PA (INVI-) INVITROGEN CORP.
Percent Similarity: 36.64%
Best Local Similarity: 25.34%
Query Match: 6.81%
Conservative: 33
Mismatches: 113
Indels: 74
RESULT 528
ID ACC77962 standard; DNA; 3221 BP.
DE Thermus thermophilus mutant DNA polymerase encoding DNA.
PN WO2003025132-A2.
PD 27-MAR-2003.
PA (INVI-) INVITROGEN CORP.
Percent Similarity: 36.64%
Best Local Similarity: 25.34%
Query Match: 6.81%
Conservative: 33
Mismatches: 113
Indels: 74
RESULT 529
ID ACC77972 standard; DNA; 3221 BP.
DE Thermus thermophilus mutant DNA polymerase encoding DNA.
PN WO2003025132-A2.
PD 27-MAR-2003.
PA (INVI-) INVITROGEN CORP.
Percent Similarity: 36.64%
Best Local Similarity: 25.34%
Query Match: 6.81%
Conservative: 33
Mismatches: 113
Indels: 74
RESULT 530
ID ACC77874 standard; DNA; 3221 BP.

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Percent Similarity: 36.64%
Best Local Similarity: 25.34%
Query Match: 6.81%
Conservative: 33
Mismatch: 113
Indels: 74
RESULT 563
ID ACC77934 standard; DNA; 3221 BP.
DE Thermus thermophilus mutant DNA polymerase encoding DNA.
PN WO2003025132-A2.
PD 27-MAR-2003.
PA (INVI-) INVITROGEN CORP.
Percent Similarity: 38.11%
Best Local Similarity: 26.22%
Mismatch: 117
Indels: 62
Query Match: 6.81%
RESULT 564
ID ACC77875 standard; DNA; 3221 BP.
DE Thermus thermophilus mutant DNA polymerase encoding DNA.
PN WO2003025132-A2.
PD 27-MAR-2003.
PA (INVI-) INVITROGEN CORP.
Percent Similarity: 36.64%
Best Local Similarity: 25.34%
Mismatch: 113
Indels: 74
Query Match: 6.81%
RESULT 565
ID ACC77895 standard; DNA; 3221 BP.
DE Thermus thermophilus mutant DNA polymerase encoding DNA.
PN WO2003025132-A2.
PD 27-MAR-2003.
PA (INVI-) INVITROGEN CORP.
Percent Similarity: 36.64%
Best Local Similarity: 25.34%
Mismatch: 113
Indels: 74
Query Match: 6.81%
RESULT 566
ID ACC77868 standard; DNA; 3221 BP.
DE Thermus thermophilus mutant DNA polymerase encoding DNA.
PN WO2003025132-A2.
PD 27-MAR-2003.
PA (INVI-) INVITROGEN CORP.
Percent Similarity: 36.64%
Best Local Similarity: 25.34%
Mismatch: 113
Indels: 74
Query Match: 6.81%
RESULT 567
ID ACC77869 standard; DNA; 3221 BP.
DE Thermus thermophilus mutant DNA polymerase encoding DNA.
PN WO2003025132-A2.
PD 27-MAR-2003.
PA (INVI-) INVITROGEN CORP.
Percent Similarity: 36.64%
Best Local Similarity: 25.34%
Mismatch: 113
Indels: 74
Query Match: 6.81%
RESULT 568
ID ACC77887 standard; DNA; 3221 BP.
DE Thermus thermophilus mutant DNA polymerase encoding DNA.
PN WO2003025132-A2.
PD 27-MAR-2003.
PA (INVI-) INVITROGEN CORP.
Percent Similarity: 36.64%
Best Local Similarity: 25.34%
Mismatch: 113
Indels: 74
Query Match: 6.81%
RESULT 569
ID ACC77897 standard; DNA; 3221 BP.
DE Thermus thermophilus mutant DNA polymerase encoding DNA.
PN WO2003025132-A2.
PD 27-MAR-2003.
PA (INVI-) INVITROGEN CORP.
Percent Similarity: 36.64%
Best Local Similarity: 25.34%
Mismatch: 113
Indels: 74
Query Match: 6.81%
RESULT 570
ID ACC77922 standard; DNA; 3221 BP.
DE Thermus thermophilus mutant DNA polymerase encoding DNA.
PN WO2003025132-A2.
PD 27-MAR-2003.
PA (INVI-) INVITROGEN CORP.
Percent Similarity: 36.64%
Best Local Similarity: 25.34%
Mismatch: 113
Indels: 74
Query Match: 6.81%
Conservative: 33
Mismatch: 113
Indels: 74

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Best Local Similarity: 25.34%
Query Match: 6.81%
Mismatch: 113
Indels: 74
RESULT 571
ID ACC77925 standard; DNA; 3221 BP.
DE Thermus thermophilus mutant DNA polymerase encoding DNA.
PN WO2003025132-A2.
PD 27-MAR-2003.
PA (INVI-) INVITROGEN CORP.
Percent Similarity: 36.64%
Best Local Similarity: 25.34%
Mismatch: 113
Indels: 74
Query Match: 6.81%
RESULT 572
ID ACC77940 standard; DNA; 3221 BP.
DE Thermus thermophilus mutant DNA polymerase encoding DNA.
PN WO2003025132-A2.
PD 27-MAR-2003.
PA (INVI-) INVITROGEN CORP.
Percent Similarity: 36.64%
Best Local Similarity: 25.34%
Mismatch: 113
Indels: 74
Query Match: 6.81%
RESULT 573
ID ACC77878 standard; DNA; 3221 BP.
DE Thermus thermophilus mutant DNA polymerase encoding DNA.
PN WO2003025132-A2.
PD 27-MAR-2003.
PA (INVI-) INVITROGEN CORP.
Percent Similarity: 36.64%
Best Local Similarity: 25.34%
Mismatch: 113
Indels: 74
Query Match: 6.81%
RESULT 574
ID ACC77882 standard; DNA; 3221 BP.
DE Thermus thermophilus mutant DNA polymerase encoding DNA.
PN WO2003025132-A2.
PD 27-MAR-2003.
PA (INVI-) INVITROGEN CORP.
Percent Similarity: 36.64%
Best Local Similarity: 25.34%
Mismatch: 113
Indels: 74
Query Match: 6.81%
RESULT 575
ID ACC77899 standard; DNA; 3221 BP.
DE Thermus thermophilus mutant DNA polymerase encoding DNA.
PN WO2003025132-A2.
PD 27-MAR-2003.
PA (INVI-) INVITROGEN CORP.
Percent Similarity: 36.64%
Best Local Similarity: 25.34%
Mismatch: 113
Indels: 74
Query Match: 6.81%
RESULT 576
ID ACC77905 standard; DNA; 3221 BP.
DE Thermus thermophilus mutant DNA polymerase encoding DNA.
PN WO2003025132-A2.
PD 27-MAR-2003.
PA (INVI-) INVITROGEN CORP.
Percent Similarity: 36.64%
Best Local Similarity: 25.34%
Mismatch: 113
Indels: 74
Query Match: 6.81%
RESULT 577
ID ACC77932 standard; DNA; 3221 BP.
DE Thermus thermophilus mutant DNA polymerase encoding DNA.
PN WO2003025132-A2.
PD 27-MAR-2003.
PA (INVI-) INVITROGEN CORP.
Percent Similarity: 36.64%
Best Local Similarity: 25.34%
Mismatch: 113
Indels: 74
Query Match: 6.81%
RESULT 578
ID ACC77963 standard; DNA; 3221 BP.
DE Thermus thermophilus mutant DNA polymerase encoding DNA.
PN WO2003025132-A2.
PD 27-MAR-2003.
PA (INVI-) INVITROGEN CORP.
Percent Similarity: 36.64%
Best Local Similarity: 25.34%
Mismatch: 113
Indels: 74
Query Match: 6.81%
Conservative: 33
Mismatch: 113
Indels: 74

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RESULT 587			
ID	ACC77876 standard; DNA; 3221 BP.		
DE	Thermus thermophilus mutant DNA polymerase encoding DNA.		
PN	W02003025132-A2.		
PD	27-MAR-2003.		
PA	(INVI-) INVITROGEN CORP.		
Percent Similarity:	36.64%	Conservative:	33
Best Local Similarity:	25.34%	Mismatches:	113
Query Match:	6.81%	Indels:	74
RESULT 588			
ID	ACC77896 standard; DNA; 3221 BP.		
DE	Thermus thermophilus mutant DNA polymerase encoding DNA.		
PN	W02003025132-A2.		
PD	27-MAR-2003.		
PA	(INVI-) INVITROGEN CORP.		
Percent Similarity:	36.64%	Conservative:	33
Best Local Similarity:	25.34%	Mismatches:	113
Query Match:	6.81%	Indels:	74
RESULT 589			
ID	ACC77908 standard; DNA; 3221 BP.		
DE	Thermus thermophilus mutant DNA polymerase encoding DNA.		
PN	W02003025132-A2.		
PD	27-MAR-2003.		
PA	(INVI-) INVITROGEN CORP.		
Percent Similarity:	36.64%	Conservative:	33
Best Local Similarity:	25.34%	Mismatches:	113
Query Match:	6.81%	Indels:	74
RESULT 590			
ID	ACC77910 standard; DNA; 3221 BP.		
DE	Thermus thermophilus mutant DNA polymerase encoding DNA.		
PN	W02003025132-A2.		
PD	27-MAR-2003.		
PA	(INVI-) INVITROGEN CORP.		
Percent Similarity:	36.64%	Conservative:	33
Best Local Similarity:	25.34%	Mismatches:	113
Query Match:	6.81%	Indels:	74
RESULT 591			
ID	ACC77917 standard; DNA; 3221 BP.		
DE	Thermus thermophilus mutant DNA polymerase encoding DNA.		
PN	W02003025132-A2.		
PD	27-MAR-2003.		
PA	(INVI-) INVITROGEN CORP.		
Percent Similarity:	36.64%	Conservative:	33
Best Local Similarity:	25.34%	Mismatches:	113
Query Match:	6.81%	Indels:	74
RESULT 592			
ID	ACC77926 standard; DNA; 3221 BP.		
DE	Thermus thermophilus mutant DNA polymerase encoding DNA.		
PN	W02003025132-A2.		
PD	27-MAR-2003.		
PA	(INVI-) INVITROGEN CORP.		
Percent Similarity:	36.64%	Conservative:	33
Best Local Similarity:	25.34%	Mismatches:	113
Query Match:	6.81%	Indels:	74
RESULT 593			
ID	ACC77933 standard; DNA; 3221 BP.		
DE	Thermus thermophilus mutant DNA polymerase encoding DNA.		
PN	W02003025132-A2.		
PD	27-MAR-2003.		
PA	(INVI-) INVITROGEN CORP.		
Percent Similarity:	36.64%	Conservative:	33
Best Local Similarity:	25.34%	Mismatches:	113
Query Match:	6.81%	Indels:	74
RESULT 594			
ID	ACC77968 standard; DNA; 3221 BP.		
DE	Thermus thermophilus mutant DNA polymerase encoding DNA.		
PN	W02003025132-A2.		
PD	27-MAR-2003.		
PA	(INVI-) INVITROGEN CORP.		
Percent Similarity:	36.64%	Conservative:	33
Best Local Similarity:	25.34%	Mismatches:	113
Query Match:	6.81%	Indels:	74
RESULT 595			
ID	ACC77968 standard; DNA; 3221 BP.		
DE	Thermus thermophilus mutant DNA polymerase encoding DNA.		
PN	W02003025132-A2.		
PD	27-MAR-2003.		
PA	(INVI-) INVITROGEN CORP.		
Percent Similarity:	36.64%	Conservative:	33
Best Local Similarity:	25.34%	Mismatches:	113
Query Match:	6.81%	Indels:	74

[illegible]

PN WO2003025132-A2.
 PD 27-MAR-2003.
 PA (INVI-) INVITROGEN CORP.
 Percent Similarity: 38.11% Conservative: 34
 Best Local Similarity: 26.22% Mismatches: 117
 Query Match: 6.81% Indels: 62
 RESULT 612
 ID ACC77938 standard; DNA; 3221 BP.
 DE Thermus thermophilus mutant DNA polymerase encoding DNA.
 PN WO2003025132-A2.
 PD 27-MAR-2003.
 PA (INVI-) INVITROGEN CORP.
 Percent Similarity: 26.64% Conservative: 33
 Best Local Similarity: 25.34% Mismatches: 113
 Query Match: 6.81% Indels: 74
 RESULT 613
 ID ABD13665 standard; DNA; 3660 BP.
 DE Pseudomonas aeruginosa polynucleotide #12269.
 PN US6551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Percent Similarity: 35.90% Conservative: 21
 Best Local Similarity: 26.92% Mismatches: 83
 Query Match: 6.81% Indels: 68
 RESULT 614
 ID ADD48688 standard; DNA; 5352 BP.
 DE Rat gene M34384, SEQ ID NO 14397.
 PN WO2003016475-A2.
 PD 27-FEB-2003.
 PA (GENO) GEN HOSPITAL CORP.
 Percent Similarity: 36.32% Conservative: 18
 Best Local Similarity: 28.25% Mismatches: 96
 Query Match: 6.81% Indels: 47
 RESULT 615
 ID ACA35857 standard; DNA; 846 BP.
 DE Prokaryotic essential gene #17514.
 PN WO20027183-A2.
 PD 03-OCT-2002.
 PA (ELIT-) ELITRA PHARM INC.
 Percent Similarity: 33.74% Conservative: 19
 Best Local Similarity: 26.02% Mismatches: 74
 Query Match: 6.78% Indels: 90
 RESULT 616
 ID ACH97285 standard; DNA; 906 BP.
 DE Klebsiella pneumoniae polynucleotide seqid 3080.
 PN US6610836-B1.
 PD 26-AUG-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Percent Similarity: 31.25% Conservative: 19
 Best Local Similarity: 24.26% Mismatches: 70
 Query Match: 6.78% Indels: 118
 RESULT 617
 ID ABD14669 standard; DNA; 966 BP.
 DE Pseudomonas aeruginosa polynucleotide #13273.
 PN US6551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Percent Similarity: 36.55% Conservative: 16
 Best Local Similarity: 28.43% Mismatches: 86
 Query Match: 6.78% Indels: 39
 RESULT 618
 ID ABD08723 standard; DNA; 1083 BP.
 DE Pseudomonas aeruginosa polynucleotide #7327.
 PN US6551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Percent Similarity: 36.72% Conservative: 23
 Best Local Similarity: 27.73% Mismatches: 101
 Query Match: 6.78% Indels: 62
 RESULT 619
 ID ABD16105 standard; DNA; 1200 BP.
 DE Pseudomonas aeruginosa polynucleotide #14709.

PN US6551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Percent Similarity: 38.60% Conservative: 29
 Best Local Similarity: 25.88% Mismatches: 91
 Query Match: 6.78% Indels: 49
 RESULT 620
 ID ABD16436 standard; DNA; 1290 BP.
 DE Pseudomonas aeruginosa polynucleotide #15040.
 PN US6551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Percent Similarity: 38.60% Conservative: 29
 Best Local Similarity: 25.88% Mismatches: 91
 Query Match: 6.78% Indels: 49
 RESULT 621
 ID ABD15673 standard; DNA; 1299 BP.
 DE Pseudomonas aeruginosa polynucleotide #14277.
 PN US6551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Percent Similarity: 35.00% Conservative: 20
 Best Local Similarity: 27.31% Mismatches: 108
 Query Match: 6.78% Indels: 61
 RESULT 622
 ID ABD14522 standard; DNA; 1428 BP.
 DE Pseudomonas aeruginosa polynucleotide #13126.
 PN US6551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Percent Similarity: 38.86% Conservative: 14
 Best Local Similarity: 30.86% Mismatches: 77
 Query Match: 6.78% Indels: 31
 RESULT 623
 ID ABD16317 standard; DNA; 1449 BP.
 DE Pseudomonas aeruginosa polynucleotide #14921.
 PN US6551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Percent Similarity: 38.60% Conservative: 29
 Best Local Similarity: 25.88% Mismatches: 91
 Query Match: 6.78% Indels: 49
 RESULT 624
 ID ACF39359 standard; DNA; 1509 BP.
 DE Mycobacterium tuberculosis mycobacterial antigen DNA SEQ ID NO:96.
 PN WO2003033530-A2.
 PD 24-APR-2003.
 PA (MICR-) MICROBIOLOGICAL RES AUTHORITY.
 Percent Similarity: 37.84% Conservative: 16
 Best Local Similarity: 29.19% Mismatches: 83
 Query Match: 6.78% Indels: 32
 RESULT 625
 ID ABD14362 standard; DNA; 1515 BP.
 DE Pseudomonas aeruginosa polynucleotide #12966.
 PN US6551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Percent Similarity: 38.86% Conservative: 14
 Best Local Similarity: 30.86% Mismatches: 77
 Query Match: 6.78% Indels: 31
 RESULT 626
 ID ACA53421 standard; DNA; 1590 BP.
 DE 'Prokaryotic essential gene #35078.
 PN WO20027183-A2.
 PD 03-OCT-2002.
 PA (ELIT-) ELITRA PHARM INC.
 Percent Similarity: 34.89% Conservative: 28
 Best Local Similarity: 24.82% Mismatches: 74
 Query Match: 6.78% Indels: 107
 RESULT 627
 ID ABD15703 standard; DNA; 1824 BP.
 DE Pseudomonas aeruginosa polynucleotide #14307.
 PN US6551795-B1.

PN US2003036180-A1.
 PD 20-FEB-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 30.08%
 Best Local Similarity: 19.92%
 Mismatches: 72
 Indels: 100
 Query Match:
 RESULT 642
 ID ACA71805 standard; cDNA; 2749 BP.
 DE Human secreted and transmembrane polypeptide PRO846 cDNA.
 PN US2002177553-A1.
 PD 28-NOV-2002.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 30.08%
 Best Local Similarity: 19.92%
 Mismatches: 72
 Indels: 100
 Query Match:
 RESULT 643
 ID ABX89333 standard; cDNA; 2749 BP.
 DE DNA encoding novel secreted and transmembrane protein PRO846.
 PN US2003017563-A1.
 PD 23-JAN-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 30.08%
 Best Local Similarity: 19.92%
 Mismatches: 72
 Indels: 100
 Query Match:
 RESULT 644
 ID ABX92445 standard; cDNA; 2749 BP.
 DE cDNA encoding human PRO846 polypeptide.
 PN US2002169284-A1.
 PD 14-NOV-2002.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 30.08%
 Best Local Similarity: 19.92%
 Mismatches: 72
 Indels: 100
 Query Match:
 RESULT 645
 ID ABX80979 standard; cDNA; 2749 BP.
 DE Human secreted/transmembrane protein cDNA, #183.
 PN US2003027162-A1.
 PD 06-FEB-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 30.08%
 Best Local Similarity: 19.92%
 Mismatches: 72
 Indels: 100
 Query Match:
 RESULT 646
 ID ACD4488 standard; cDNA; 2749 BP.
 DE cDNA encoding human PRO846 polypeptide.
 PN US2002127576-A1.
 PD 12-SEP-2002.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 30.08%
 Best Local Similarity: 19.92%
 Mismatches: 72
 Indels: 100
 Query Match:
 RESULT 647
 ID ACD41987 standard; cDNA; 2749 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #193.
 PN US2003036179-A1.
 PD 20-FEB-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 30.08%
 Best Local Similarity: 19.92%
 Mismatches: 72
 Indels: 100
 Query Match:
 RESULT 648
 ID ACA66186 standard; cDNA; 2749 BP.
 DE Human cDNA encoding secreted/transmembrane protein PRO846.
 PN US2003004102-A1.
 PD 02-JAN-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 30.08%
 Best Local Similarity: 19.92%
 Mismatches: 72
 Indels: 100
 Query Match:
 RESULT 649
 ID ABX79659 standard; cDNA; 2749 BP.
 DE Human secreted/transmembrane protein cDNA, #183.
 PN US2002142961-A1.
 PD 03-OCT-2002.

PA (GETH) GENENTECH INC.
 Percent Similarity: 30.08%
 Best Local Similarity: 19.92%
 Mismatches: 72
 Indels: 100
 Query Match:
 RESULT 650
 ID ACA93680 standard; cDNA; 2749 BP.
 DE Novel human secreted and transmembrane protein PRO846 cDNA.
 PN US2003022187-A1.
 PD 30-JAN-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 30.08%
 Best Local Similarity: 19.92%
 Mismatches: 72
 Indels: 100
 Query Match:
 RESULT 651
 ID ABX81362 standard; DNA; 2749 BP.
 DE Human secreted or transmembrane protein related PCR primer #149.
 PN US2003027985-A1.
 PD 06-FEB-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 30.08%
 Best Local Similarity: 19.92%
 Mismatches: 72
 Indels: 100
 Query Match:
 RESULT 652
 ID ACA04216 standard; cDNA; 2749 BP.
 DE Human cDNA encoding a secreted/transmembrane protein, SEQ ID 385.
 PN US2003032155-A1.
 PD 13-FEB-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 30.08%
 Best Local Similarity: 19.92%
 Mismatches: 72
 Indels: 100
 Query Match:
 RESULT 653
 ID ACA93178 standard; cDNA; 2749 BP.
 DE Novel human secreted and transmembrane protein PRO846 cDNA.
 PN US2003017476-A1.
 PD 23-JAN-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 30.08%
 Best Local Similarity: 19.92%
 Mismatches: 72
 Indels: 100
 Query Match:
 RESULT 654
 ID ABX17262 standard; cDNA; 2749 BP.
 DE Human PRO polynucleotide #147.
 PN US2002123463-A1.
 PD 05-SEP-2002.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 30.08%
 Best Local Similarity: 19.92%
 Mismatches: 72
 Indels: 100
 Query Match:
 RESULT 655
 ID ACA68117 standard; cDNA; 2749 BP.
 DE Novel human secreted and transmembrane protein PRO846 cDNA.
 PN US2002177164-A1.
 PD 28-NOV-2002.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 30.08%
 Best Local Similarity: 19.92%
 Mismatches: 72
 Indels: 100
 Query Match:
 RESULT 656
 ID ACA88566 standard; cDNA; 2749 BP.
 DE Human secreted and transmembrane polypeptide PRO846 cDNA.
 PN US2002197615-A1.
 PD 26-DEC-2002.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 30.08%
 Best Local Similarity: 19.92%
 Mismatches: 72
 Indels: 100
 Query Match:
 RESULT 657
 ID ACD82073 standard; cDNA; 2749 BP.
 DE cDNA encoding human PRO846 polypeptide.
 PN US2003017981-A1.
 PD 23-JAN-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 30.08%
 Best Local Similarity: 19.92%
 Mismatches: 72
 Indels: 100
 Query Match:
 RESULT 658
 ID ABX79659 standard; cDNA; 2749 BP.
 DE Human secreted/transmembrane protein cDNA, #183.
 PN US2002142961-A1.
 PD 03-OCT-2002.

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ID ADA45904 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003022328-A1.
PD 30-JAN-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 659
ID ADA76335 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
PN US2003073212-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 660
ID ADA18985 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
PN US2003054517-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 661
ID ADA61608 standard; cDNA; 2749 BP.
DE Homo sapiens.
PN US2003049816-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 662
ID ADB19393 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003068796-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 663
ID ADB27934 standard; cDNA; 2749 BP.
DE cDNA encoding human PRO polypeptide #193.
PN US2003082704-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 664
ID ADA86413 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003082711-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 665
ID ADB15977 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
PN US2003087350-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 666
ID ADA38027 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003082705-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 667
ID ADA47763 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
PN US2003073215-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 668
ID ADA21713 standard; cDNA; 2749 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO846.
PN US2003054404-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 669
ID ADA10500 standard; cDNA; 2749 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO846.
PN US2003059831-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 670
ID ADA67558 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
PN US2003068795-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 671
ID ADB30565 standard; cDNA; 2749 BP.
DE cDNA encoding human PRO polypeptide #193.
PN US2003068794-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 672
ID ADA85861 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003082693-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 673
ID ADA18044 standard; cDNA; 2749 BP.
DE cDNA encoding human PRO846 polypeptide.
PN US2003054987-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 674
ID ADA97073 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
PN US2003082705-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100

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Percent Similarity:	30.08%	Conservative:	25
Best Local Similarity:	19.92%	Mismatches:	72
Query Match:	6.78%	Indels:	100
RESULT 675			
ID ADA79377 standard; cDNA; 2749 BP.			
DE Human PRO polynucleotide #193.			
PN US2003082763-A1.			
PD 01-MAY-2003.			
PA (GETH) GENENTECH INC.			
Percent Similarity:	30.08%	Conservative:	25
Best Local Similarity:	19.92%	Mismatches:	72
Query Match:	6.78%	Indels:	100
RESULT 676			
ID ADA87516 standard; cDNA; 2749 BP.			
DE Novel human secreted and transmembrane protein PRO846 CDNA.			
PN US2003087345-A1.			
PD 08-MAY-2003.			
PA (GETH) GENENTECH INC.			
Percent Similarity:	30.08%	Conservative:	25
Best Local Similarity:	19.92%	Mismatches:	72
Query Match:	6.78%	Indels:	100
RESULT 677			
ID ADB16718 standard; cDNA; 2749 BP.			
DE Human PRO polynucleotide #193.			
PN US2003087349-A1.			
PD 08-MAY-2003.			
PA (GETH) GENENTECH INC.			
Percent Similarity:	30.08%	Conservative:	25
Best Local Similarity:	19.92%	Mismatches:	72
Query Match:	6.78%	Indels:	100
RESULT 678			
ID ADA28152 standard; cDNA; 2749 BP.			
DE Human CDNA encoding secreted/transmembrane protein PRO846.			
PN US2003054359-A1.			
PD 20-MAR-2003.			
PA (GETH) GENENTECH INC.			
Percent Similarity:	30.08%	Conservative:	25
Best Local Similarity:	19.92%	Mismatches:	72
Query Match:	6.78%	Indels:	100
RESULT 679			
ID ADA91810 standard; cDNA; 2749 BP.			
DE Novel human secreted and transmembrane protein PRO846 CDNA.			
PN US2003082694-A1.			
PD 01-MAY-2003.			
PA (GETH) GENENTECH INC.			
Percent Similarity:	30.08%	Conservative:	25
Best Local Similarity:	19.92%	Mismatches:	72
Query Match:	6.78%	Indels:	100
RESULT 680			
ID ADB14873 standard; cDNA; 2749 BP.			
DE Human PRO polynucleotide #193.			
PN US2003087351-A1.			
PD 08-MAY-2003.			
PA (GETH) GENENTECH INC.			
Percent Similarity:	30.08%	Conservative:	25
Best Local Similarity:	19.92%	Mismatches:	72
Query Match:	6.78%	Indels:	100
RESULT 681			
ID ADA24754 standard; cDNA; 2749 BP.			
DE Novel human secreted and transmembrane protein PRO846 CDNA.			
PN US2003050241-A1.			
PD 13-MAR-2003.			
PA (GETH) GENENTECH INC.			
Percent Similarity:	30.08%	Conservative:	25
Best Local Similarity:	19.92%	Mismatches:	72
Query Match:	6.78%	Indels:	100
RESULT 682			
ID ADB18834 standard; cDNA; 2749 BP.			
DE Novel human secreted and transmembrane protein PRO846 CDNA.			
PN US2003073211-A1.			
PD 17-APR-2003.			
PA (GETH) GENENTECH INC.			
Percent Similarity:	30.08%	Conservative:	25
Best Local Similarity:	19.92%	Mismatches:	72
Query Match:	6.78%	Indels:	100
RESULT 683			
ID ADB18834 standard; cDNA; 2749 BP.			
DE Novel human secreted and transmembrane protein PRO846 CDNA.			
PN US2003073211-A1.			
PD 17-APR-2003.			
PA (GETH) GENENTECH INC.			
Percent Similarity:	30.08%	Conservative:	25
Best Local Similarity:	19.92%	Mismatches:	72
Query Match:	6.78%	Indels:	100

Query Match:	6.78%	Indels:	100
RESULT 683			
ID ADA94049 standard; cDNA; 2749 BP.			
DE Human PRO polynucleotide #193.			
PN US2003077722-A1.			
PD 24-APR-2003.			
PA (GETH) GENENTECH INC.			
Percent Similarity: 30.08%			
Best Local Similarity: 19.92%			
Query Match:	6.78%	Conservative: 25	
		Mismatches: 72	
		Indels: 100	
RESULT 684			
ID ADB19945 standard; cDNA; 2749 BP.			
DE Novel human secreted and transmembrane protein PRO846 cDNA.			
PN US2003082691-A1.			
PD 01-MAY-2003.			
PA (GETH) GENENTECH INC.			
Percent Similarity: 30.08%			
Best Local Similarity: 19.92%			
Query Match:	6.78%	Conservative: 25	
		Mismatches: 72	
		Indels: 100	
RESULT 685			
ID ADB13257 standard; cDNA; 2749 BP.			
DE Human PRO polynucleotide #193.			
PN US2003082710-A1.			
PD 01-MAY-2003.			
PA (GETH) GENENTECH INC.			
Percent Similarity: 30.08%			
Best Local Similarity: 19.92%			
Query Match:	6.78%	Conservative: 25	
		Mismatches: 72	
		Indels: 100	
RESULT 686			
ID ACD98616 standard; cDNA; 2749 BP.			
DE Novel human secreted and transmembrane protein PRO846 cDNA.			
PN US2003044945-A1.			
PD 06-MAR-2003.			
PA (GETH) GENENTECH INC.			
Percent Similarity: 30.08%			
Best Local Similarity: 19.92%			
Query Match:	6.78%	Conservative: 25	
		Mismatches: 72	
		Indels: 100	
RESULT 687			
ID ACD29787 standard; cDNA; 2749 BP.			
DE Novel human secreted and transmembrane protein PRO846 cDNA.			
PN US2003050240-A1.			
PD 13-MAR-2003.			
PA (GETH) GENENTECH INC.			
Percent Similarity: 30.08%			
Best Local Similarity: 19.92%			
Query Match:	6.78%	Conservative: 25	
		Mismatches: 72	
		Indels: 100	
RESULT 688			
ID ADA12415 standard; cDNA; 2749 BP.			
DE Human cDNA encoding secreted/transmembrane polypeptide PRO846.			
PN US2003055216-A1.			
PD 20-MAR-2003.			
PA (GETH) GENENTECH INC.			
Percent Similarity: 30.08%			
Best Local Similarity: 19.92%			
Query Match:	6.78%	Conservative: 25	
		Mismatches: 72	
		Indels: 100	
RESULT 689			
ID ADA94732 standard; cDNA; 2749 BP.			
DE Human cDNA encoding secreted/transmembrane protein PRO846.			
PN US2003059832-A1.			
PD 27-MAR-2003.			
PA (GETH) GENENTECH INC.			
Percent Similarity: 30.08%			
Best Local Similarity: 19.92%			
Query Match:	6.78%	Conservative: 25	
		Mismatches: 72	
		Indels: 100	
RESULT 690			
ID ADA74511 standard; cDNA; 2749 BP.			
DE Human PRO polynucleotide #193.			
PN US2003068798-A1.			
PD 10-APR-2003.			
PA (GETH) GENENTECH INC.			
Percent Similarity: 30.08%			
Best Local Similarity: 19.92%			
Query Match:	6.78%	Conservative: 25	
		Mismatches: 72	
		Indels: 100	
RESULT 691			
ID ADA74511 standard; cDNA; 2749 BP.			
DE Human PRO polynucleotide #193.			
PN US2003068798-A1.			
PD 10-APR-2003.			
PA (GETH) GENENTECH INC.			
Percent Similarity: 30.08%			
Best Local Similarity: 19.92%			
Query Match:	6.78%	Conservative: 25	
		Mismatches: 72	
		Indels: 100	

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ID ADB24744 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide SEQ ID NO 385.
PN US2003077713-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 692
ID ADB2268 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
PN US2003082701-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 693
ID ADA75231 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
PN US2003073216-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 694
ID ADA85309 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003082695-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 695
ID ADA84757 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003082708-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 696
ID ADB30013 standard; cDNA; 2749 BP.
DE cDNA encoding human PRO polypeptide #193.
PN US2003073214-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 697
ID ADA80541 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
PN US2003082761-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 698
ID ADA75783 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
PN US2003082703-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 699
ID ADA38957 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
PN US2003077714-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
DE Human cDNA encoding secreted/transmembrane protein PRO846.
PN US2003059780-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 700
ID ADA47008 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
PN US2003073210-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 701
ID ADB25304 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide SEQ ID NO 385.
PN US2003077715-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 702
ID ADA93480 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
PN US2003077721-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 703
ID ADB26830 standard; cDNA; 2749 BP.
DE cDNA encoding human PRO polypeptide #193.
PN US2003092147-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 704
ID ADB31117 standard; cDNA; 2749 BP.
DE cDNA encoding human PRO polypeptide #193.
PN US2003096386-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 705
ID ADA93078 standard; cDNA; 2749 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO846.
PN US2003060407-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 706
ID ADA61045 standard; cDNA; 2749 BP.
DE Homo sapiens.
PN US2003049817-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 707
ID ADB24192 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide SEQ ID NO 385.
PN US2003077714-A1.
PD 24-APR-2003.

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ID ADA8620 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003073213-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 725
ID ADA97625 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
PN US2003082686-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 726
ID ADB27382 standard; cDNA; 2749 BP.
DE cDNA encoding human PRO polypeptide #193.
PN US2003022239-A1.
PD 30-JAN-2003.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 727
ID ADB22315 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003087344-A1.
PD 08-MAY-2003.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 728
ID ACD39624 standard; DNA; 2749 BP.
DE Human PRO 846 PCR primer #1.
PN US2003017982-A1.
PD 23-JAN-2003.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 729
ID ADA06805 standard; cDNA; 2749 BP.
DE Human secreted/transmembrane PRO polypeptide cDNA #147.
PN US2003049638-A1.
PD 13-MAR-2003.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 730
ID ADA39498 standard; cDNA; 2749 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO846.
PN US2003059782-A1.
PD 27-MAR-2003.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 731
ID ADA67006 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
PN US2003068793-A1.
PD 10-APR-2003.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 732
ID ADB2867 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
PN US2003077711-A1.
PD 24-APR-2003.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 733
ID ADB23640 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide SEQ ID NO 385.
PN US2003077712-A1.
PD 24-APR-2003.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 734
ID ADA92362 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003082712-A1.
PD 01-MAY-2003.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 735
ID ADB15425 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
PN US2003087352-A1.
PD 08-MAY-2003.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 736
ID ADB38677 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003082766-A1.
PD 01-MAY-2003.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 737
ID ADB96524 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #147.
PN US2003054403-A1.
PD 20-MAR-2003.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 738
ID ADB38125 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003087347-A1.
PD 08-MAY-2003.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 739
ID ADB66597 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003082689-A1.
PD 01-MAY-2003.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 740
ID ADB89677 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
PN US2003082698-A1.
PD 01-MAY-2003.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100

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RESULT 741
 ID ADB90409 standard; cDNA; 2749 BP.
 DE Human PRO polynucleotide #193.
 PN US2003082762-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 30.08%
 Best Local Similarity: 19.92%
 Query Match: 6.78%
 Indels: 100
 Conservative: 25
 Mismatches: 72
 Indels: 100
 RESULT 742
 ID ADB39510 standard; cDNA; 2749 BP.
 DE Novel human secreted and transmembrane protein PRO846 cDNA.
 PN US2003082764-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 30.08%
 Best Local Similarity: 19.92%
 Query Match: 6.78%
 Indels: 100
 Conservative: 25
 Mismatches: 72
 Indels: 100
 RESULT 743
 ID ADB73721 standard; cDNA; 2749 BP.
 DE Human PRO polynucleotide sequence #46.
 PN US2003045462-A1.
 PD 06-MAR-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 30.08%
 Best Local Similarity: 19.92%
 Query Match: 6.78%
 Indels: 100
 Conservative: 25
 Mismatches: 72
 Indels: 100
 RESULT 744
 ID ADB47133 standard; cDNA; 2749 BP.
 DE Novel human secreted and transmembrane protein PRO846 cDNA.
 PN US2003082687-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 30.08%
 Best Local Similarity: 19.92%
 Query Match: 6.78%
 Indels: 100
 Conservative: 25
 Mismatches: 72
 Indels: 100
 RESULT 745
 ID ADB86740 standard; cDNA; 2749 BP.
 DE Human PRO polynucleotide #193.
 PN US2003082697-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 30.08%
 Best Local Similarity: 19.92%
 Query Match: 6.78%
 Indels: 100
 Conservative: 25
 Mismatches: 72
 Indels: 100
 RESULT 746
 ID ADB76437 standard; cDNA; 2749 BP.
 DE Human PRO polynucleotide sequence #46.
 PN US2003083248-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 30.08%
 Best Local Similarity: 19.92%
 Query Match: 6.78%
 Indels: 100
 Conservative: 25
 Mismatches: 72
 Indels: 100
 RESULT 747
 ID ADB77345 standard; cDNA; 2749 BP.
 DE Novel human secreted and transmembrane protein PRO846 cDNA.
 PN US2003082696-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 30.08%
 Best Local Similarity: 19.92%
 Query Match: 6.78%
 Indels: 100
 Conservative: 25
 Mismatches: 72
 Indels: 100
 RESULT 748
 ID ADB34502 standard; cDNA; 2749 BP.
 DE Human PRO polynucleotide SEQ ID NO 385.
 PN US2003077717-A1.
 PD 24-APR-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 30.08%
 Best Local Similarity: 19.92%
 Query Match: 6.78%
 Indels: 100
 Conservative: 25
 Mismatches: 72
 Indels: 100
 RESULT 749
 ID ADB12227 standard; cDNA; 2749 BP.
 DE Human cDNA encoding secreted/transmembrane protein PRO846.
 PN US2003049681-A1.

ID ADB35606 standard; cDNA; 2749 BP.
 DE Human PRO polynucleotide SEQ ID NO 385.
 PN US2003077719-A1.
 PD 24-APR-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 30.08%
 Best Local Similarity: 19.92%
 Query Match: 6.78%
 Indels: 100
 Conservative: 25
 Mismatches: 72
 Indels: 100
 RESULT 750
 ID ADB33950 standard; cDNA; 2749 BP.
 DE Human PRO polynucleotide SEQ ID NO 385.
 PN US2003077716-A1.
 PD 24-APR-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 30.08%
 Best Local Similarity: 19.92%
 Query Match: 6.78%
 Indels: 100
 Conservative: 25
 Mismatches: 72
 Indels: 100
 RESULT 751
 ID ADB35054 standard; cDNA; 2749 BP.
 DE Human PRO polynucleotide SEQ ID NO 385.
 PN US2003077718-A1.
 PD 24-APR-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 30.08%
 Best Local Similarity: 19.92%
 Query Match: 6.78%
 Indels: 100
 Conservative: 25
 Mismatches: 72
 Indels: 100
 RESULT 752
 ID ADB36158 standard; cDNA; 2749 BP.
 DE Human PRO polynucleotide SEQ ID NO 385.
 PN US2003077720-A1.
 PD 24-APR-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 30.08%
 Best Local Similarity: 19.92%
 Query Match: 6.78%
 Indels: 100
 Conservative: 25
 Mismatches: 72
 Indels: 100
 RESULT 753
 ID ADB46553 standard; cDNA; 2749 BP.
 DE Novel human secreted and transmembrane protein PRO846 cDNA.
 PN US2003082692-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 30.08%
 Best Local Similarity: 19.92%
 Query Match: 6.78%
 Indels: 100
 Conservative: 25
 Mismatches: 72
 Indels: 100
 RESULT 754
 ID ADC43863 standard; cDNA; 2749 BP.
 DE Human cDNA encoding secreted/transmembrane protein, PRO846.
 PN US2003054986-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 30.08%
 Best Local Similarity: 19.92%
 Query Match: 6.78%
 Indels: 100
 Conservative: 25
 Mismatches: 72
 Indels: 100
 RESULT 755
 ID ADC57996 standard; cDNA; 2749 BP.
 DE Human PRO polynucleotide #147.
 PN US2003027754-A1.
 PD 06-FEB-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 30.08%
 Best Local Similarity: 19.92%
 Query Match: 6.78%
 Indels: 100
 Conservative: 25
 Mismatches: 72
 Indels: 100
 RESULT 756
 ID ADC53360 standard; cDNA; 2749 BP.
 DE Human PRO polynucleotide #147.
 PN US2003045463-A1.
 PD 06-MAR-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 30.08%
 Best Local Similarity: 19.92%
 Query Match: 6.78%
 Indels: 100
 Conservative: 25
 Mismatches: 72
 Indels: 100
 RESULT 757
 ID ADC12227 standard; cDNA; 2749 BP.
 DE Human cDNA encoding secreted/transmembrane protein PRO846.
 PN US2003049681-A1.

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PD 13-MAR-2003.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 758
ID ADC61623 standard; cDNA; 2749 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO846.
PN US2003049684-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 759
ID ADC63587 standard; cDNA; 2749 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO846.
PN US2003054405-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 760
ID ADC66687 standard; cDNA; 2749 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO846.
PN US2003060406-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 761
ID ADC56649 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #147.
PN US2003064375-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 762
ID ADC68811 standard; cDNA; 2749 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO846.
PN US2003064407-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 763
ID ADC62871 standard; cDNA; 2749 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO846.
PN US2003068648-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 764
ID ADC7936 standard; cDNA; 2749 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO846.
PN US2003069178-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 765
ID ADC11694 standard; cDNA; 2749 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO846.
PN US2003069403-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 766
ID ADC41256 standard; cDNA; 2749 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO846.
PN US2003072745-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 767
ID ADC67311 standard; cDNA; 2749 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO846.
PN US2003073131-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 768
ID ADC62247 standard; cDNA; 2749 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO846.
PN US2003073624-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 769
ID ADC41880 standard; cDNA; 2749 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO846.
PN US2003104998-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 770
ID ADC50426 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003092106-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 771
ID ADC71973 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003092107-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 772
ID ADC59952 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003092105-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 773
ID ADC52959 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID385.
PN US2003087365-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100

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RESULT 774
ID ADC57313 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID385.
FN US2003087366-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indel: 100
RESULT 775
ID ADC60504 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
FN US2003087367-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indel: 100
RESULT 776
ID ADC50979 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
FN US2003087361-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indel: 100
RESULT 777
ID ADC65506 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
FN US2003087362-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indel: 100
RESULT 778
ID ADC54604 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID385.
FN US2003087363-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indel: 100
RESULT 779
ID ADC53565 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID385.
FN US2003087364-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indel: 100
RESULT 780
ID ADC59088 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID385.
FN US2003087359-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indel: 100
RESULT 781
ID ADC5966 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID385.
FN US2003087360-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indel: 100
RESULT 782
ID ADC5966 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID385.
FN US2003087360-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indel: 100

RESULT 783
ID ADC14816 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
FN US2003082546-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indel: 100
RESULT 784
ID ADD08348 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
FN US2003086823-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indel: 100
RESULT 785
ID ADD03210 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
FN US2003092104-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indel: 100
RESULT 786
ID ADC90202 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
FN US2003087348-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indel: 100
RESULT 787
ID ADC82173 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #147.
FN US2003083461-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indel: 100
RESULT 788
ID ADC69621 standard; cDNA; 2749 BP.
DE cDNA encoding human PRO polypeptide #193.
FN US2003194770-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indel: 100
RESULT 789
ID ADC48510 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
FN US2003194773-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indel: 100
RESULT 790
ID ADD10039 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
FN US2003194776-A1.
PD 16-OCT-2003.

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PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 791
ID ADD07815 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2002193299-A1.
PD 19-DEC-2002.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 792
ID ADD04614 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003087354-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 793
ID ADC82706 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #147.
PN US2003059833-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 794
ID ADC80570 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003092103-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 795
ID ADD11077 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
PN US2003194774-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 796
ID ADD10348 standard; cDNA; 2749 BP.
DE Human secreted/transmembrane PRO polypeptide cDNA #30.
PN US2003105011-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 797
ID ADC47958 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
PN US2003194771-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 798
ID ADD08886 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003073090-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 799
ID ADC80018 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003087358-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 800
ID ADD07135 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2002193300-A1.
PD 19-DEC-2002.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 801
ID ADD11308 standard; cDNA; 2749 BP.
DE Human secreted/transmembrane PRO polypeptide cDNA #30.
PN US2003105013-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 802
ID ADD09487 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
PN US2003194775-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 803
ID ADC83382 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #147.
PN US2003059783-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 804
ID ADD41200 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003203438-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 805
ID ADD52339 standard; cDNA; 2749 BP.
DE cDNA encoding human PRO polypeptide #193.
PN US2003194769-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 806
ID ADD53079 standard; cDNA; 2749 BP.
DE cDNA encoding human PRO polypeptide #193.
PN US2003194792-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 807
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ID	ADD53631 standard; cDNA; 2749 BP.		
DE	Novel human secreted and transmembrane protein PRO846 cDNA.		
FN	US2003203437-A1.		
PD	30-OCT-2003.		
PA	(GETH) GENENTECH INC.		
Percent Similarity:	30.08%	Conservative:	25
Best Local Similarity:	19.92%	Mismatches:	72
Query Match:	6.78%	Indels:	100
RESULT 808			
ID	ADD55489 standard; cDNA; 2749 BP.		
DE	Human PRO polynucleotide #147.		
FN	US2003077593-A1.		
PD	24-APR-2003.		
Percent Similarity:	30.08%	Conservative:	25
Best Local Similarity:	19.92%	Mismatches:	72
Query Match:	6.78%	Indels:	100
RESULT 809			
ID	ADD37101 standard; cDNA; 2749 BP.		
DE	Human secreted/transmembrane PRO polypeptide cDNA #30.		
FN	US2003105012-A1.		
PD	05-JUN-2003.		
PA	(GETH) GENENTECH INC.		
Percent Similarity:	30.08%	Conservative:	25
Best Local Similarity:	19.92%	Mismatches:	72
Query Match:	6.78%	Indels:	100
RESULT 810			
ID	ADD56447 standard; cDNA; 2749 BP.		
DE	Human PRO polynucleotide #147.		
FN	US2003077594-A1.		
PD	24-APR-2003.		
Percent Similarity:	30.08%	Conservative:	25
Best Local Similarity:	19.92%	Mismatches:	72
Query Match:	6.78%	Indels:	100
RESULT 811			
ID	ADD51787 standard; cDNA; 2749 BP.		
DE	cDNA encoding human PRO polypeptide #193.		
FN	US2003194779-A1.		
PD	16-OCT-2003.		
PA	(GETH) GENENTECH INC.		
Percent Similarity:	30.08%	Conservative:	25
Best Local Similarity:	19.92%	Mismatches:	72
Query Match:	6.78%	Indels:	100
RESULT 812			
ID	ADD02586 standard; cDNA; 2749 BP.		
DE	Human PRO polynucleotide #193.		
FN	US2003203431-A1.		
PD	30-OCT-2003.		
PA	(GETH) GENENTECH INC.		
Percent Similarity:	30.08%	Conservative:	25
Best Local Similarity:	19.92%	Mismatches:	72
Query Match:	6.78%	Indels:	100
RESULT 813			
ID	ADD02020 standard; cDNA; 2749 BP.		
DE	Human PRO polynucleotide #193.		
FN	US2003203430-A1.		
PD	30-OCT-2003.		
PA	(GETH) GENENTECH INC.		
Percent Similarity:	30.08%	Conservative:	25
Best Local Similarity:	19.92%	Mismatches:	72
Query Match:	6.78%	Indels:	100
RESULT 814			
ID	ADD54202 standard; cDNA; 2749 BP.		
DE	Human PRO polynucleotide #193.		
FN	US2003203430-A1.		
PD	30-OCT-2003.		
PA	(GETH) GENENTECH INC.		
Percent Similarity:	30.08%	Conservative:	25
Best Local Similarity:	19.92%	Mismatches:	72
Query Match:	6.78%	Indels:	100
RESULT 815			
ID	ADD54885 standard; cDNA; 2749 BP.		
DE	Human PRO polynucleotide #147.		
FN	US2002132253-A1.		
PD	30-OCT-2003.		
PA	(GETH) GENENTECH INC.		
Percent Similarity:	30.08%	Conservative:	25
Best Local Similarity:	19.92%	Mismatches:	72
Query Match:	6.78%	Indels:	100

PD	19-SEP-2002.
PA	(GETH) GENENTECH INC.
Percent Similarity:	30.08%
Best Local Similarity:	19.92%
Query Match:	6.78%
RESULT 816	
ID	AD8494249 standard; cDNA; 2749 BP.
DE	Human cDNA encoding secreted/transmembrane protein, PRO846.
FN	US2003096744-A1.
PD	22-MAY-2003.
PA	(GETH) GENENTECH INC.
Percent Similarity:	30.08%
Best Local Similarity:	19.92%
Query Match:	6.78%
RESULT 817	
ID	ADD92519 standard; cDNA; 2749 BP.
DE	Human PRO polynucleotide #193.
FN	US2003199030-A1.
PD	23-OCT-2003.
PA	(GETH) GENENTECH INC.
Percent Similarity:	30.08%
Best Local Similarity:	19.92%
Query Match:	6.78%
RESULT 818	
ID	ADD91415 standard; cDNA; 2749 BP.
DE	Human PRO polynucleotide #193.
FN	US2003199055-A1.
PD	23-OCT-2003.
PA	(GETH) GENENTECH INC.
Percent Similarity:	30.08%
Best Local Similarity:	19.92%
Query Match:	6.78%
RESULT 819	
ID	ADR04029 standard; cDNA; 2749 BP.
DE	Human PRO polynucleotide #193.
FN	US2003199057-A1.
PD	23-OCT-2003.
PA	(GETH) GENENTECH INC.
Percent Similarity:	30.08%
Best Local Similarity:	19.92%
Query Match:	6.78%
RESULT 820	
ID	ADR31904 standard; cDNA; 2749 BP.
DE	Human cDNA encoding secreted/transmembrane protein PRO846.
FN	US2003068647-A1.
PD	10-APR-2003.
PA	(GETH) GENENTECH INC.
Percent Similarity:	30.08%
Best Local Similarity:	19.92%
Query Match:	6.78%
RESULT 821	
ID	ADE27039 standard; cDNA; 2749 BP.
DE	Novel human secreted and transmembrane protein PRO846 cDNA.
FN	US2003087304-A1.
PD	08-MAY-2003.
PA	(GETH) GENENTECH INC.
Percent Similarity:	30.08%
Best Local Similarity:	19.92%
Query Match:	6.78%
RESULT 822	
ID	ADE32326 standard; cDNA; 2749 BP.
DE	Novel human secreted and transmembrane protein PRO846 cDNA.
FN	US2003194765-A1.
PD	16-OCT-2003.
PA	(GETH) GENENTECH INC.
Percent Similarity:	30.08%
Best Local Similarity:	19.92%
Query Match:	6.78%
RESULT 823	
ID	ADE22528 standard; cDNA; 2749 BP.
DE	cDNA encoding human PRO polypeptide #193.
FN	US2003199056-A1.
PD	23-OCT-2003.
PA	(GETH) GENENTECH INC.
Percent Similarity:	30.08%
Best Local Similarity:	19.92%
Query Match:	6.78%
RESULT 824	
ID	AD8494249 standard; cDNA; 2749 BP.
DE	Human cDNA encoding secreted/transmembrane protein, PRO846.
FN	US2003096744-A1.
PD	22-MAY-2003.
PA	(GETH) GENENTECH INC.
Percent Similarity:	30.08%
Best Local Similarity:	19.92%
Query Match:	6.78%
RESULT 825	
ID	ADD92519 standard; cDNA; 2749 BP.
DE	Human PRO polynucleotide #193.
FN	US2003199030-A1.
PD	23-OCT-2003.
PA	(GETH) GENENTECH INC.
Percent Similarity:	30.08%
Best Local Similarity:	19.92%
Query Match:	6.78%
RESULT 826	
ID	ADD91415 standard; cDNA; 2749 BP.
DE	Human PRO polynucleotide #193.
FN	US2003199055-A1.
PD	23-OCT-2003.
PA	(GETH) GENENTECH INC.
Percent Similarity:	30.08%
Best Local Similarity:	19.92%
Query Match:	6.78%
RESULT 827	
ID	ADR04029 standard; cDNA; 2749 BP.
DE	Human PRO polynucleotide #193.
FN	US2003199057-A1.
PD	23-OCT-2003.
PA	(GETH) GENENTECH INC.
Percent Similarity:	30.08%
Best Local Similarity:	19.92%
Query Match:	6.78%
RESULT 828	
ID	ADR31904 standard; cDNA; 2749 BP.
DE	Human cDNA encoding secreted/transmembrane protein PRO846.
FN	US2003068647-A1.
PD	10-APR-2003.
PA	(GETH) GENENTECH INC.
Percent Similarity:	30.08%
Best Local Similarity:	19.92%
Query Match:	6.78%
RESULT 829	
ID	ADE27039 standard; cDNA; 2749 BP.
DE	Novel human secreted and transmembrane protein PRO846 cDNA.
FN	US2003087304-A1.
PD	08-MAY-2003.
PA	(GETH) GENENTECH INC.
Percent Similarity:	30.08%
Best Local Similarity:	19.92%
Query Match:	6.78%
RESULT 830	
ID	ADE32326 standard; cDNA; 2749 BP.
DE	Novel human secreted and transmembrane protein PRO846 cDNA.
FN	US2003194765-A1.
PD	16-OCT-2003.
PA	(GETH) GENENTECH INC.
Percent Similarity:	30.08%
Best Local Similarity:	19.92%
Query Match:	6.78%
RESULT 831	
ID	ADE22528 standard; cDNA; 2749 BP.
DE	cDNA encoding human PRO polypeptide #193.
FN	US2003199056-A1.
PD	23-OCT-2003.
PA	(GETH) GENENTECH INC.
Percent Similarity:	30.08%
Best Local Similarity:	19.92%
Query Match:	6.78%
RESULT 832	
ID	AD8494249 standard; cDNA; 2749 BP.
DE	Human cDNA encoding secreted/transmembrane protein, PRO846.
FN	US2003096744-A1.
PD	22-MAY-2003.
PA	(GETH) GENENTECH INC.
Percent Similarity:	30.08%
Best Local Similarity:	19.92%
Query Match:	6.78%
RESULT 833	
ID	ADD92519 standard; cDNA; 2749 BP.
DE	Human PRO polynucleotide #193.
FN	US2003199030-A1.
PD	23-OCT-2003.
PA	(GETH) GENENTECH INC.
Percent Similarity:	30.08%
Best Local Similarity:	19.92%
Query Match:	6.78%
RESULT 834	
ID	ADD91415 standard; cDNA; 2749 BP.
DE	Human PRO polynucleotide #193.
FN	US2003199

Query Match:	Best Local Similarity:	19.92%	6.78%	Mismatches:	72	Indels:	100
Query Match:	Best Local Similarity:	19.92%	6.78%	Mismatches:	72	Indels:	100
RESULT 832	ID ADE33982 standard; cDNA; 2749 BP.						
DE	Novel human secreted and transmembrane protein PRO846 cDNA.						
PN	US2003194791-A1.						
PD	16-OCT-2003.						
PA	(GETH) GENENTECH INC.						
Percent Similarity:	30.08%			Conservative:	25		
Best Local Similarity:	19.92%			Mismatches:	72		
Query Match:	Best Local Similarity:	19.92%	6.78%	Indels:	100		
RESULT 833	ID ADD80034 standard; cDNA; 2749 BP.						
DE	cDNA encoding human PRO polypeptide #193.						
PN	US2003207417-A1.						
PD	06-NOV-2003.						
PA	(GETH) GENENTECH INC.						
Percent Similarity:	30.08%			Conservative:	25		
Best Local Similarity:	19.92%			Mismatches:	72		
Query Match:	Best Local Similarity:	19.92%	6.78%	Indels:	100		
RESULT 834	ID ADD93071 standard; cDNA; 2749 BP.						
DE	Human PRO polynucleotide #193.						
PN	US2003194768-A1.						
PD	16-OCT-2003.						
PA	(GETH) GENENTECH INC.						
Percent Similarity:	30.08%			Conservative:	25		
Best Local Similarity:	19.92%			Mismatches:	72		
Query Match:	Best Local Similarity:	19.92%	6.78%	Indels:	100		
RESULT 835	ID ADD72390 standard; cDNA; 2749 BP.						
DE	Human cDNA encoding secreted/transmembrane protein, PRO846.						
PN	US2003194781-A1.						
PD	16-OCT-2003.						
PA	(GETH) GENENTECH INC.						
Percent Similarity:	30.08%			Conservative:	25		
Best Local Similarity:	19.92%			Mismatches:	72		
Query Match:	Best Local Similarity:	19.92%	6.78%	Indels:	100		
RESULT 836	ID ADE19491 standard; cDNA; 2749 BP.						
DE	Human PRO polynucleotide #193.						
PN	US2003199025-A1.						
PD	23-OCT-2003.						
PA	(GETH) GENENTECH INC.						
Percent Similarity:	30.08%			Conservative:	25		
Best Local Similarity:	19.92%			Mismatches:	72		
Query Match:	Best Local Similarity:	19.92%	6.78%	Indels:	100		
RESULT 837	ID ADE18939 standard; cDNA; 2749 BP.						
DE	Human PRO polynucleotide #193.						
PN	US2003199026-A1.						
PD	23-OCT-2003.						
PA	(GETH) GENENTECH INC.						
Percent Similarity:	30.08%			Conservative:	25		
Best Local Similarity:	19.92%			Mismatches:	72		
Query Match:	Best Local Similarity:	19.92%	6.78%	Indels:	100		
RESULT 838	ID ADE43135 standard; cDNA; 2749 BP.						
DE	Human PRO polynucleotide #193.						
PN	US2003199033-A1.						
PD	23-OCT-2003.						
PA	(GETH) GENENTECH INC.						
Percent Similarity:	30.08%			Conservative:	25		
Best Local Similarity:	19.92%			Mismatches:	72		
Query Match:	Best Local Similarity:	19.92%	6.78%	Indels:	100		
RESULT 839	ID ADD95924 standard; cDNA; 2749 BP.						
DE	Human PRO polynucleotide #193.						
PN	US2003199059-A1.						
PD	23-OCT-2003.						
PA	(GETH) GENENTECH INC.						
Percent Similarity:	30.08%			Conservative:	25		
Best Local Similarity:	19.92%			Mismatches:	72		
Query Match:	Best Local Similarity:	19.92%	6.78%	Indels:	100		
RESULT 840	ID ADD91967 standard; cDNA; 2749 BP.						
DE	Human PRO polynucleotide #193.						
PN	US2003199053-A1.						
PD	23-OCT-2003.						
PA	(GETH) GENENTECH INC.						
Percent Similarity:	30.08%			Conservative:	25		
Best Local Similarity:	19.92%			Mismatches:	72		
Query Match:	Best Local Similarity:	19.92%	6.78%	Indels:			

RESULT 840
ID ADE22810 standard; cDNA; 2749 BP.
DE cDNA encoding human PRO polypeptide #193.
PN US2003199064-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 841
ID ADD78928 standard; cDNA; 2749 BP.
DE cDNA encoding human PRO polypeptide #193.
PN US2003203429-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 842
ID ADE26506 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003087305-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 843
ID ADE32878 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003194766-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 844
ID ADP42570 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
PN US2003199032-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 845
ID ADE17041 standard; cDNA; 2749 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO846.
PN US2003203433-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 846
ID ADB80586 standard; cDNA; 2749 BP.
DE cDNA encoding human PRO polypeptide #193.
PN US2003207418-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 847
ID ADD89614 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
PN US2003199028-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 848
ID ADE40898 standard; cDNA; 2749 BP.

DE Human PRO polynucleotide #193.
PN US2003199031-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 849
ID ADE04697 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
PN US2003199034-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 850
ID ADE92826 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
PN US2003194777-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 851
ID ADF47055 standard; cDNA; 2749 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO846.
PN US2003195333-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 852
ID ADP67443 standard; cDNA; 2749 BP.
DE Human PRO846 nucleotide sequence SEQ ID NO:516.
PN US2002198148-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 853
ID ADG21535 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003207355-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 854
ID ADG23176 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003207384-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 855
ID ADF97511 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
PN US2003207370-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 856
ID ADG80575 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.

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PN US2003207373-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100

RESULT 857
ID ADG52812 standard; cDNA; 2749 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO846.
PN US2003216561-A1.
PD 20-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100

RESULT 858
ID ADG60132 standard; cDNA; 2749 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO846.
PN US2003206915-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100

RESULT 859
ID ADG80023 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
PN US2003207372-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100

RESULT 860
ID ADH55315 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003207381-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100

RESULT 861
ID ADH55867 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003207379-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100

RESULT 862
ID ADI35697 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #147.
PN US2003050457-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100

RESULT 863
ID ADI60892 standard; cDNA; 2749 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO846.
PN US2003077700-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100

RESULT 864
ID ADI64086 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003207385-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100

RESULT 865
ID ADI65035 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003207386-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100

RESULT 866
ID ADH81948 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003207388-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100

RESULT 867
ID ADI00190 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003049682-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100

RESULT 868
ID ADH81396 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003207377-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100

RESULT 869
ID ABX78063 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #147.
PN US2003027163-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100

RESULT 870
ID ABX80475 standard; cDNA; 2749 BP.
DE Human secreted or transmembrane protein related PCR primer #149.
PN US2002132252-A1.
PD 19-SEP-2002.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100

RESULT 871
ID ACA69381 standard; cDNA; 2749 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO846.
PN US2003032023-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100

RESULT 872
ID ACD24045 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003032156-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100

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RESULT 873
ID ABX90452 standard; cDNA; 2749 BP.
DE Human secreted/transmembrane protein cDNA, #183.
PN US2002160384-A1.
PD 31-OCT-2002.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatches: 72
Indels: 100
RESULT 874
ID ACDA4266 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003050239-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatches: 72
Indels: 100
RESULT 875
ID ABX64298 standard; cDNA; 2749 BP.
DE CDNA encoding human PRO846 polypeptide.
PN US2002103125-A1.
PD 01-AUG-2002.
PA (GETH ) GENENTECH LTD.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatches: 72
Indels: 100
RESULT 876
ID ACA67186 standard; cDNA; 2749 BP.
DE CDNA encoding human PRO polypeptide #193.
PN US2003004311-A1.
PD 02-JAN-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatches: 72
Indels: 100
RESULT 877
ID ADM82565 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003087355-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatches: 72
Indels: 100
RESULT 878
ID ADN15964 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003087353-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatches: 72
Indels: 100
RESULT 879
ID ADN16593 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003087385-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatches: 72
Indels: 100
RESULT 880
ID ADN15412 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003087356-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatches: 72
Indels: 100
RESULT 881
ID ADE23362 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003100497-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatches: 72
Indels: 100
RESULT 882
ID ADC81122 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003092115-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatches: 72
Indels: 100
RESULT 883
ID ADD76570 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
PN US2003100087-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatches: 72
Indels: 100
RESULT 884
ID ADD87934 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
PN US2003092113-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatches: 72
Indels: 100
RESULT 885
ID ADD86338 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
PN US2003203440-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatches: 72
Indels: 100
RESULT 886
ID AD875786 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
PN US2003211571-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatches: 72
Indels: 100
RESULT 887
ID AD848549 standard; cDNA; 2749 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO846.
PN US2003104536-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatches: 72
Indels: 100
RESULT 888
ID AD841309 standard; cDNA; 2749 BP.
DE Human secreted/transmembrane PRO polypeptide cDNA #30.
PN US2003100497-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatches: 72
Indels: 100
RESULT 889
ID ADE23362 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA, #183.
PN US2002160384-A1.
PD 31-OCT-2002.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatches: 72
Indels: 100
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DE cDNA encoding human PRO polypeptide #193.
PN US2003092108-A1.
PA (GAOW//) FONG S.
PA (GERB//) GERBER H.
PA (GERR//) GERRITSEN M E.
PA (GODD//) GODDARD A.
PA (GODO//) GODOWSKI P J.
PA (GIEM//) GIRMALDI J C.
PA (GURN//) GURNEY A L.
PA (HILL//) HILLAN K J.
PA (KLJA//) KLJAVIN I J.
PA (KUOS//) KUO S S.
PA (NAPJ//) NAPIER M A.
PA (PANJ//) PAN J.
PA (PAON//) PAONI N F.
PA (ROYM//) ROY M A.
PA (SHEL//) SHELTON D L.
PA (STEW//) STEWART T A.
PA (TUMA//) TUMAS D.
PA (WILL//) WILLIAMS P M.
PA (WOOD//) WOOD W I.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Indels: 100
Query Match:
RESULT 890
ID ADE23914 standard; cDNA; 2749 BP.
DE cDNA encoding human PRO polypeptide #193.
PN US2003092110-A1.
PA (GETH//) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Indels: 100
Query Match:
RESULT 891
ID ADE24557 standard; cDNA; 2749 BP.
DE cDNA encoding human PRO polypeptide #193.
PN US2003092111-A1.
PA (GETH//) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Indels: 100
Query Match:
RESULT 892
ID ADD87382 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
PN US2003203439-A1.
PA (GETH//) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Indels: 100
Query Match:
RESULT 893
ID ADE89248 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
PN US2003199062-A1.
PA (GETH//) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Indels: 100
Query Match:
RESULT 894
ID ADE18387 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
PN US2003194794-A1.
PA (GETH//) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Indels: 100
Query Match:
RESULT 895
ID ADE88696 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
PN US2003199054-A1.
PA (GETH//) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Indels: 100
Query Match:
RESULT 896
ID ADE89650 standard; cDNA; 2749 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO846.
PN US2003130181-A1.
PA (ASHK//) ASHKENAZI A J.
PA (BAKE//) BAKER K P.
PA (BOTS//) BOTSTEIN D.
PA (DESN//) DESNOVERS L.
PA (EATO//) EATON D L.
PA (FERR//) FERRARA N.
PA (FILV//) FILVAROFF E.
PA (FONG//) FONG S.
PA (GAOW//) GAO W.
PA (GERB//) GERBER H.
PA (GERR//) GERRITSEN M E.
PA (GODD//) GODDARD A.
PA (GODO//) GODOWSKI P J.
PA (GIEM//) GIRMALDI J C.
PA (GURN//) GURNEY A L.
PA (HILL//) HILLAN K J.
PA (KLJA//) KLJAVIN I J.
PA (KUOS//) KUO S S.
PA (NAPJ//) NAPIER M A.
PA (PANJ//) PAN J.
PA (PAON//) PAONI N F.
PA (ROYM//) ROY M A.
PA (SHEL//) SHELTON D L.
PA (STEW//) STEWART T A.
PA (TUMA//) TUMAS D.
PA (WILL//) WILLIAMS P M.
PA (WOOD//) WOOD W I.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Indels: 100
Query Match:
RESULT 897
ID ADF61290 standard; cDNA; 2749 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO846.
PN US2003195345-A1.
PA (GETH//) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Indels: 100
Query Match:
RESULT 898
ID ADF39982 standard; cDNA; 2749 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO846.
PN US2003198994-A1.
PA (GETH//) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Indels: 100
Query Match:
RESULT 899
ID ADF45778 standard; cDNA; 2749 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO846.
PN US2003195148-A1.
PA (GETH//) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Indels: 100
Query Match:
RESULT 900
ID ADE94716 standard; cDNA; 2749 BP.
DE cDNA encoding human PRO polypeptide #193.
PN US2003199027-A1.
PA (GETH//) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Indels: 100
Query Match:
RESULT 901
ID ADE91127 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
PN US2003199061-A1.
PA (GETH//) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Indels: 100
Query Match:
RESULT 902
ID ADF35642 standard; cDNA; 2749 BP.
DE cDNA encoding human PRO846 polypeptide.
PN US2003194760-A1.
PN 16-OCT-2003.

```


Query Match: 6.78% Indels: 100

RESULT 919
ID ADF46402 standard; cDNA; 2749 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO846.
PN US2003195344-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Indels: 100

Conservative: 25
Mismatch: 72

RESULT 920
ID ADE91722 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003199058-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Indels: 100

Conservative: 25
Mismatch: 72

RESULT 921
ID ADG11892 standard; cDNA; 2749 BP.
DE cDNA encoding human PRO846 polypeptide.
PN US2003228655-A1.
PD 11-DEC-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Indels: 100

Conservative: 25
Mismatch: 72

RESULT 922
ID ADG02301 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
PN US2003207352-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Indels: 100

Conservative: 25
Mismatch: 72

RESULT 923
ID ADG22087 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003207360-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Indels: 100

Conservative: 25
Mismatch: 72

RESULT 924
ID ADG20157 standard; cDNA; 2749 BP.
DE cDNA encoding human PRO polypeptide #193.
PN US2003207376-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Indels: 100

Conservative: 25
Mismatch: 72

RESULT 925
ID ADF98063 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
PN US2003207422-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Indels: 100

Conservative: 25
Mismatch: 72

RESULT 926
ID ADG24280 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003207426-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Indels: 100

Conservative: 25
Mismatch: 72

RESULT 927
ID ADF98634 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
PN US2003208055-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Indels: 100

Conservative: 25
Mismatch: 72

RESULT 928
ID ADG03465 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
PN US2003207351-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Indels: 100

Conservative: 25
Mismatch: 72

RESULT 929
ID ADF99186 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
PN US2003207353-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Indels: 100

Conservative: 25
Mismatch: 72

RESULT 930
ID ADG16771 standard; cDNA; 2749 BP.
DE cDNA encoding human PRO polypeptide #193.
PN US2003207359-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Indels: 100

Conservative: 25
Mismatch: 72

RESULT 931
ID ADG05230 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
PN US2003207375-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Indels: 100

Conservative: 25
Mismatch: 72

RESULT 932
ID ADG19497 standard; cDNA; 2749 BP.
DE cDNA encoding human PRO polypeptide #193.
PN US2003207425-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Indels: 100

Conservative: 25
Mismatch: 72

RESULT 933
ID ADG13334 standard; cDNA; 2749 BP.
DE cDNA encoding human PRO polypeptide #193.
PN US2003207357-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Indels: 100

Conservative: 25
Mismatch: 72

RESULT 934
ID ADG08391 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003207424-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Indels: 100

Conservative: 25
Mismatch: 72

ID ADG15561 standard; cDNA; 2749 BP.
DE CDNA encoding human PRO polypeptide #193.4
PN US2003219885-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 936

ID ADF96959 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
PN US2003207371-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 937

ID ADG06144 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
PN US2003207374-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 938

ID ADG23728 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003207389-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 939

ID ADG04017 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
PN US2003207423-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 940

ID ADG24918 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003207427-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 941

ID ADG07215 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003207350-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 942

ID ADG07767 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003207356-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 943

ID ADG55262 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003207358-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 944

ID ADG60926 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003207390-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 945

ID ADG62030 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003207428-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 946

ID ADG82231 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
PN US2003207358-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 947

ID ADG57470 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003207362-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 948

ID ADG56918 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003207364-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 949

ID ADG55814 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003207365-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 950

ID ADG58574 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003207368-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 951

ID ADG70940 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003207368-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 951

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PN US2003207420-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 952
ID ADG58022 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003207363-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 953
ID ADG51636 standard; cDNA; 2749 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO846.
PN US2003215908-A1.
PD 20-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 954
ID ADG5430 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003207414-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 955
ID ADG50388 standard; cDNA; 2749 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO846.
PN US2003207803-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 956
ID ADG81679 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
PN US2003207805-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 957
ID ADH19762 standard; cDNA; 2749 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO846.
PN US2003228656-A1.
PD 11-DEC-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 958
ID ADH30641 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
PN US2003077723-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 959
ID ADH12008 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003207419-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 960
ID ADG49764 standard; cDNA; 2749 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO846.
PN US2003215905-A1.
PD 20-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 961
ID ADG51636 standard; cDNA; 2749 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO846.
PN US2003215908-A1.
PD 20-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 962
ID ADG5430 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003207414-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 963
ID ADG54158 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003207416-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 964
ID ADG49140 standard; cDNA; 2749 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO846.
PN US2003216305-A1.
PD 20-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 965
ID ADG81127 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
PN US2003194793-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 966
ID ADG56366 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003207366-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 967
ID ADH12632 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003207378-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100

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Percent Similarity: 30.08% Conservative: 25
Best Local Similarity: 19.92% Mismatches: 72
Query Match: 6.78% Indels: 100
RESULT 968
ID ADG48516 standard; cDNA; 2749 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO846.
PN US2003216560-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 30.08% Conservative: 25
Best Local Similarity: 19.92% Mismatches: 72
Query Match: 6.78% Indels: 100
RESULT 969
ID ADH21255 standard; cDNA; 2749 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO846.
PN US2003224358-A1.
PD 04-DEC-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 30.08% Conservative: 25
Best Local Similarity: 19.92% Mismatches: 72
Query Match: 6.78% Indels: 100
RESULT 970
ID ADG61478 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003207429-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 30.08% Conservative: 25
Best Local Similarity: 19.92% Mismatches: 72
Query Match: 6.78% Indels: 100
RESULT 971
ID ADH20295 standard; cDNA; 2749 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO846.
PN US2003219856-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 30.08% Conservative: 25
Best Local Similarity: 19.92% Mismatches: 72
Query Match: 6.78% Indels: 100
RESULT 972
ID ADH28565 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
PN US2003022331-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 30.08% Conservative: 25
Best Local Similarity: 19.92% Mismatches: 72
Query Match: 6.78% Indels: 100
RESULT 973
ID ADG54710 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003207367-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 30.08% Conservative: 25
Best Local Similarity: 19.92% Mismatches: 72
Query Match: 6.78% Indels: 100
RESULT 974
ID ADG59750 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003207369-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 30.08% Conservative: 25
Best Local Similarity: 19.92% Mismatches: 72
Query Match: 6.78% Indels: 100
RESULT 975
ID ADG51012 standard; cDNA; 2749 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO846.
PN US2004005312-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Percent Similarity: 30.08% Conservative: 25
Best Local Similarity: 19.92% Mismatches: 72

Query Match: 6.78% Indels: 100
RESULT 976
ID ADH43492 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #30.
PN US2003224984-A1.
PD 04-DEC-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 30.08% Conservative: 25
Best Local Similarity: 19.92% Mismatches: 72
Query Match: 6.78% Indels: 100
RESULT 977
ID ADG58956 standard; cDNA; 2749 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO846.
PN US2004005657-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Percent Similarity: 30.08% Conservative: 25
Best Local Similarity: 19.92% Mismatches: 72
Query Match: 6.78% Indels: 100
RESULT 978
ID ADG62412 standard; cDNA; 2749 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO846.
PN US2004006219-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Percent Similarity: 30.08% Conservative: 25
Best Local Similarity: 19.92% Mismatches: 72
Query Match: 6.78% Indels: 100
RESULT 979
ID ADI81174 standard; cDNA; 2749 BP.
DE cDNA encoding human PRO polypeptide #193.
PN US2003207361-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 30.08% Conservative: 25
Best Local Similarity: 19.92% Mismatches: 72
Query Match: 6.78% Indels: 100
RESULT 980
ID ADH25437 standard; cDNA; 2749 BP.
DE Human neurotrophin homologue related nucleotide sequence SEQ ID NO:215.
PN EPI386931-A1.
PD 04-FEB-2004.
PA (GETH) GENENTECH INC.
Percent Similarity: 30.08% Conservative: 25
Best Local Similarity: 19.92% Mismatches: 72
Query Match: 6.78% Indels: 100
RESULT 981
ID ADG09917 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2004009548-A1.
PD 15-JAN-2004.
PA (GETH) GENENTECH INC.
Percent Similarity: 30.08% Conservative: 25
Best Local Similarity: 19.92% Mismatches: 72
Query Match: 6.78% Indels: 100
RESULT 982
ID ADI15388 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003207382-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 30.08% Conservative: 25
Best Local Similarity: 19.92% Mismatches: 72
Query Match: 6.78% Indels: 100
RESULT 983
ID ADG09265 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2004009547-A1.
PD 15-JAN-2004.
PA (GETH) GENENTECH INC.
Percent Similarity: 30.08% Conservative: 25
Best Local Similarity: 19.92% Mismatches: 72
Query Match: 6.78% Indels: 100

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RESULT 984
ID AD114720 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003207383-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Conservative: 25
Mismatch: 72
Indels: 100
Query Match:
RESULT 985
ID AD118315 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003207349-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Conservative: 25
Mismatch: 72
Indels: 100
Query Match:
RESULT 986
ID ADJ63596 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2004039164-A1.
PD 26-FEB-2004.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Conservative: 25
Mismatch: 72
Indels: 100
Query Match:
RESULT 987
ID ADJ77491 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
PN US2004038336-A1.
PD 26-FEB-2004.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Conservative: 25
Mismatch: 72
Indels: 100
Query Match:
RESULT 988
ID ADK82837 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #30.
PN US2004043927-A1.
PD 04-MAR-2004.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Conservative: 25
Mismatch: 72
Indels: 100
Query Match:
RESULT 989
ID ADJ65613 standard; cDNA; 2749 BP.
DE cDNA encoding human PRO polypeptide #193.
PN US2004038335-A1.
PD 26-FEB-2004.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Conservative: 25
Mismatch: 72
Indels: 100
Query Match:
RESULT 990
ID ADM27749 standard; cDNA; 2749 BP.
DE cDNA encoding human PRO polypeptide #193.
PN US2004048333-A1.
PD 11-MAR-2004.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Conservative: 25
Mismatch: 72
Indels: 100
Query Match:
RESULT 991
ID ADM17214 standard; cDNA; 2749 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO846.
PN US2004048332-A1.
PD 11-MAR-2004.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Conservative: 25
Mismatch: 72
Indels: 100
Query Match:
RESULT 992
ID ADL07048 standard; cDNA; 2749 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO846.
PN US2004063921-A1.
PD 01-APR-2004.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Conservative: 25
Mismatch: 72
Indels: 100
Query Match:
RESULT 993
ID ADM42473 standard; cDNA; 2749 BP.
DE cDNA encoding human PRO polypeptide #193.
PN US2004058424-A1.
PD 25-MAR-2004.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Conservative: 25
Mismatch: 72
Indels: 100
Query Match:
RESULT 994
ID ADM28335 standard; cDNA; 2749 BP.
DE cDNA encoding human PRO polypeptide #193.
PN US2004077064-A1.
PD 22-APR-2004.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Conservative: 25
Mismatch: 72
Indels: 100
Query Match:
RESULT 995
ID ACC77620 standard; DNA; 3026 BP.
DE Thermus aquaticus mutant DNA polymerase encoding DNA.
PN WO2003025132-A2.
PD 27-MAR-2003.
PA (INVI-) INVITROGEN CORP.
Percent Similarity: 39.31%
Best Local Similarity: 24.83%
Conservative: 42
Mismatch: 99
Indels: 79
Query Match:
RESULT 996
ID ACC77632 standard; DNA; 3026 BP.
DE Thermus aquaticus mutant DNA polymerase encoding DNA.
PN WO2003025132-A2.
PD 27-MAR-2003.
PA (INVI-) INVITROGEN CORP.
Percent Similarity: 39.31%
Best Local Similarity: 24.83%
Conservative: 42
Mismatch: 99
Indels: 79
Query Match:
RESULT 997
ID ACC77632 standard; DNA; 3026 BP.
DE Thermus aquaticus mutant DNA polymerase encoding DNA.
PN WO2003025132-A2.
PD 27-MAR-2003.
PA (INVI-) INVITROGEN CORP.
Percent Similarity: 39.31%
Best Local Similarity: 24.83%
Conservative: 42
Mismatch: 99
Indels: 79
Query Match:
RESULT 998
ID ACC77632 standard; DNA; 3026 BP.
DE Thermus aquaticus mutant DNA polymerase encoding DNA.
PN WO2003025132-A2.
PD 27-MAR-2003.
PA (INVI-) INVITROGEN CORP.
Percent Similarity: 39.31%
Best Local Similarity: 24.83%
Conservative: 42
Mismatch: 99
Indels: 79
Query Match:
RESULT 999
ID ACC77632 standard; DNA; 3026 BP.
DE Thermus aquaticus mutant DNA polymerase encoding DNA.
PN WO2003025132-A2.
PD 27-MAR-2003.
PA (INVI-) INVITROGEN CORP.
Percent Similarity: 39.31%
Best Local Similarity: 24.83%
Conservative: 42
Mismatch: 99
Indels: 79
Query Match:
RESULT 1000
ID ADJ40534 standard; cDNA; 1611 BP.
DE Plant cDNA #1534.
PN US2004016025-A1.
PD 22-JAN-2004.
PA (BUDW/) BUDWORTH P.
PA (MOUG/) MOUGHAMER T.
PA (BRIG/) BRIGGS S P.
PA (COOP/) COOPER B.
PA (GLAZ/) GLAZEBROOK J.
PA (GOFF/) GOFF S A.
PA (KATA/) KATAGIRI F.
PA (KREP/) KREPS J.

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PA (PROV/) PROVART N.
 PA (RICK/) RICK D.
 PA (ZHUT/) ZHU T.
 Percent Similarity: 38.91% Conservative: 24
 Best Local Similarity: 28.87% Mismatches: 87
 Query Match: 6.74% Indels: 60
 RESULT 1002
 ID AD057711 standard; DNA; 1950 BP.
 DE Actinobacillus actinomycetemcomitans immunogenic polypeptide gene #81.
 PN WO2004045499-A2.
 PD 03-JUN-2004.
 PA (UYEL) UNIV FLORIDA.
 Percent Similarity: 37.25% Conservative: 35
 Best Local Similarity: 23.08% Mismatches: 127
 Query Match: 6.74% Indels: 28
 RESULT 1003
 ID ABD14922 standard; DNA; 2496 BP.
 DE Pseudomonas aeruginosa polynucleotide #13526.
 PN US6551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Percent Similarity: 35.91% Conservative: 25
 Best Local Similarity: 26.25% Mismatches: 90
 Query Match: 6.74% Indels: 77
 RESULT 1004
 ID ABD15329 standard; DNA; 2622 BP.
 DE Pseudomonas aeruginosa polynucleotide #13933.
 PN US6551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Percent Similarity: 35.91% Conservative: 25
 Best Local Similarity: 26.25% Mismatches: 90
 Query Match: 6.74% Indels: 77
 RESULT 1005
 ID ABD15222 standard; DNA; 2685 BP.
 DE Pseudomonas aeruginosa polynucleotide #13826.
 PN US6551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Percent Similarity: 35.91% Conservative: 25
 Best Local Similarity: 26.25% Mismatches: 90
 Query Match: 6.74% Indels: 77
 RESULT 1006
 ID AAV02312 standard; CDNA; 3065 BP.
 DE C16N gene for promoting neuron survival and type 1 collagen production.
 PN WO9740150-A1.
 PD 30-OCT-1997.
 PA (SUMU) SUMITOMO PHARM CO LTD.
 Percent Similarity: 30.84% Conservative: 30
 Best Local Similarity: 22.19% Mismatches: 95
 Query Match: 6.74% Indels: 146
 RESULT 1007
 ID ACCT7798 standard; DNA; 3221 BP.
 DE Thermus thermophilus mutant DNA polymerase encoding DNA.
 PN WO2003025132-A2.
 PD 27-MAR-2003.
 PA (INVI-) INVITROGEN CORP.
 Percent Similarity: 36.64% Conservative: 33
 Best Local Similarity: 25.34% Mismatches: 113
 Query Match: 6.74% Indels: 74
 RESULT 1008
 ID ACCT77981 standard; DNA; 3221 BP.
 DE Thermus thermophilus mutant DNA polymerase encoding DNA.
 PN WO2003025132-A2.
 PD 27-MAR-2003.
 PA (INVI-) INVITROGEN CORP.
 Percent Similarity: 36.64% Conservative: 33
 Best Local Similarity: 25.34% Mismatches: 113
 Query Match: 6.74% Indels: 74
 RESULT 1009
 ID ACCT78005 standard; DNA; 3221 BP.
 DE Thermus thermophilus mutant DNA polymerase encoding DNA.
 PN WO2003025132-A2.

PD 27-MAR-2003.
 PA (INVI-) INVITROGEN CORP.
 Percent Similarity: 36.64% Conservative: 33
 Best Local Similarity: 25.34% Mismatches: 113
 Query Match: 6.74% Indels: 74
 RESULT 1010
 ID ACCT77997 standard; DNA; 3221 BP.
 DE Thermus thermophilus mutant DNA polymerase encoding DNA.
 PN WO2003025132-A2.
 PD 27-MAR-2003.
 PA (INVI-) INVITROGEN CORP.
 Percent Similarity: 36.64% Conservative: 33
 Best Local Similarity: 25.34% Mismatches: 113
 Query Match: 6.74% Indels: 74
 RESULT 1011
 ID AA240178 standard; CDNA; 3337 BP.
 DE Mouse C16N-2 coding sequence.
 PN JP11308995-A.
 PD 09-NOV-1999.
 PA (SUMU) SUMITOMO SEIYAKU KK.
 Percent Similarity: 30.84% Conservative: 30
 Best Local Similarity: 22.19% Mismatches: 95
 Query Match: 6.74% Indels: 146
 RESULT 1012
 ID AA244729 standard; CDNA; 3337 BP.
 DE Murine C16N-2 CDNA.
 PN WO200001405-A1.
 PD 13-JAN-2000.
 PA (SUMU) SUMITOMO PHARM CO LTD.
 Percent Similarity: 30.84% Conservative: 30
 Best Local Similarity: 22.19% Mismatches: 95
 Query Match: 6.74% Indels: 146
 RESULT 1013
 ID AA240177 standard; CDNA; 3674 BP.
 DE Mouse C16N-1 coding sequence.
 PN JP11308995-A.
 PD 09-NOV-1999.
 PA (SUMU) SUMITOMO SEIYAKU KK.
 Percent Similarity: 30.84% Conservative: 30
 Best Local Similarity: 22.19% Mismatches: 95
 Query Match: 6.74% Indels: 146
 RESULT 1014
 ID AA244728 standard; CDNA; 3674 BP.
 DE Murine C16N-1 CDNA.
 PN WO200001405-A1.
 PD 13-JAN-2000.
 PA (SUMU) SUMITOMO PHARM CO LTD.
 Percent Similarity: 30.84% Conservative: 30
 Best Local Similarity: 22.19% Mismatches: 95
 Query Match: 6.74% Indels: 146
 RESULT 1015
 ID AAD07024 standard; DNA; 5054 BP.
 DE Pseudomonas putida PHA synthase DNA.
 PN WO200123596-A2.
 PD 05-APR-2001.
 PA (PION-) PIONEER HI-BRED INT INC.
 PA (DUPO) DU PONT DE NEMOURS & CO E I.
 Percent Similarity: 39.16% Conservative: 35
 Best Local Similarity: 25.86% Mismatches: 72
 Query Match: 6.74% Indels: 89
 RESULT 1016
 ID ABA17139 standard; DNA; 32179 BP.
 DE Human nervous system related polynucleotide SEQ ID NO 9470.
 PN WO200159063-A2.
 PD 16-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Percent Similarity: 32.89% Conservative: 31
 Best Local Similarity: 22.59% Mismatches: 79
 Query Match: 6.74% Indels: 123
 RESULT 1017
 Percent Similarity: 36.25% Conservative: 34
 Best Local Similarity: 25.62% Mismatches: 119
 Query Match: 6.74% Indels: 85

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RESULT 1018
ID ABX34289 standard; DNA; 135638 BP.
DE S. atroolivaceus leinamycin biosynthesis gene cluster.
PN WO200271179-A2.
PD 03-OCT-2002.
PA (REGC) UNIV CALIFORNIA.
PA (KYOW) KYOWA HAKKO KOGYO KK.
Percent Similarity: 33
Conservative: 33
Mismatches: 78
Indels: 48
Best Local Similarity: 41.04%
Query Match: 25.47%
Query Match: 6.74%
Query Match: 6.74%
RESULT 1019
ID AAH64966 standard; DNA; 349980 BP.
DE C Glutamicum coding sequence fragment SEQ ID NO: 1.
PN EPI108790-A2.
PD 20-JUN-2001.
PA (KYOW) KYOWA HAKKO KOGYO KK.
Percent Similarity: 39.29%
Conservative: 28
Mismatches: 78
Indels: 41
Best Local Similarity: 25.00%
Query Match: 6.74%
Query Match: 6.74%
RESULT 1020
ID ACD93801 standard; cDNA; 536 BP.
DE Human colon cancer cell expressed cDNA #2213.
PN US2002155438-A1.
PD 24-OCT-2002.
PA (SIMP/) SIMPSON A J G.
PA (NETO/) NETO D D.
PA (BREN/) BRENTANI R R.
Percent Similarity: 34.64%
Conservative: 11
Mismatches: 71
Indels: 46
Best Local Similarity: 28.49%
Query Match: 6.70%
Query Match: 6.70%
Query Match: 6.70%
RESULT 1021
ID ADM94403 standard; cDNA; 1069 BP.
DE Wheat MRP4 ABC transporter cDNA #2.
PN US6677502-B1.
PD 13-JAN-2004.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
PA (PION-) PIONEER HI-BRED INT INC.
Percent Similarity: 37.59%
Conservative: 39
Mismatches: 82
Indels: 94
Best Local Similarity: 23.76%
Query Match: 6.70%
Query Match: 6.70%
RESULT 1022
ID ADJ79603 standard; DNA; 1521 BP.
DE Glyphosphate resistant corn EPSPS DNA with corn codon usage ID10.
PN WO2004009761-A2.
PD 29-JAN-2004.
PA (MONS) MONSANTO TECHNOLOGY LLC.
Percent Similarity: 36.79%
Conservative: 34
Mismatches: 103
Indels: 87
Best Local Similarity: 25.42%
Query Match: 6.70%
Query Match: 6.70%
RESULT 1023
ID ADH76897 standard; cDNA; 1670 BP.
DE Human SOX18 cDNA.
PN US2002142415-A1.
PD 03-OCT-2002.
PA (KOOP/) KOOPMAN P A.
PA (MUSC/) MUSCAT G E O.
Percent Similarity: 34.28%
Conservative: 30
Mismatches: 105
Indels: 81
Best Local Similarity: 23.67%
Query Match: 6.70%
Query Match: 6.70%
RESULT 1024
ID ABD08413 standard; DNA; 1929 BP.
DE Pseudomonas aeruginosa polynucleotide #7017.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Percent Similarity: 36.79%
Conservative: 20
Mismatches: 104
Indels: 45
Best Local Similarity: 28.21%
Query Match: 6.70%
Query Match: 6.70%
RESULT 1025
ID ABD08507 standard; DNA; 1947 BP.
DE Pseudomonas aeruginosa polynucleotide #7111.
PN US6551795-B1.
PD 22-APR-2003.

PA (GENO-) GENOME THERAPEUTICS CORP.
Percent Similarity: 36.75%
Conservative: 20
Mismatches: 104
Indels: 45
Best Local Similarity: 28.21%
Query Match: 6.70%
Query Match: 6.70%
RESULT 1026
ID ADA69772 standard; DNA; 2016 BP.
DE Rice gene, SEQ ID 3095.
PN WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Percent Similarity: 32.14%
Conservative: 23
Mismatches: 98
Indels: 92
Best Local Similarity: 23.93%
Query Match: 6.70%
Query Match: 6.70%
RESULT 1027
ID ADB84163 standard; DNA; 2160 BP.
DE Gene expression estimation method-related DNA sequence #23.
PN WO2003044227-A1.
PD 30-MAY-2003.
PA (NAAG-) NAT INST AGROBIOLOGICAL SCI.
Percent Similarity: 32.14%
Conservative: 23
Mismatches: 98
Indels: 92
Best Local Similarity: 23.93%
Query Match: 6.70%
Query Match: 6.70%
RESULT 1028
ID AAV62155 standard; DNA; 2341 BP.
DE HSV-2 strain SB5 Contig ID 11 DNA sequence.
PN WO9820016-A1.
PD 14-MAY-1998.
PA (SMIK) SMITHKLINE BEECHAM CORP.
Percent Similarity: 34.46%
Conservative: 22
Mismatches: 109
Indels: 86
Best Local Similarity: 27.03%
Query Match: 6.70%
Query Match: 6.70%
RESULT 1029
ID ABK14883 standard; DNA; 2499 BP.
DE DNA encoding Taq DNA polymerase cold-sensitive mutant Cs#3.
PN US6333159-B1.
PD 25-DEC-2001.
PA (UNIW) UNIV WASHINGTON.
Percent Similarity: 41.79%
Conservative: 44
Mismatches: 107
Indels: 57
Best Local Similarity: 26.07%
Query Match: 6.70%
Query Match: 6.70%
RESULT 1030
ID ABA97303 standard; DNA; 2499 BP.
DE Cold sensitive mutant DNA polymerase DNA #3.
PN US6316202-B1.
PD 13-NOV-2001.
PA (UNIW) UNIV WASHINGTON.
Percent Similarity: 41.79%
Conservative: 44
Mismatches: 107
Indels: 57
Best Local Similarity: 26.07%
Query Match: 6.70%
Query Match: 6.70%
RESULT 1031
ID AAV62145 standard; DNA; 2694 BP.
DE HSV-2 strain SB5 Contig ID 90 DNA sequence.
PN WO9820016-A1.
PD 14-MAY-1998.
PA (SMIK) SMITHKLINE BEECHAM CORP.
Percent Similarity: 34.46%
Conservative: 22
Mismatches: 109
Indels: 86
Best Local Similarity: 27.03%
Query Match: 6.70%
Query Match: 6.70%
RESULT 1032
ID ACC78004 standard; DNA; 3221 BP.
DE Thermus thermophilus mutant DNA polymerase encoding DNA.
PN WO2003025132-A2.
PD 27-MAR-2003.
PA (INVT-) INVITROGEN CORP.
Percent Similarity: 36.64%
Conservative: 33
Mismatches: 113
Indels: 74
Best Local Similarity: 25.34%
Query Match: 6.70%
Query Match: 6.70%
RESULT 1033
ID AAK90702 standard; DNA; 3281 BP.
DE Human digestive system antigen genomic sequence SEQ ID NO: 4278.
PN WO200155314-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.

Percent Similarity: 34.23% Conservative: 16
 Best Local Similarity: 28.08% Mismatches: 101
 Query Match: 6.70% Indels: 70
 RESULT 1034
 ID AAK90701 standard; DNA; 3704 BP.
 DE Human digestive system antigen genomic sequence SEQ ID NO: 4277.
 PN WO200155314-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Percent Similarity: 34.23% Conservative: 16
 Best Local Similarity: 28.08% Mismatches: 101
 Query Match: 6.70% Indels: 70
 RESULT 1035
 ID AAL44297 standard; DNA; 8651 BP.
 DE Agromyces mediolanus Y1 operon (C50 carotenoid producing operon).
 PN WO200241833-A2.
 PD 30-MAY-2002.
 PA (CRGI) CARGILL INC.
 Percent Similarity: 34.55% Conservative: 21
 Best Local Similarity: 26.02% Mismatches: 87
 Query Match: 6.70% Indels: 74
 RESULT 1036
 ID AAZ23904 standard; DNA; 49999 BP.
 DE Human LOBO homologue genomic DNA fragment 6.
 PN WO9950284-A2.
 PD 07-OCT-1999.
 PA (ROSE/) ROSENTHAL A.
 Percent Similarity: 36.11% Conservative: 22
 Best Local Similarity: 25.93% Mismatches: 80
 Query Match: 6.70% Indels: 58
 RESULT 1037
 Percent Similarity: 31.61% Conservative: 27
 Best Local Similarity: 23.85% Mismatches: 85
 Query Match: 6.70% Indels: 154
 RESULT 1038
 Percent Similarity: 38.04% Conservative: 29
 Best Local Similarity: 26.67% Mismatches: 106
 Query Match: 6.70% Indels: 52
 RESULT 1039
 Percent Similarity: 38.04% Conservative: 29
 Best Local Similarity: 26.67% Mismatches: 106
 Query Match: 6.70% Indels: 52
 RESULT 1040
 Percent Similarity: 38.04% Conservative: 29
 Best Local Similarity: 26.67% Mismatches: 106
 Query Match: 6.70% Indels: 52
 RESULT 1041
 Percent Similarity: 38.04% Conservative: 29
 Best Local Similarity: 26.67% Mismatches: 106
 Query Match: 6.70% Indels: 52
 RESULT 1042
 Percent Similarity: 38.04% Conservative: 29
 Best Local Similarity: 26.67% Mismatches: 106
 Query Match: 6.70% Indels: 52
 RESULT 1043
 Percent Similarity: 38.04% Conservative: 29
 Best Local Similarity: 26.67% Mismatches: 106
 Query Match: 6.70% Indels: 52
 RESULT 1044
 ID AD122705 standard; DNA; 1052 BP.
 DE S. pristinamycin papM gene SEQ ID NO:1.
 PN WO2004003012-A2.
 PD 08-JAN-2004.
 PA (AVET) AVENTIS PHARMA SA.
 Percent Similarity: 31.87% Conservative: 25
 Best Local Similarity: 22.71% Mismatches: 121
 Query Match: 6.66% Indels: 65
 RESULT 1045
 ID AD122711 standard; DNA; 1052 BP.
 DE S. pristinamycin papM gene G828A mutant.
 PN WO2004003012-A2.
 PD 08-JAN-2004.
 PA (AVET) AVENTIS PHARMA SA.

Percent Similarity: 31.87% Conservative: 25
 Best Local Similarity: 22.71% Mismatches: 121
 Query Match: 6.66% Indels: 65
 RESULT 1046
 ID ABD14793 standard; DNA; 1266 BP.
 DE Pseudomonas aeruginosa polynucleotide #13397.
 PN US5551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Percent Similarity: 32.39% Conservative: 32
 Best Local Similarity: 22.33% Mismatches: 100
 Query Match: 6.66% Indels: 115
 RESULT 1047
 ID ABD1488 standard; DNA; 1359 BP.
 DE Pseudomonas aeruginosa polynucleotide #13492.
 PN US5551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Percent Similarity: 32.39% Conservative: 32
 Best Local Similarity: 22.33% Mismatches: 100
 Query Match: 6.66% Indels: 115
 RESULT 1048
 ID ABD05006 standard; DNA; 1605 BP.
 DE Pseudomonas aeruginosa polynucleotide #3610.
 PN US5551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Percent Similarity: 33.77% Conservative: 24
 Best Local Similarity: 25.97% Mismatches: 105
 Query Match: 6.66% Indels: 101
 RESULT 1049
 ID ACC77989 standard; DNA; 3221 BP.
 DE Thermus thermophilus mutant DNA polymerase encoding DNA.
 PN WO2003025132-A2.
 PD 27-MAR-2003.
 PA (INVI-) INVITROGEN CORP.
 Percent Similarity: 36.84% Conservative: 33
 Best Local Similarity: 25.34% Mismatches: 113
 Query Match: 6.66% Indels: 74
 RESULT 1050
 ID ABD05159 standard; DNA; 3270 BP.
 DE Pseudomonas aeruginosa polynucleotide #3763.
 PN US5551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Percent Similarity: 33.77% Conservative: 24
 Best Local Similarity: 25.97% Mismatches: 105
 Query Match: 6.66% Indels: 101
 RESULT 1051
 ID AAF90037 standard; DNA; 6462 BP.
 DE Nucleotide sequence of a type I polyketide synthase.
 PN WO200140497-A2.
 PD 07-JUN-2001.
 PA (AVET) AVENTIS PHARMA SA.
 Percent Similarity: 36.63% Conservative: 40
 Best Local Similarity: 23.43% Mismatches: 89
 Query Match: 6.66% Indels: 104
 RESULT 1052
 ID AAS32623 standard; DNA; 10646 BP.
 DE Human genomic DNA for novel endocrine antigen, SEQ ID NO 577.
 PN WO200155319-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Percent Similarity: 39.23% Conservative: 19
 Best Local Similarity: 30.14% Mismatches: 69
 Query Match: 6.66% Indels: 59
 RESULT 1053
 ID AAA81519 standard; DNA; 16677 BP.
 DE N. meningitidis partial DNA sequence gnm_66 SEQ ID NO:66.
 PN WO200022430-A2.
 PD 20-APR-2000.
 PA (CHIR) CHIRON CORP.
 Percent Similarity: 37.80% Conservative: 33

PD 17-OCT-2002.			
PA (ISIS-) ISIS INNOVATION LTD.			
Percent Similarity:	32.26%	Conservative:	20
Best Local Similarity:	25.81%	Mismatches:	96
Query Match:	6.63%	Indels:	114
RESULT 1063			
ID AAN90395 standard; DNA; 1905 BP.			
DE Genomic/cDNA composite DNA of bovine Mullerian inhibiting substance.			
PN WO9006695-A.			
PD 27-JUL-1989.			
PA (BIOJ) BIOGEN INC.			
Percent Similarity:	35.28%	Conservative:	30
Best Local Similarity:	25.57%	Mismatches:	123
Query Match:	6.63%	Indels:	77
RESULT 1064			
ID ACT77602 standard; DNA; 3026 BP.			
DE Thermus aquaticus mutant DNA polymerase encoding DNA.			
PN WO200302532-A2.			
PD 27-MAR-2003.			
PA (INVI-) INVITROGEN CORP.			
Percent Similarity:	39.31%	Conservative:	42
Best Local Similarity:	24.83%	Mismatches:	99
Query Match:	6.63%	Indels:	79
RESULT 1065			
ID ACT77583 standard; DNA; 3026 BP.			
DE Thermus aquaticus mutant DNA polymerase encoding DNA.			
PN WO200302532-A2.			
PD 27-MAR-2003.			
PA (INVI-) INVITROGEN CORP.			
Percent Similarity:	42.09%	Conservative:	43
Best Local Similarity:	26.62%	Mismatches:	109
Query Match:	6.63%	Indels:	53
RESULT 1066			
ID ABL27024 standard; DNA; 4706 BP.			
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 32545.			
PN WO200171042-A2.			
PD 27-SEP-2001.			
PA (PEKS) PE CORP NY.			
Percent Similarity:	35.80%	Conservative:	18
Best Local Similarity:	28.40%	Mismatches:	102
Query Match:	6.63%	Indels:	55
RESULT 1067			
ID ADP21336 standard; DNA; 8374 BP.			
DE Gene CACNA1C for screening for cardiac therapeutic preparation.			
PN WO2004050894-A2.			
PD 17-JUN-2004.			
PA (ARTE-) ARTESIAN THERAPEUTICS INC.			
Percent Similarity:	32.52%	Conservative:	30
Best Local Similarity:	23.40%	Mismatches:	96
Query Match:	6.63%	Indels:	127
RESULT 1068			
ID ADG75175 standard; DNA; 9369 BP.			
DE Human herpesvirus 2 strain HG52 UL36 DNA - SEQ ID 247.			
PN WO2003086308-A2.			
PD 23-OCT-2003.			
PA (CORI-) CORIXA CORP.			
Percent Similarity:	34.46%	Conservative:	22
Best Local Similarity:	27.03%	Mismatches:	109
Query Match:	6.63%	Indels:	86
RESULT 1069			
ID ADG75118 standard; DNA; 9369 BP.			
DE Human herpesvirus 2 UL36 ORF DNA - SEQ ID 190.			
PN WO2003086308-A2.			
PD 23-OCT-2003.			
PA (CORI-) CORIXA CORP.			
Percent Similarity:	34.46%	Conservative:	22
Best Local Similarity:	27.03%	Mismatches:	109
Query Match:	6.63%	Indels:	86
RESULT 1070			
ID ADG75118 standard; DNA; 9369 BP.			
DE Human herpesvirus 2 UL36 ORF DNA - SEQ ID 190.			
PN WO2003086308-A2.			
PD 23-OCT-2003.			
PA (CORI-) CORIXA CORP.			
Percent Similarity:	34.46%	Conservative:	22
Best Local Similarity:	27.03%	Mismatches:	109
Query Match:	6.63%	Indels:	86
RESULT 1071			
ID ADG75118 standard; DNA; 9369 BP.			
DE Human herpesvirus 2 UL36 ORF DNA - SEQ ID 190.			
PN WO2003086308-A2.			
PD 23-OCT-2003.			
PA (CORI-) CORIXA CORP.			
Percent Similarity:	34.46%	Conservative:	22
Best Local Similarity:	27.03%	Mismatches:	109
Query Match:	6.63%	Indels:	86
RESULT 1070			
ID ADG75118 standard; DNA; 9369 BP.			
DE Human herpesvirus 2 UL36 ORF DNA - SEQ ID 190.			
PN WO2003086308-A2.			
PD 23-OCT-2003.			
PA (CORI-) CORIXA CORP.			
Percent Similarity:	34.46%	Conservative:	22
Best Local Similarity:	27.03%	Mismatches:	109
Query Match:	6.63%	Indels:	86
RESULT 1071			
ID ADG75118 standard; DNA; 9369 BP.			
DE Human herpesvirus 2 UL36 ORF DNA - SEQ ID 190.			
PN WO2003086308-A2.			
PD 23-OCT-2003.			
PA (CORI-) CORIXA CORP.			
Percent Similarity:	34.46%	Conservative:	22
Best Local Similarity:	27.03%	Mismatches:	109
Query Match:	6.63%	Indels:	86
RESULT 1071			
ID ADG75118 standard; DNA; 9369 BP.			
DE Human herpesvirus 2 UL36 ORF DNA - SEQ ID 190.			
PN WO2003086308-A2.			
PD 23-OCT-2003.			
PA (CORI-) CORIXA CORP.			
Percent Similarity:	34.46%	Conservative:	22
Best Local Similarity:	27.03%	Mismatches:	109
Query Match:	6.63%	Indels:	86
RESULT 1071			
ID ADG75118 standard; DNA; 9369 BP.			
DE Human herpesvirus 2 UL36 ORF DNA - SEQ ID 190.			
PN WO2003086308-A2.			
PD 23-OCT-2003.			
PA (CORI-) CORIXA CORP.			
Percent Similarity:			

Percent Similarity: 40.54% Conservative: 17
 Best Local Similarity: 29.05% Mismatches: 54
 Query Match: 6.63% Indels: 34
 RESULT 1072
 ID ABD10237 standard; DNA; 969 BP.
 DE Pseudomonas aeruginosa polynucleotide #8841.
 PN US6551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Percent Similarity: 34.52% Conservative: 15
 Best Local Similarity: 26.90% Mismatches: 83
 Query Match: 6.59% Indels: 46
 RESULT 1073
 ID ABD10349 standard; DNA; 1008 BP.
 DE Pseudomonas aeruginosa polynucleotide #8953.
 PN US6551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Percent Similarity: 34.52% Conservative: 15
 Best Local Similarity: 26.90% Mismatches: 83
 Query Match: 6.59% Indels: 46
 RESULT 1074
 ID AAS54191 standard; DNA; 1014 BP.
 DE Pseudomonas aeruginosa DNA for cellular proliferation protein #322.
 PN WO200170955-A2.
 PD 27-SEP-2001.
 PA (ELIT-) ELITRA PHARM INC.
 Percent Similarity: 34.63% Conservative: 22
 Best Local Similarity: 25.11% Mismatches: 85
 Query Match: 6.59% Indels: 66
 RESULT 1075
 ID ACA42441 standard; DNA; 1014 BP.
 DE Prokaryotic essential gene #24098.
 PN WO200277183-A2.
 PD 03-OCT-2002.
 PA (ELIT-) ELITRA PHARM INC.
 Percent Similarity: 34.63% Conservative: 22
 Best Local Similarity: 25.11% Mismatches: 85
 Query Match: 6.59% Indels: 66
 RESULT 1076
 ID ABD01581 standard; DNA; 1035 BP.
 DE Pseudomonas aeruginosa polynucleotide #185.
 PN US6551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Percent Similarity: 34.63% Conservative: 22
 Best Local Similarity: 25.11% Mismatches: 85
 Query Match: 6.59% Indels: 66
 RESULT 1077
 ID ABD01558 standard; DNA; 1074 BP.
 DE Pseudomonas aeruginosa polynucleotide #162.
 PN US6551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Percent Similarity: 34.63% Conservative: 22
 Best Local Similarity: 25.11% Mismatches: 85
 Query Match: 6.59% Indels: 66
 RESULT 1078
 ID ACA23686 standard; DNA; 1263 BP.
 DE Prokaryotic essential gene #5343.
 PN WO200277183-A2.
 PD 03-OCT-2002.
 PA (ELIT-) ELITRA PHARM INC.
 Percent Similarity: 34.63% Conservative: 37
 Best Local Similarity: 22.52% Mismatches: 82
 Query Match: 6.59% Indels: 54
 RESULT 1079
 ID ABD13880 standard; DNA; 1293 BP.
 DE Pseudomonas aeruginosa polynucleotide #12484.
 PN US6551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Percent Similarity: 31.03% Conservative: 23

Best Local Similarity: 23.82% Mismatches: 88
 Query Match: 6.59% Indels: 132
 RESULT 1080
 ID ABD14385 standard; DNA; 1422 BP.
 DE Pseudomonas aeruginosa polynucleotide #12989.
 PN US6551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Percent Similarity: 31.03% Conservative: 23
 Best Local Similarity: 23.82% Mismatches: 88
 Query Match: 6.59% Indels: 132
 RESULT 1081
 ID ABD01554 standard; DNA; 1455 BP.
 DE Pseudomonas aeruginosa polynucleotide #158.
 PN US6551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Percent Similarity: 34.63% Conservative: 22
 Best Local Similarity: 25.11% Mismatches: 85
 Query Match: 6.59% Indels: 66
 RESULT 1082
 ID ABX70924 standard; cDNA; 1696 BP.
 DE Novel human cDNA sequence #149.
 PN WO200281731-A2.
 PD 17-OCT-2002.
 PA (HYSE-) HYSEQ INC.
 Percent Similarity: 34.55% Conservative: 23
 Best Local Similarity: 26.18% Mismatches: 81
 Query Match: 6.59% Indels: 100
 RESULT 1083
 ID AAN70309 standard; cDNA; 1814 BP.
 DE Sequence of bovine mullerian inhibiting substance (MIS) cDNA.
 PN EP221761-A.
 PD 13-MAY-1987.
 PA (BIOJ) BIOGEN NV.
 Percent Similarity: 32.03% Conservative: 22
 Best Local Similarity: 24.84% Mismatches: 99
 Query Match: 6.59% Indels: 109
 RESULT 1084
 ID AAS87226 standard; cDNA; 2327 BP.
 DE DNA encoding novel human diagnostic protein #23030.
 PN WO200175067-A2.
 PD 11-OCT-2001.
 PA (HYSE-) HYSEQ INC.
 Percent Similarity: 32.92% Conservative: 18
 Best Local Similarity: 25.51% Mismatches: 101
 Query Match: 6.59% Indels: 63
 RESULT 1085
 ID AAX87254 standard; cDNA; 2413 BP.
 DE cDNA clone encoding human PRO201, amplified in tumour cells.
 PN WO9935170-A2.
 PD 15-JUL-1999.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 32.92% Conservative: 18
 Best Local Similarity: 25.51% Mismatches: 101
 Query Match: 6.59% Indels: 63
 RESULT 1086
 ID AAZ32137 standard; cDNA; 2413 BP.
 DE Human PRO201 (Nsp1) protein encoding cDNA clone DNA30676.
 PN WO9954467-A1.
 PD 28-OCT-1999.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 32.92% Conservative: 18
 Best Local Similarity: 25.51% Mismatches: 101
 Query Match: 6.59% Indels: 63
 RESULT 1087
 ID AAZ89573 standard; cDNA; 2413 BP.
 DE Human PRO201 cDNA.
 PN US6051403-A.
 PD 18-APR-2000.
 PA (GETH) GENENTECH INC.

Percent Similarity: 32.92% Conservative: 18
Best Local Similarity: 25.51% Mismatches: 101
Query Match: 6.59% Indels: 63
RESULT 1088
ID AA289585 standard; cDNA; 2413 BP.
DE Human PRO201 cDNA.
FN US6051690-A.
PD 18-APR-2000.
PA (GETH) GENENTECH INC.
Percent Similarity: 32.92% Conservative: 18
Best Local Similarity: 25.51% Mismatches: 101
Query Match: 6.59% Indels: 63
RESULT 1089
ID AAA46900 standard; cDNA; 2413 BP.
DE cDNA encoding novel polypeptide PRO201.
FN WO200037640-A2.
PD 29-JUN-2000.
PA (GETH) GENENTECH INC.
Percent Similarity: 32.92% Conservative: 18
Best Local Similarity: 25.51% Mismatches: 101
Query Match: 6.59% Indels: 63
RESULT 1090
ID ADJ58630 standard; cDNA; 2413 BP.
DE Human DNA30676 cDNA encoding PRO201 (Nspl) protein.
FN US2003191283-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 32.92% Conservative: 18
Best Local Similarity: 25.51% Mismatches: 101
Query Match: 6.59% Indels: 63
RESULT 1091
ID AAV63400 standard; DNA; 2507 BP.
DE DNA sequence encoding a DNA polymerase enzyme.
FN US5837450-A.
PD 17-NOV-1998.
PA (THIR-) THIRD WAVE TECHNOLOGIES INC.
Percent Similarity: 40.43% Conservative: 40
Best Local Similarity: 25.92% Mismatches: 115
Query Match: 6.59% Indels: 52
RESULT 1092
ID ABD10528 standard; DNA; 2511 BP.
DE Pseudomonas aeruginosa polynucleotide #9132.
FN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Percent Similarity: 34.52% Conservative: 15
Best Local Similarity: 26.90% Mismatches: 83
Query Match: 6.59% Indels: 46
RESULT 1093
ID ADD69661 standard; cDNA; 2846 BP.
DE Human REMAP cDNA - SEQ ID 90.
FN WO2003048305-A2.
PD 12-JUN-2003.
PA (INCY-) INCYTE GENOMICS INC.
Percent Similarity: 37.83% Conservative: 30
Best Local Similarity: 24.78% Mismatches: 69
Query Match: 6.59% Indels: 74
RESULT 1094
ID AAA38444 standard; DNA; 2893 BP.
DE Human desmin gene 5' flanking region, including the promoter region.
FN EP999278-A1.
PD 10-MAY-2000.
PA (UYPA-) UNIV PARIS VII.
Percent Similarity: 33.33% Conservative: 41
Best Local Similarity: 21.02% Mismatches: 106
Query Match: 6.59% Indels: 116
RESULT 1095
ID ACC77986 standard; DNA; 3221 BP.
DE Thermus thermophilus mutant DNA polymerase encoding DNA.
FN WO2003025132-A2.
PD 27-MAR-2003.
PA (INVI-) INVITROGEN CORP.
Percent Similarity: 36.64% Conservative: 34
Best Local Similarity: 25.00% Mismatches: 113
Query Match: 6.59% Indels: 74
RESULT 1096
ID ACC77950 standard; DNA; 3221 BP.
DE Thermus thermophilus mutant DNA polymerase encoding DNA.
FN WO2003025132-A2.
PD 27-MAR-2003.
PA (INVI-) INVITROGEN CORP.
Percent Similarity: 36.64% Conservative: 34
Best Local Similarity: 25.00% Mismatches: 113
Query Match: 6.59% Indels: 74
RESULT 1097
ID ACC77982 standard; DNA; 3221 BP.
DE Thermus thermophilus mutant DNA polymerase encoding DNA.
FN WO2003025132-A2.
PD 27-MAR-2003.
PA (INVI-) INVITROGEN CORP.
Percent Similarity: 36.64% Conservative: 34
Best Local Similarity: 25.00% Mismatches: 113
Query Match: 6.59% Indels: 74
RESULT 1098
ID ACC77982 standard; DNA; 3221 BP.
DE Thermus thermophilus mutant DNA polymerase encoding DNA.
FN WO2003025132-A2.
PD 27-MAR-2003.
PA (INVI-) INVITROGEN CORP.
Percent Similarity: 36.64% Conservative: 34
Best Local Similarity: 25.00% Mismatches: 113
Query Match: 6.59% Indels: 74
RESULT 1099
ID ADQ23554 standard; DNA; 3289 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 6374.
FN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Percent Similarity: 32.78% Conservative: 25
Best Local Similarity: 24.50% Mismatches: 85
Query Match: 6.59% Indels: 118
RESULT 1100
ID ABK84417 standard; cDNA; 3633 BP.
DE Human cDNA differentially expressed in granulocytic cells #988.
FN WO200228999-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Percent Similarity: 38.80% Conservative: 39
Best Local Similarity: 23.20% Mismatches: 97
Query Match: 6.59% Indels: 57
RESULT 1101
ID ABL30051 standard; DNA; 4567 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 41626.
FN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Percent Similarity: 39.64% Conservative: 27
Best Local Similarity: 27.48% Mismatches: 77
Query Match: 6.59% Indels: 57
RESULT 1102
ID ADN41761 standard; DNA; 22459 BP.
DE Novel human secreted protein polynucleotide seqid 883.
FN US200404191-A1.
PD 04-MAR-2004.
PA (FISC/) FISCHER C L.
PA (ROSE/) ROSEN C A.
PA (SOPP/) SOPPET D R.
PA (RUBE/) RUBEN S M.
PA (KYAW/) KYAW H.
PA (LIYV/) LI Y.
PA (ZENG/) ZENG Z.
PA (LAF/) LAFLEUR D W.
PA (MOOR/) MOORE P A.
PA (SHIY/) SHI Y.
PA (OLSE/) OLSEN H.
PA (EBNE/) EBNER R.

Best Local Similarity: 25.34% Mismatches: 113
Query Match: 6.59% Indels: 74
RESULT 1096
ID ACC77953 standard; DNA; 3221 BP.
DE Thermus thermophilus mutant DNA polymerase encoding DNA.
FN WO2003025132-A2.
PD 27-MAR-2003.
PA (INVI-) INVITROGEN CORP.
Percent Similarity: 36.64% Conservative: 34
Best Local Similarity: 25.00% Mismatches: 113
Query Match: 6.59% Indels: 74
RESULT 1097
ID ACC77950 standard; DNA; 3221 BP.
DE Thermus thermophilus mutant DNA polymerase encoding DNA.
FN WO2003025132-A2.
PD 27-MAR-2003.
PA (INVI-) INVITROGEN CORP.
Percent Similarity: 36.64% Conservative: 34
Best Local Similarity: 25.00% Mismatches: 113
Query Match: 6.59% Indels: 74
RESULT 1098
ID ACC77982 standard; DNA; 3221 BP.
DE Thermus thermophilus mutant DNA polymerase encoding DNA.
FN WO2003025132-A2.
PD 27-MAR-2003.
PA (INVI-) INVITROGEN CORP.
Percent Similarity: 36.64% Conservative: 34
Best Local Similarity: 25.00% Mismatches: 113
Query Match: 6.59% Indels: 74
RESULT 1099
ID ADQ23554 standard; DNA; 3289 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 6374.
FN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Percent Similarity: 32.78% Conservative: 25
Best Local Similarity: 24.50% Mismatches: 85
Query Match: 6.59% Indels: 118
RESULT 1100
ID ABK84417 standard; cDNA; 3633 BP.
DE Human cDNA differentially expressed in granulocytic cells #988.
FN WO200228999-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Percent Similarity: 38.80% Conservative: 39
Best Local Similarity: 23.20% Mismatches: 97
Query Match: 6.59% Indels: 57
RESULT 1101
ID ABL30051 standard; DNA; 4567 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 41626.
FN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Percent Similarity: 39.64% Conservative: 27
Best Local Similarity: 27.48% Mismatches: 77
Query Match: 6.59% Indels: 57
RESULT 1102
ID ADN41761 standard; DNA; 22459 BP.
DE Novel human secreted protein polynucleotide seqid 883.
FN US200404191-A1.
PD 04-MAR-2004.
PA (FISC/) FISCHER C L.
PA (ROSE/) ROSEN C A.
PA (SOPP/) SOPPET D R.
PA (RUBE/) RUBEN S M.
PA (KYAW/) KYAW H.
PA (LIYV/) LI Y.
PA (ZENG/) ZENG Z.
PA (LAF/) LAFLEUR D W.
PA (MOOR/) MOORE P A.
PA (SHIY/) SHI Y.
PA (OLSE/) OLSEN H.
PA (EBNE/) EBNER R.

PA (BIRSE/) BIRSE C E.
 Percent Similarity: 39.73%
 Best Local Similarity: 29.45%
 Query Match: 6.59%
 RESULT 1103
 ID ABV99730 standard; cDNA; 30350 BP.
 DE Human Ras-like protein encoding cDNA.
 Percent Similarity: 36.03%
 Best Local Similarity: 28.31%
 Query Match: 6.59%
 RESULT 1104
 ID ABZ66810 standard; DNA; 37116 BP.
 DE Orthomyxovirin biosynthetic gene cluster SEQ ID NO 279.
 PN WO200279505-A2.
 PD 10-OCT-2002.
 PA (ECOP-) ECOPIA BIOSCIENCES INC.
 Percent Similarity: 33.58%
 Best Local Similarity: 28.30%
 Query Match: 6.59%
 RESULT 1105
 ID AAAL1992 standard; DNA; 37856 BP.
 DE S. cellulosum DNA encoding polyketide and hereropolyketide enzymes.
 PN DE19846493-A1.
 PD 13-APR-2000.
 PA (GBPB-) GES BIOTECHNOLOGISCHE FORSCHUNG MBH.
 Percent Similarity: 37.27%
 Best Local Similarity: 25.83%
 Query Match: 6.59%
 RESULT 1106
 ID ADM45913 standard; DNA; 84428 BP.
 DE Streptomyces mycarofaciens midcamycin polyketide synthetase DNA.
 PN JP2004049100-A.
 PD 19-FEB-2004.
 PA (MBIJ-) MBIJI SEIKA KAISHA LTD.
 Percent Similarity: 33.33%
 Best Local Similarity: 25.17%
 Query Match: 6.59%
 RESULT 1107
 ID AAS08693 standard; DNA; 109519 BP.
 DE Micromonospora DNA encoding biosynthetic enzymes for Everninomycin.
 PN WO2004048598-A2.
 PD 07-AUG-2003.
 PA (GENE-) GENE LOGIC INC.
 Percent Similarity: 33.83%
 Best Local Similarity: 23.74%
 Query Match: 6.55%
 RESULT 1110
 ID ADD40759 standard; cDNA; 3885 BP.
 DE Human tenascin-W coding sequence.
 PN WO2003080663-A2.
 PD 02-OCT-2003.
 PA (NOVS-) NOVARTIS FORSCHUNGSSSTIFTUNG ZWEIGNIEDERL.
 Percent Similarity: 35.88%
 Best Local Similarity: 27.57%
 Query Match: 6.55%
 RESULT 1112
 ID ADOL19282 standard; DNA; 4750 BP.
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 2101.
 PN WO2004048938-A2.
 PD 10-JUN-2004.
 PA (PROT-) PROTEIN DESIGN LABS INC.
 Percent Similarity: 35.88%
 Best Local Similarity: 27.57%
 Query Match: 6.55%
 RESULT 1113
 ID ABK84242 standard; cDNA; 43599 BP.
 DE Human cDNA differentially expressed in granulocytic cells #813.
 PN WO200228999-A2.
 PD 11-APR-2002.
 PA (GENE-) GENE LOGIC INC.
 Percent Similarity: 35.61%
 Best Local Similarity: 24.62%

Best Local Similarity: 27.34%
 Query Match: 6.59%
 Mismatches: 93
 Indels: 76
 ID ADL08116 standard; DNA; 160361 BP.
 DE Human gene associated with low HDL-C FAPB-3.
 PN US2004043389-A1.
 PD 04-MAR-2004.
 PA (VITI-) VITIVITY INC.
 Percent Similarity: 40.43%
 Best Local Similarity: 29.08%
 Query Match: 6.59%
 RESULT 1117
 ID AC445126 standard; DNA; 2487 BP.
 DE Prokaryotic essential gene #26783.
 PN WO20027183-A2.
 PD 03-OCT-2002.
 PA (ELIT-) ELITRA PHARM INC.
 Percent Similarity: 35.86%
 Best Local Similarity: 23.03%
 Query Match: 6.55%
 RESULT 1118
 ID ABK62569 standard; cDNA; 3730 BP.
 DE Rat sequence differentially expressed in response to a hepatotoxin #476.
 PN WO200210453-A2.
 PD 07-FEB-2002.
 PA (GENE-) GENE LOGIC INC.
 Percent Similarity: 33.83%
 Best Local Similarity: 23.74%
 Query Match: 6.55%
 RESULT 1119
 ID ADS8760 standard; DNA; 3730 BP.
 DE Toxicity-related gene, SEQ ID 3786.
 PN WO2003064624-A2.
 PD 07-AUG-2003.
 PA (GENE-) GENE LOGIC INC.
 Percent Similarity: 33.83%
 Best Local Similarity: 23.74%
 Query Match: 6.55%
 RESULT 1120
 ID ADP71852 standard; DNA; 3730 BP.
 DE Renal toxin progression gene marker #441.
 PN WO2004048598-A2.
 PD 10-JUN-2004.
 PA (GENE-) GENE LOGIC INC.
 Percent Similarity: 33.83%
 Best Local Similarity: 23.74%
 Query Match: 6.55%
 RESULT 1121
 ID ADD40759 standard; cDNA; 3885 BP.
 DE Human tenascin-W coding sequence.
 PN WO2003080663-A2.
 PD 02-OCT-2003.
 PA (NOVS-) NOVARTIS FORSCHUNGSSSTIFTUNG ZWEIGNIEDERL.
 Percent Similarity: 35.88%
 Best Local Similarity: 27.57%
 Query Match: 6.55%
 RESULT 1122
 ID ADOL19282 standard; DNA; 4750 BP.
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 2101.
 PN WO2004048938-A2.
 PD 10-JUN-2004.
 PA (PROT-) PROTEIN DESIGN LABS INC.
 Percent Similarity: 35.88%
 Best Local Similarity: 27.57%
 Query Match: 6.55%
 RESULT 1123
 ID ABK84242 standard; cDNA; 43599 BP.
 DE Human cDNA differentially expressed in granulocytic cells #813.
 PN WO200228999-A2.
 PD 11-APR-2002.
 PA (GENE-) GENE LOGIC INC.
 Percent Similarity: 35.61%
 Best Local Similarity: 24.62%

Query Match:	6.55%	Indels:	69
RESULT 1124			
ID ADE86070 standard; DNA; 47988 BP.			
DE Streptomyces hygroscopicus non-ribosomal peptide synthetase complex DNA.			
PN WO2003082309-A1.			
PD 09-OCT-2003.			
PA (AMHP) WYETH.			
Percent Similarity:	38.10%	Conservative:	18
Best Local Similarity:	28.57%	Mismatches:	83
Query Match:	6.55%	Indels:	34
RESULT 1125			
ID ABD02013 standard; DNA; 849 BP.			
DE Pseudomonas aeruginosa polynucleotide #617.			
PN US651795-B1.			
PD 22-APR-2003.			
PA (GENO-) GENOME THERAPEUTICS CORP.			
Percent Similarity:	35.29%	Conservative:	13
Best Local Similarity:	26.80%	Mismatches:	46
Query Match:	6.52%	Indels:	53
RESULT 1126			
ID AAD11173 standard; DNA; 1053 BP.			
DE Pseudomonas stutzeri open reading frame-P (ORF-P) DNA.			
PN WO200153309-A1.			
PD 26-JUL-2001.			
PA (IDAH-) IDAHO RES FOUND INC.			
PA (PASZ-) PASZCZYNSKI A.			
PA (SEBA-) SEBAT J L.			
Percent Similarity:	38.24%	Conservative:	21
Best Local Similarity:	29.41%	Mismatches:	88
Query Match:	6.52%	Indels:	60
RESULT 1127			
ID ADH76980 standard; DNA; 1402 BP.			
DE Human SOX18 related DNA.			
PN US2002142415-A1.			
PD 03-OCT-2002.			
PA (KOOP/) KOOPMAN P A.			
PA (MUSC/) MUSCAT G E O.			
Percent Similarity:	35.76%	Conservative:	37
Best Local Similarity:	22.92%	Mismatches:	109
Query Match:	6.52%	Indels:	78
RESULT 1128			
ID ABD04496 standard; DNA; 1575 BP.			
DE Pseudomonas aeruginosa polynucleotide #3100.			
PN US6551795-B1.			
PD 22-APR-2003.			
PA (GENO-) GENOME THERAPEUTICS CORP.			
Percent Similarity:	40.00%	Conservative:	23
Best Local Similarity:	29.55%	Mismatches:	90
Query Match:	6.52%	Indels:	42
RESULT 1129			
ID ABD17609 standard; DNA; 1866 BP.			
DE Pseudomonas aeruginosa polynucleotide #16213.			
PN US6551795-B1.			
PD 22-APR-2003.			
PA (GENO-) GENOME THERAPEUTICS CORP.			
Percent Similarity:	37.37%	Conservative:	35
Best Local Similarity:	25.26%	Mismatches:	80
Query Match:	6.52%	Indels:	102
RESULT 1130			
ID ABD04585 standard; DNA; 1956 BP.			
DE Pseudomonas aeruginosa polynucleotide #3189.			
PN US6551795-B1.			
PD 22-APR-2003.			
PA (GENO-) GENOME THERAPEUTICS CORP.			
Percent Similarity:	40.00%	Conservative:	23
Best Local Similarity:	29.55%	Mismatches:	90
Query Match:	6.52%	Indels:	42
RESULT 1131			
ID ADB63152 standard; cDNA; 2082 BP.			
DE Human cDNA encoding clone SPLEN20043460.			
PN EPI308459-A2.			
PD 07-MAY-2003.			
PA (HELI-) HELIX RES INST.			
Query Match:	6.52%	Indels:	42
RESULT 1132			
ID ABD02082 standard; DNA; 2379 BP.			
DE Pseudomonas aeruginosa polynucleotide #686.			
PN US6551795-B1.			
PD 22-APR-2003.			
PA (GENO-) GENOME THERAPEUTICS CORP.			
Percent Similarity:	34.24%	Conservative:	32
Best Local Similarity:	23.39%	Mismatches:	87
Query Match:	6.52%	Indels:	107
RESULT 1133			
ID ABD02092 standard; DNA; 2499 BP.			
DE Pseudomonas aeruginosa polynucleotide #696.			
PN US6551795-B1.			
PD 22-APR-2003.			
PA (GENO-) GENOME THERAPEUTICS CORP.			
Percent Similarity:	34.24%	Conservative:	32
Best Local Similarity:	23.39%	Mismatches:	87
Query Match:	6.52%	Indels:	107
RESULT 1134			
ID ADI21750 standard; cDNA; 3212 BP.			
DE Novel human protein cDNA #9.			
PN WO2003025148-A2.			
PD 27-MAR-2003.			
PA (HYSE-) HYSEQ INC.			
Percent Similarity:	34.92%	Conservative:	21
Best Local Similarity:	26.59%	Mismatches:	83
Query Match:	6.52%	Indels:	82
RESULT 1135			
ID AAI57998 standard; cDNA; 4071 BP.			
DE Human polynucleotide SEQ ID NO 201.			
PN WO200153312-A1.			
PD 26-JUL-2001.			
PA (HYSE-) HYSEQ INC.			
Percent Similarity:	38.63%	Conservative:	26
Best Local Similarity:	27.47%	Mismatches:	70
Query Match:	6.52%	Indels:	74
RESULT 1136			
ID ADR07615 standard; DNA; 4989 BP.			
DE Novel coding sequence (useful for identifying genetic disorders) #681.			
PN WO2003054152-A2.			
PD 03-JUL-2003.			
PA (HYSE-) HYSEQ INC.			
Percent Similarity:	49.30%	Conservative:	8
Best Local Similarity:	38.03%	Mismatches:	24
Query Match:	6.52%	Indels:	12
RESULT 1137			
ID AB11939 standard; cDNA; 7335 BP.			
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 30299.			
PN WO200171042-A2.			
PD 27-SEP-2001.			
PA (PEKE) PE CORP NY.			
Percent Similarity:	34.27%	Conservative:	34
Best Local Similarity:	22.38%	Mismatches:	83
Query Match:	6.52%	Indels:	106
RESULT 1138			
ID AAH98395 standard; cDNA; 8836 BP.			
DE Human EST-derived coding sequence SEQ ID NO: 252.			
PN WO200154477-A2.			
PD 02-AUG-2001.			
PA (HYSE-) HYSEQ INC.			
Percent Similarity:	32.74%	Conservative:	27
Best Local Similarity:	24.78%	Mismatches:	90
Query Match:	6.52%	Indels:	138
RESULT 1139			
ID AAS36759 standard; DNA; 9745 BP.			
DE Human cardiovascular system antigen genomic DNA SEQ ID NO 2959.			
PN WO200155321-A2.			
PD 02-AUG-2001.			
PA (HUMA-) HUMAN GENOME SCI INC.			
Query Match:	6.52%	Indels:	138

Percent Similarity: 34.82% Conservative: 20
 Best Local Similarity: 25.88% Mismatches: 74
 Query Match: 6.52% Indels: 72
 RESULT 1140
 ID ADB47453 standard; DNA; 9745 BP.
 DE Human cardiovascular system related genomic DNA #1019.
 PN US2003059908-A1.
 PD 27-MAR-2003.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Percent Similarity: 34.82% Conservative: 20
 Best Local Similarity: 25.88% Mismatches: 74
 Query Match: 6.52% Indels: 72
 RESULT 1141
 ID ABL1938 standard; cDNA; 10026 BP.
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 30296.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Percent Similarity: 34.27% Conservative: 34
 Best Local Similarity: 22.38% Mismatches: 83
 Query Match: 6.52% Indels: 106
 RESULT 1142
 ID AAS36758 standard; DNA; 12149 BP.
 DE Human cardiovascular system antigen genomic DNA SEQ ID NO 2258.
 PN WO200155321-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Percent Similarity: 34.82% Conservative: 20
 Best Local Similarity: 25.89% Mismatches: 74
 Query Match: 6.52% Indels: 72
 RESULT 1143
 ID ADB47452 standard; DNA; 12149 BP.
 DE Human cardiovascular system related genomic DNA #1018.
 PN US2003059908-A1.
 PD 27-MAR-2003.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Percent Similarity: 34.82% Conservative: 20
 Best Local Similarity: 25.89% Mismatches: 74
 Query Match: 6.52% Indels: 72
 RESULT 1144
 ID AB274518 standard; DNA; 13361 BP.
 DE Secreted protein gene 330 genomic fragment HTLCX82, SEQ ID NO:1665.
 PN WO200277013-A2.
 PD 03-OCT-2002.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Percent Similarity: 35.06% Conservative: 15
 Best Local Similarity: 26.44% Mismatches: 60
 Query Match: 6.52% Indels: 53
 RESULT 1145
 ID ADC20950 standard; DNA; 13361 BP.
 DE Human secreted protein-related DNA sequence #368.
 PN WO200292787-A2.
 PD 21-NOV-2002.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Percent Similarity: 35.06% Conservative: 15
 Best Local Similarity: 26.44% Mismatches: 60
 Query Match: 6.52% Indels: 53
 RESULT 1146
 ID ADC26981 standard; DNA; 20922 BP.
 DE Sorangium cellulosum tmbA gene cluster tmbB DNA.
 PN US2003054547-A1.
 PD 20-MAR-2003.
 PA (JULI/) JULIEN B.
 Percent Similarity: 34.55% Conservative: 25
 Best Local Similarity: 25.45% Mismatches: 116
 Query Match: 6.52% Indels: 65
 RESULT 1147
 ID AAD11177 standard; DNA; 25801 BP.
 DE Pseudomonas stutzeri cosmid pT31 DNA.
 PN WO200153309-A1.
 PD 26-JUL-2001.
 PA (IDAH-) IDAHO RES FOUND INC.
 (PASZ/) PASZCZYNSKI A.

PA (SEBA/) SEBAT J L.
 Percent Similarity: 38.24% Conservative: 21
 Best Local Similarity: 29.41% Mismatches: 88
 Query Match: 6.52% Indels: 60
 RESULT 1148
 Percent Similarity: 35.22% Conservative: 21
 Best Local Similarity: 22.01% Mismatches: 48
 Query Match: 6.52% Indels: 55
 RESULT 1149
 Percent Similarity: 35.22% Conservative: 21
 Best Local Similarity: 22.01% Mismatches: 48
 Query Match: 6.52% Indels: 55
 RESULT 1150
 Percent Similarity: 35.22% Conservative: 21
 Best Local Similarity: 22.01% Mismatches: 48
 Query Match: 6.52% Indels: 55
 RESULT 1151
 Percent Similarity: 35.22% Conservative: 21
 Best Local Similarity: 22.01% Mismatches: 48
 Query Match: 6.52% Indels: 55
 RESULT 1152
 Percent Similarity: 35.22% Conservative: 21
 Best Local Similarity: 22.01% Mismatches: 48
 Query Match: 6.52% Indels: 55
 RESULT 1153
 Percent Similarity: 35.22% Conservative: 21
 Best Local Similarity: 22.01% Mismatches: 48
 Query Match: 6.52% Indels: 55
 RESULT 1154
 Percent Similarity: 37.10% Conservative: 28
 Best Local Similarity: 25.81% Mismatches: 112
 Query Match: 6.52% Indels: 44
 RESULT 1155
 Percent Similarity: 37.10% Conservative: 28
 Best Local Similarity: 25.81% Mismatches: 112
 Query Match: 6.52% Indels: 44
 RESULT 1156
 Percent Similarity: 37.10% Conservative: 28
 Best Local Similarity: 25.81% Mismatches: 112
 Query Match: 6.52% Indels: 44
 RESULT 1157
 Percent Similarity: 37.10% Conservative: 28
 Best Local Similarity: 25.81% Mismatches: 112
 Query Match: 6.52% Indels: 44
 RESULT 1158
 Percent Similarity: 37.10% Conservative: 28
 Best Local Similarity: 25.81% Mismatches: 112
 Query Match: 6.52% Indels: 44
 RESULT 1159
 Percent Similarity: 37.10% Conservative: 28
 Best Local Similarity: 25.81% Mismatches: 112
 Query Match: 6.52% Indels: 44
 RESULT 1160
 Percent Similarity: 37.10% Conservative: 28
 Best Local Similarity: 25.81% Mismatches: 112
 Query Match: 6.52% Indels: 44
 RESULT 1161
 Percent Similarity: 37.10% Conservative: 28
 Best Local Similarity: 25.81% Mismatches: 112
 Query Match: 6.52% Indels: 44
 RESULT 1162
 Percent Similarity: 37.10% Conservative: 28
 Best Local Similarity: 25.81% Mismatches: 112
 Query Match: 6.52% Indels: 44
 RESULT 1163
 Percent Similarity: 35.22% Conservative: 21
 Best Local Similarity: 22.01% Mismatches: 48
 Query Match: 6.52% Indels: 55
 RESULT 1164
 Percent Similarity: 35.22% Conservative: 21
 Best Local Similarity: 22.01% Mismatches: 48
 Query Match: 6.52% Indels: 55
 RESULT 1165

ID AD113694 standard; DNA; 247509 BP.
 DE Osteoarthritis-associated polymorphic nucleotide #216.
 PN WO20030304166-A2.
 PD 03-JUL-2003.
 PA (INCY-) INCYTE GENOMICS INC.
 Percent Similarity: 34.82%
 Best Local Similarity: 25.89%
 Query Match: 6.52%
 RESULT 1166
 ID ABD08014 standard; DNA; 930 BP.
 DE Pseudomonas aeruginosa polynucleotide #5618.
 PN US6551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Percent Similarity: 35.53%
 Best Local Similarity: 27.19%
 Query Match: 6.48%
 RESULT 1167
 ID ACA36198 standard; DNA; 1027 BP.
 DE Prokaryotic essential gene #17855.
 PN WO20027183-A2.
 PD 03-OCT-2002.
 PA (ELIT-) ELITRA PHARM INC.
 Percent Similarity: 37.32%
 Best Local Similarity: 25.35%
 Query Match: 6.48%
 RESULT 1168
 ID AA291271 standard; DNA; 1074 BP.
 DE Nucleotide sequence fccr seq ID NO:36.
 PN WO200004158-A2.
 PD 27-JAN-2000.
 PA (PION-) PIONEER HI-BRED INT INC.
 Percent Similarity: 37.76%
 Best Local Similarity: 24.13%
 Query Match: 6.48%
 RESULT 1169
 ID ABD15610 standard; DNA; 1158 BP.
 DE Pseudomonas aeruginosa polynucleotide #14214.
 PN US6551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Percent Similarity: 35.65%
 Best Local Similarity: 26.09%
 Query Match: 6.48%
 RESULT 1170
 ID ABD08045 standard; DNA; 1308 BP.
 DE Pseudomonas aeruginosa polynucleotide #6649.
 PN US6551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Percent Similarity: 35.53%
 Best Local Similarity: 27.19%
 Query Match: 6.48%
 RESULT 1171
 ID AA291259 standard; DNA; 1377 BP.
 DE CoA ligase fccf nucleotide sequence SEQ ID NO:12.
 PN WO200004158-A2.
 PD 27-JAN-2000.
 PA (PION-) PIONEER HI-BRED INT INC.
 Percent Similarity: 37.76%
 Best Local Similarity: 24.13%
 Query Match: 6.48%
 RESULT 1172
 ID AAT74890 standard; DNA; 1535 BP.
 DE Human neurogenic differentiation protein (NeuroD2) DNA clone 14B1.
 PN WO9716548-A1.
 PD 09-MAY-1997.
 PA (HUTC-) HUTCHINSON CANCER RES CENT FRED.
 PA (WEIN-) WEINTRAUB N.
 Percent Similarity: 38.71%
 Best Local Similarity: 31.61%
 Query Match: 6.48%
 RESULT 1173

ID AAV42931 standard; DNA; 1535 BP.
 DE DNA encoding human neuroD2 protein, which is a bHLH protein.
 PN US5795723-A.
 PD 18-AUG-1998.
 PA (HUTC-) HUTCHINSON CANCER RES CENT FRED.
 Percent Similarity: 38.71%
 Best Local Similarity: 31.61%
 Query Match: 6.48%
 RESULT 1174
 ID ABS56389 standard; DNA; 1535 BP.
 DE Human bHLH family neuroD2 genomic DNA, clone 14B1.
 PN US6444463-B1.
 PD 03-SEP-2002.
 PA (HUTC-) HUTCHINSON CANCER RES CENT FRED.
 Percent Similarity: 38.71%
 Best Local Similarity: 31.61%
 Query Match: 6.48%
 RESULT 1175
 ID ADP72550 standard; DNA; 1580 BP.
 DE Renal toxin progression gene marker #1139.
 PN WO2004048598-A2.
 PD 10-JUN-2004.
 PA (GENE-) GENE LOGIC INC.
 Percent Similarity: 34.11%
 Best Local Similarity: 22.09%
 Query Match: 6.48%
 RESULT 1176
 ID AB211712 standard; cDNA; 1625 BP.
 DE Human polynucleotide SEQ ID NO 594.
 PN WO200270539-A2.
 PD 12-SEP-2002.
 PA (HYSE-) HYSEQ INC.
 Percent Similarity: 41.10%
 Best Local Similarity: 24.58%
 Query Match: 6.48%
 RESULT 1177
 ID ADM44230 standard; cDNA; 1625 BP.
 DE Novel human arginine-rich protein cDNA #594.
 PN US2004053250-A1.
 PD 18-MAR-2004.
 PA (TANG/) TANG Y T.
 PA (XUEA/) XUE A.
 PA (DRNA/) DRMANAC R T.
 Percent Similarity: 41.10%
 Best Local Similarity: 24.58%
 Query Match: 6.48%
 RESULT 1178
 ID ABD11546 standard; DNA; 1650 BP.
 DE Pseudomonas aeruginosa polynucleotide #10150.
 PN US6551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Percent Similarity: 33.91%
 Best Local Similarity: 23.88%
 Query Match: 6.48%
 RESULT 1179
 ID ABD11322 standard; DNA; 1725 BP.
 DE Pseudomonas aeruginosa polynucleotide #9926.
 PN US6551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Percent Similarity: 33.91%
 Best Local Similarity: 23.88%
 Query Match: 6.48%
 RESULT 1180
 ID ABD14631 standard; DNA; 2145 BP.
 DE Pseudomonas aeruginosa polynucleotide #13235.
 PN US6551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Percent Similarity: 32.99%
 Best Local Similarity: 24.83%
 Query Match: 6.48%
 RESULT 1181
 ID ABD14631 standard; DNA; 2145 BP.
 DE Pseudomonas aeruginosa polynucleotide #13235.
 PN US6551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Percent Similarity: 32.99%
 Best Local Similarity: 24.83%
 Query Match: 6.48%
 RESULT 1182

RESULT 1181
ID ADA52692 standard; cDNA; 2198 BP.
DE Human coding sequence, SEQ ID 260.
PN EPI293569-A2.
PD 19-MAR-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Percent Similarity: 37.44%
Best Local Similarity: 27.59%
Query Match: 6.48%
Conservative: 20
Mismatches: 49
Indels: 78
RESULT 1182
ID ABL24533 standard; DNA; 2244 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 25072.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Percent Similarity: 41.61%
Best Local Similarity: 26.85%
Query Match: 6.48%
Conservative: 22
Mismatches: 58
Indels: 29
RESULT 1183
ID ABA97188 standard; DNA; 2326 BP.
DE Goat lactoferrin-associated DNA #2.
PN KR98043944-A.
PD 05-SEP-1998.
PA (KORAD) KOREA ADV INST SCI & TECHNOLOGY.
Percent Similarity: 34.95%
Best Local Similarity: 25.61%
Query Match: 6.48%
Conservative: 27
Mismatches: 97
Indels: 91
RESULT 1184
ID AC77593 standard; DNA; 3026 BP.
DE Thermus aquaticus mutant DNA polymerase encoding DNA.
PN WO2003025132-A2.
PD 27-MAR-2003.
PA (INVI-) INVITROGEN CORP.
Percent Similarity: 39.38%
Best Local Similarity: 26.71%
Query Match: 6.48%
Conservative: 37
Mismatches: 97
Indels: 81
RESULT 1185
ID AC77767 standard; DNA; 3026 BP.
DE Thermus aquaticus mutant DNA polymerase encoding DNA.
PN WO2003025132-A2.
PD 27-MAR-2003.
PA (INVI-) INVITROGEN CORP.
Percent Similarity: 38.14%
Best Local Similarity: 25.09%
Query Match: 6.48%
Conservative: 38
Mismatches: 102
Indels: 79
RESULT 1186
ID AAH02112 standard; DNA; 3297 BP.
DE Mycobacterium tuberculosis nucleotide sequence SEQ ID NO:2105.
PN WO200123604-A2.
PD 05-APR-2001.
PA (INFE-) INFECTIO DIAGNOSTIC (IDI) INC.
Percent Similarity: 36.73%
Best Local Similarity: 26.94%
Query Match: 6.48%
Conservative: 24
Mismatches: 100
Indels: 56
RESULT 1187
ID AAH52090 standard; DNA; 3297 BP.
DE Mycobacterium tuberculosis potential drug target gene SEQ ID 144.
PN WO200135317-A1.
PD 17-MAY-2001.
PA (REGC) UNIV CALIFORNIA.
Percent Similarity: 36.73%
Best Local Similarity: 26.94%
Query Match: 6.48%
Conservative: 24
Mismatches: 100
Indels: 56
RESULT 1188
ID ACH97234 standard; DNA; 3390 BP.
DE Klebsiella pneumoniae polynucleotide segid 3029.
PN US6610836-B1.
PD 26-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Percent Similarity: 26.88%
Best Local Similarity: 20.58%
Query Match: 6.48%
Conservative: 26
Mismatches: 101
Indels: 201

RESULT 1189
ID ABD07965 standard; DNA; 3741 BP.
DE Pseudomonas aeruginosa polynucleotide #8569.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Percent Similarity: 35.53%
Best Local Similarity: 27.19%
Query Match: 6.48%
Conservative: 19
Mismatches: 106
Indels: 41
RESULT 1190
ID AAJ59784 standard; cDNA; 3913 BP.
DE Human polynucleotide SEQ ID NO 3773.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 38.57%
Best Local Similarity: 27.35%
Query Match: 6.48%
Conservative: 25
Mismatches: 64
Indels: 74
RESULT 1191
ID ABD14252 standard; DNA; 4431 BP.
DE Pseudomonas aeruginosa polynucleotide #12856.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Percent Similarity: 30.34%
Best Local Similarity: 24.34%
Query Match: 6.48%
Conservative: 16
Mismatches: 79
Indels: 109
RESULT 1192
ID ABL24532 standard; DNA; 4649 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 25069.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Percent Similarity: 41.61%
Best Local Similarity: 26.85%
Query Match: 6.48%
Conservative: 22
Mismatches: 58
Indels: 29
RESULT 1193
ID AAS59642 standard; DNA; 5870 BP.
DE Propionibacterium acnes immunogenic protein encoding DNA #137.
PN WO200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Percent Similarity: 36.22%
Best Local Similarity: 26.38%
Query Match: 6.48%
Conservative: 25
Mismatches: 87
Indels: 75
RESULT 1194
ID ACF64571 standard; DNA; 5870 BP.
DE Propionibacterium acnes DNA contig sequence #137.
PN WO2003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Percent Similarity: 36.22%
Best Local Similarity: 26.38%
Query Match: 6.48%
Conservative: 25
Mismatches: 87
Indels: 75
RESULT 1195
ID ADH13157 standard; DNA; 6131 BP.
DE Human malignant neoplasia-related gene SeqID6.
PN EPI365034-A2.
PD 26-NOV-2003.
PA (FARB) BAYER AG.
Percent Similarity: 38.71%
Best Local Similarity: 31.61%
Query Match: 6.48%
Conservative: 11
Mismatches: 59
Indels: 36
RESULT 1196
ID ACA26658 standard; DNA; 7802 BP.
DE Prokaryotic essential gene #8315.
PN WO20027183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Percent Similarity: 33.33%
Best Local Similarity: 24.21%
Query Match: 6.48%
Conservative: 23
Mismatches: 90
Indels: 78
RESULT 1197

ID AAV58938 standard; DNA; 10095 BP.
 DE Mycobacterium tuberculosis embCAB operon.
 PN WO9841533-A1.
 PD 24-SEP-1998.
 PA (YSSH) UNIV YESHIVA EINSTEIN COLLEGE.
 Percent Similarity: 36.73% Conservative: 24
 Best Local Similarity: 26.94% Mismatches: 100
 Query Match: 6.48% Indels: 56
 RESULT 1198
 ID ADN36912 standard; DNA; 20640 BP.
 DE X. albilineans XALB1 gene cluster DNA encoding protein Albi.
 PN WO2004035760-A2.
 PD 29-APR-2004.
 PA (UVEL) UNIV FLORIDA.
 Percent Similarity: 38.13% Conservative: 32
 Best Local Similarity: 25.68% Mismatches: 116
 Query Match: 6.48% Indels: 44
 RESULT 1199
 ID AA291253 standard; DNA; 24494 BP.
 DE Bacterium 2412.1 fumonis-catabolising gene cluster.
 PN WO200004158-A2.
 PD 27-JAN-2000.
 PA (PION-) PIONEER HI-BRED INT INC.
 Percent Similarity: 37.76% Conservative: 39
 Best Local Similarity: 24.13% Mismatches: 101
 Query Match: 6.48% Indels: 79
 RESULT 1200
 ID ADN36893 standard; DNA; 55839 BP.
 DE X. albilineans XALB1 gene cluster DNA.
 PN WO2004035760-A2.
 PD 29-APR-2004.
 PA (UVEL) UNIV FLORIDA.
 Percent Similarity: 38.13% Conservative: 32
 Best Local Similarity: 25.68% Mismatches: 116
 Query Match: 6.48% Indels: 44
 RESULT 1201
 ID ADC26995 standard; DNA; 67251 BP.
 DE Sorangium cellulosum tmbA gene cluster.
 PN US2003054547-A1.
 PD 20-MAR-2003.
 PA (JULI) JULIEN B.
 Percent Similarity: 40.59% Conservative: 28
 Best Local Similarity: 26.73% Mismatches: 71
 Query Match: 6.48% Indels: 50
 RESULT 1202
 Percent Similarity: 37.03% Conservative: 43
 Best Local Similarity: 23.42% Mismatches: 107
 Query Match: 6.48% Indels: 93
 RESULT 1203
 Percent Similarity: 36.73% Conservative: 24
 Best Local Similarity: 26.94% Mismatches: 100
 Query Match: 6.48% Indels: 56
 RESULT 1204
 Percent Similarity: 37.03% Conservative: 43
 Best Local Similarity: 23.42% Mismatches: 107
 Query Match: 6.48% Indels: 93
 RESULT 1205
 Percent Similarity: 36.73% Conservative: 24
 Best Local Similarity: 26.94% Mismatches: 100
 Query Match: 6.48% Indels: 56
 RESULT 1206
 Percent Similarity: 49.53% Conservative: 23
 Best Local Similarity: 28.04% Mismatches: 36
 Query Match: 6.48% Indels: 18
 RESULT 1207
 ID ABZ38468 standard; DNA; 507 BP.
 DE N. gonorrhoeae nucleotide sequence SEQ ID 1525.
 PN WO200279243-A2.
 PD 10-OCT-2002.
 PA (CHIR-) CHIRON SPA.
 Percent Similarity: 43.45% Conservative: 26

Best Local Similarity: 27.98% Mismatches: 64
 Query Match: 6.44% Indels: 31
 RESULT 1208
 ID ACA39058 standard; DNA; 855 BP.
 DE Prokaryotic essential gene #20715.
 PN WO20027183-A2.
 PD 03-OCT-2002.
 PA (ELIT-) ELITRA PHARM INC.
 Percent Similarity: 44.26% Conservative: 20
 Best Local Similarity: 27.87% Mismatches: 53
 Query Match: 6.44% Indels: 15
 RESULT 1209
 ID ADL03828 standard; DNA; 888 BP.
 DE DNA encoding a M. catarrhalis protein #1514.
 PN US6673910-B1.
 PD 06-JAN-2004.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Percent Similarity: 44.26% Conservative: 20
 Best Local Similarity: 27.87% Mismatches: 53
 Query Match: 6.44% Indels: 15
 RESULT 1210
 ID AAH65144 standard; DNA; 921 BP.
 DE C glutamicum coding sequence fragment SEQ ID NO: 179.
 PN EP1108790-A2.
 PD 20-JUN-2001.
 PA (KYOW) KYOWA HAKKO KOGYO KK.
 Percent Similarity: 35.74% Conservative: 31
 Best Local Similarity: 23.29% Mismatches: 93
 Query Match: 6.44% Indels: 68
 RESULT 1211
 ID ABD12950 standard; DNA; 1086 BP.
 DE Pseudomonas aeruginosa polynucleotide #11554.
 PN US6551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Percent Similarity: 39.15% Conservative: 16
 Best Local Similarity: 31.60% Mismatches: 90
 Query Match: 6.44% Indels: 40
 RESULT 1212
 ID ABD05166 standard; DNA; 1251 BP.
 DE Pseudomonas aeruginosa polynucleotide #3770.
 PN US6551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Percent Similarity: 39.77% Conservative: 20
 Best Local Similarity: 28.07% Mismatches: 68
 Query Match: 6.44% Indels: 35
 RESULT 1213
 ID ABD07415 standard; DNA; 1425 BP.
 DE Pseudomonas aeruginosa polynucleotide #6019.
 PN US6551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Percent Similarity: 35.99% Conservative: 34
 Best Local Similarity: 24.22% Mismatches: 97
 Query Match: 6.44% Indels: 89
 RESULT 1214
 ID ADJ48292 standard; DNA; 1428 BP.
 DE Maize oil-associated gene #110.
 PN US2004025202-A1.
 PD 05-FEB-2004.
 PA (LAUR) LAURIE C C.
 PA (RAVA) RAVANELLO M.
 PA (SAVA) SAVAGE T.
 PA (LEDE) LEDEUX J R.
 PA (ROGE) ROGERS J A.
 Percent Similarity: 36.82% Conservative: 27
 Best Local Similarity: 27.08% Mismatches: 78
 Query Match: 6.44% Indels: 97
 RESULT 1215
 ID AAF59130 standard; DNA; 1546 BP.
 DE Streptomyces sp. SK glucose isomerase nucleotide sequence SEQ ID NO:1.
 PN JP2000333684-A.

PD 05-DEC-2000.
 PA (NOVO) NOVO NORDISK AS.
 Percent Similarity: 36.73%
 Best Local Similarity: 26.55%
 Query Match: 6.44%
 RESULT 1216
 ID AAS71366 standard; cDNA; 1588 BP.
 DE DNA encoding novel human diagnostic protein #7170.
 PN WO200175067-A2.
 PD 11-OCT-2001.
 PA (HYSE-) HYSEQ INC.
 Percent Similarity: 43.40%
 Best Local Similarity: 35.85%
 Query Match: 6.44%
 RESULT 1217
 ID ABT18484 standard; DNA; 1666 BP.
 DE Aspergillus fumigatus essential gene #842.
 PN WO200206090-A2.
 PD 31-OCT-2002.
 PA (ELIT-) ELITRA PHARM INC.
 Percent Similarity: 33.72%
 Best Local Similarity: 22.48%
 Query Match: 6.44%
 RESULT 1218
 ID ACH96895 standard; DNA; 1707 BP.
 DE Klebsiella pneumoniae polynucleotide seqid 2690.
 PN US610836-B1.
 PD 26-AUG-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Percent Similarity: 37.84%
 Best Local Similarity: 28.57%
 Query Match: 6.44%
 RESULT 1219
 ID ABD07686 standard; DNA; 1989 BP.
 DE Pseudomonas aeruginosa polynucleotide #6290.
 PN US551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Percent Similarity: 35.99%
 Best Local Similarity: 24.22%
 Query Match: 6.44%
 RESULT 1220
 ID ADQ23026 standard; DNA; 1990 BP.
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5846.
 PN WO2004048938-A2.
 PD 10-JUN-2004.
 PA (PROT-) PROTEIN DESIGN LABS INC.
 Percent Similarity: 33.90%
 Best Local Similarity: 25.42%
 Query Match: 6.44%
 RESULT 1221
 ID ADM47721 standard; DNA; 2005 BP.
 DE Polynucleotide sequence #139 useful in producing transgenic plants.
 PN US200323670-A1.
 PD 18-DEC-2003.
 PA (EDGE/) EDGERTON M D.
 PA (CHOM/) CHOMET P S.
 PA (LACC/) LACCETTI L B.
 Percent Similarity: 35.39%
 Best Local Similarity: 25.93%
 Query Match: 6.44%
 RESULT 1222
 ID ADB62264 standard; cDNA; 2165 BP.
 DE Human cDNA encoding clone CTONG20189000.
 PN EPI308459-A2.
 PD 07-MAY-2003.
 PA (HELI-) HELIX RES INST.
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.
 Percent Similarity: 38.83%
 Best Local Similarity: 28.64%
 Query Match: 6.44%
 RESULT 1223
 ID ABD02122 standard; DNA; 2367 BP.

DE Pseudomonas aeruginosa polynucleotide #726.
 PN US551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Percent Similarity: 38.89%
 Best Local Similarity: 25.93%
 Query Match: 6.44%
 RESULT 1224
 ID ABA00886 standard; DNA; 2502 BP.
 DE Novel TspJ51 DNA polymerase coding sequence.
 PN WO2003004632-A2.
 PD 16-JAN-2003.
 PA (AMSH) AMERSHAM BIOSCIENCES CORP.
 Percent Similarity: 34.44%
 Best Local Similarity: 26.30%
 Query Match: 6.44%
 RESULT 1225
 ID AAS62249 standard; cDNA; 2740 BP.
 DE cDNA sequence #36 encoding novel human secreted protein.
 PN WO200177291-A2.
 PD 18-OCT-2001.
 PA (GEMY) GENETICS INST INC.
 Percent Similarity: 37.44%
 Best Local Similarity: 26.07%
 Query Match: 6.44%
 RESULT 1226
 ID AAT32326 standard; DNA; 3049 BP.
 DE Thermus flavus DNA polymerase I coding sequence.
 PN WO9614417-A1.
 PD 17-MAY-1996.
 PA (MOLE-) MOLECULAR BIOLOGY RESOURCES INC.
 Percent Similarity: 36.86%
 Best Local Similarity: 25.94%
 Query Match: 6.44%
 RESULT 1227
 ID AAD29059 standard; cDNA; 3075 BP.
 DE Human guanine nucleotide exchange factor (GEF) 32529 cDNA.
 PN WO200206325-A2.
 PD 24-JAN-2002.
 PA (MILL-) MILLENNIUM PHARM INC.
 Percent Similarity: 38.83%
 Best Local Similarity: 28.84%
 Query Match: 6.44%
 RESULT 1228
 ID ADI81640 standard; DNA; 3213 BP.
 DE Malaria mosquito DNA encoding protein ebip7471.
 PN US2004009537-A1.
 PD 15-JAN-2004.
 PA (ROOS/) ROOS J.
 PA (STAU/) STAUDEMAN K.
 PA (VELI/) VELICELEBI G.
 Percent Similarity: 41.97%
 Best Local Similarity: 29.56%
 Query Match: 6.44%
 RESULT 1229
 ID ACC77949 standard; DNA; 3221 BP.
 DE Thermus thermophilus mutant DNA polymerase encoding DNA.
 PN WO2003025132-A2.
 PD 27-MAR-2003.
 PA (INVI-) INVITROGEN CORP.
 Percent Similarity: 36.30%
 Best Local Similarity: 25.00%
 Query Match: 6.44%
 RESULT 1230
 ID ACC77952 standard; DNA; 3221 BP.
 DE Thermus thermophilus mutant DNA polymerase encoding DNA.
 PN WO2003025132-A2.
 PD 27-MAR-2003.
 PA (INVI-) INVITROGEN CORP.
 Percent Similarity: 36.30%
 Best Local Similarity: 25.00%
 Query Match: 6.44%
 RESULT 1231
 ID ABD02122 standard; DNA; 2367 BP.

ID ACC77959 standard; DNA; 3221 BP.
DE Thermus thermophilus mutant DNA polymerase encoding DNA.
FN WO2003025132-A2.
PD 27-MAR-2003.
PA (INVI-) INVITROGEN CORP.
Percent Similarity: 36.30%
Conservative: 33
Mismatches: 114
Best Local Similarity: 25.00%
Indels: 74
Query Match: 6.44%
RESULT 1232
ID AAT17890 standard; DNA; 3666 BP.
DE Aspergillus fumigatus essential gene #248.
FN WO200286090-A2.
PD 31-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Percent Similarity: 33.72%
Conservative: 29
Mismatches: 90
Best Local Similarity: 22.48%
Indels: 81
Query Match: 6.44%
RESULT 1233
ID ADG10041 standard; DNA; 3721 BP.
DE Human NOVX polypeptide coding sequence SEQ ID NO: 61.
FN WO2003000842-A2.
PD 03-JAN-2003.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 41.70%
Conservative: 24
Mismatches: 75
Best Local Similarity: 30.94%
Indels: 57
Query Match: 6.44%
RESULT 1234
ID ABD05211 standard; DNA; 3825 BP.
DE Pseudomonas aeruginosa polynucleotide #3815.
FN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Percent Similarity: 39.77%
Conservative: 20
Mismatches: 68
Best Local Similarity: 28.07%
Indels: 35
Query Match: 6.44%
RESULT 1235
ID ABD05091 standard; DNA; 4506 BP.
DE Pseudomonas aeruginosa polynucleotide #3695.
FN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Percent Similarity: 39.77%
Conservative: 20
Mismatches: 68
Best Local Similarity: 28.07%
Indels: 35
Query Match: 6.44%
RESULT 1236
ID AAC6156 standard; cDNA; 4815 BP.
DE FCTR4 nucleic acid.
FN WO200146231-A2.
PD 28-JUN-2001.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 38.83%
Conservative: 21
Mismatches: 84
Best Local Similarity: 28.64%
Indels: 43
Query Match: 6.44%
RESULT 1237
ID AAD27271 standard; cDNA; 5540 BP.
DE Human transporter and ion channel-18 (TRICH-18) cDNA.
FN WO200192304-A2.
PD 06-DEC-2001.
PA (INCY-) INCYTE GENOMICS INC.
Percent Similarity: 37.44%
Conservative: 24
Mismatches: 92
Best Local Similarity: 26.07%
Indels: 40
Query Match: 6.44%
RESULT 1238
ID AAD54236 standard; DNA; 6297 BP.
DE Streptomyces amfibiosporus lactimidomycin ORF6 DNA.
FN WO200288176-A2.
PD 07-NOV-2002.
PA (ECOP-) ECOPIA BIOSCIENCES INC.
Percent Similarity: 39.06%
Conservative: 30
Mismatches: 90
Best Local Similarity: 26.18%
Indels: 55
Query Match: 6.44%
RESULT 1239
ID AAT06768 standard; DNA; 7000 BP.
DE Pseudomonas fluorescens pyrrolnitrin gene cluster.
FN WO9533818-A2.
PD 14-DEC-1995.
PA (CIBA) CIBA GEIGY AG.
Percent Similarity: 30.22%
Conservative: 18
Mismatches: 76
Best Local Similarity: 23.74%
Indels: 118
Query Match: 6.44%
RESULT 1240
ID AAT89955 standard; DNA; 7001 BP.
DE Pseudomonas fluorescens pyrrolnitrin gene cluster genomic DNA.
FN US5662898-A.
PD 02-SEP-1997.
PA (CIBA) CIBA GEIGY CORP.
Percent Similarity: 30.22%
Conservative: 18
Mismatches: 76
Best Local Similarity: 23.74%
Indels: 118
Query Match: 6.44%
RESULT 1241
ID AAV58730 standard; DNA; 7001 BP.
DE Pyrrolnitrin gene region.
FN US5817502-A.
PD 06-OCT-1998.
PA (NOVS) NOVARTIS FINANCE CORP.
Percent Similarity: 30.22%
Conservative: 18
Mismatches: 76
Best Local Similarity: 23.74%
Indels: 118
Query Match: 6.44%
RESULT 1242
ID AAV39840 standard; DNA; 7001 BP.
DE Pseudomonas fluorescens pyrrolnitrin gene cluster.
FN WO9824919-A1.
PD 11-JUN-1998.
PA (NOVS) NOVARTIS AG.
Percent Similarity: 30.22%
Conservative: 18
Mismatches: 76
Best Local Similarity: 23.74%
Indels: 118
Query Match: 6.44%
RESULT 1243
ID AAX99371 standard; DNA; 7001 BP.
DE P. fluorescens pyrrolnitrin gene cluster sequence.
FN US5955348-A.
PD 21-SEP-1999.
PA (NOVS) NOVARTIS AG.
Percent Similarity: 30.22%
Conservative: 18
Mismatches: 76
Best Local Similarity: 23.74%
Indels: 118
Query Match: 6.44%
RESULT 1244
ID AAA75298 standard; DNA; 7001 BP.
DE DNA sequence of Pseudomonas fluorescens pyrrolnitrin gene region.
FN US6117670-A.
PD 12-SEP-2000.
PA (NOVS) NOVARTIS FINANCE CORP.
Percent Similarity: 30.22%
Conservative: 18
Mismatches: 76
Best Local Similarity: 23.74%
Indels: 118
Query Match: 6.44%
RESULT 1245
ID AAD36299 standard; cDNA; 7610 BP.
DE Human transporter and ion channel (TRICH) 2 cDNA.
FN WO200222684-A2.
PD 21-MAR-2002.
PA (INCY-) INCYTE GENOMICS INC.
Percent Similarity: 37.44%
Conservative: 24
Mismatches: 92
Best Local Similarity: 26.07%
Indels: 40
Query Match: 6.44%
RESULT 1246
ID ACD28255 standard; DNA; 7697 BP.
DE Mouse soluble guanylyl cyclase sgc associated DNA #2.
FN US2003096240-A1.
PD 22-MAY-2003.
PA (MURA/) MURAD F.
PA (SHAR/) SHARINA I G.
PA (KRUM/) KROMENACKER J S.
PA (MART/) MARTIN E.
Percent Similarity: 41.73%
Conservative: 19
Mismatches: 53
Best Local Similarity: 28.06%
Indels: 28
Query Match: 6.44%

RESULT 1247
ID ADL33384 standard; DNA; 7706 BP.
DE Human transporter and ion channel (TRICH) gene #29.
FN WO2003083085-A2.
PD 09-OCT-2003.
PA (INCY-) INCYTE CORP.
Percent Similarity: 37.44%
Best Local Similarity: 26.07%
Query Match: 6.44%
Conservative: 24
Mismatch: 92
Indels: 40
RESULT 1248
ID ABX70982 standard; cDNA; 8037 BP.
DE Novel human cDNA sequence #207.
FN WO200281731-A2.
PD 17-OCT-2002.
PA (HYSE-) HYSEQ INC.
PA (GOOD/) GOODRICH R W.
Percent Similarity: 37.44%
Best Local Similarity: 26.07%
Query Match: 6.44%
Conservative: 24
Mismatch: 92
Indels: 40
RESULT 1249
ID AAF57452 standard; cDNA; 8040 BP.
DE Human ABCA2 transporter protein encoding cDNA.
FN WO200121798-A2.
PD 29-MAR-2001.
PA (FOXC-) FOX CHASE CANCER CENT.
Percent Similarity: 37.44%
Best Local Similarity: 26.07%
Query Match: 6.44%
Conservative: 24
Mismatch: 92
Indels: 40
RESULT 1250
ID ABV74350 standard; DNA; 8056 BP.
DE Human ABC transporter ABCA2 encoding polynucleotide SEQ ID NO 3.
FN WO200264781-A2.
PD 22-AUG-2002.
PA (ACTI-) ACTIVE PASS PHARM INC.
Percent Similarity: 37.44%
Best Local Similarity: 26.07%
Query Match: 6.44%
Conservative: 24
Mismatch: 92
Indels: 40
RESULT 1251
ID AAH75187 standard; cDNA; 8195 BP.
DE Nucleotide sequence of a human 17114 transporter polypeptide.
FN WO200164875-A2.
PD 07-SEP-2001.
PA (MILL-) MILLENNIUM PHARM INC.
Percent Similarity: 37.44%
Best Local Similarity: 26.07%
Query Match: 6.44%
Conservative: 24
Mismatch: 92
Indels: 40
RESULT 1252
ID ABI53009 standard; DNA; 8269 BP.
DE Human ATP binding cassette transporter protein, ABCA2, coding sequence.
FN WO200208424-A1.
PD 31-JAN-2002.
PA (BANY) BANYU PHARM CO LTD.
PA (INAG) INAGAKI N.
Percent Similarity: 37.44%
Best Local Similarity: 26.07%
Query Match: 6.44%
Conservative: 24
Mismatch: 92
Indels: 40
RESULT 1253
ID AAK68713 standard; DNA; 11477 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:23525.
FN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 33.33%
Best Local Similarity: 22.92%
Query Match: 6.44%
Conservative: 30
Mismatch: 101
Indels: 92
RESULT 1254
ID AAK71247 standard; DNA; 11477 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:26059.
FN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 33.33%
Best Local Similarity: 22.92%
Query Match: 6.44%
Conservative: 30
Mismatch: 101
Indels: 92

Query Match: 6.44%
Indels: 92
RESULT 1255
ID AAK68712 standard; DNA; 11482 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:23524.
FN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 33.33%
Best Local Similarity: 22.92%
Query Match: 6.44%
Conservative: 30
Mismatch: 101
Indels: 92
RESULT 1256
ID AAK71246 standard; DNA; 11482 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:26058.
FN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 33.33%
Best Local Similarity: 22.92%
Query Match: 6.44%
Conservative: 30
Mismatch: 101
Indels: 92
RESULT 1257
ID AAS59566 standard; DNA; 34088 BP.
DE Propionibacterium acnes immunogenic protein encoding DNA #61.
FN WO200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Percent Similarity: 41.06%
Best Local Similarity: 25.10%
Query Match: 6.44%
Conservative: 42
Mismatch: 80
Indels: 75
RESULT 1258
ID AC64495 standard; DNA; 34088 BP.
DE Propionibacterium acnes DNA contig sequence #61.
FN WO2003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Percent Similarity: 41.06%
Best Local Similarity: 25.10%
Query Match: 6.44%
Conservative: 42
Mismatch: 80
Indels: 75
RESULT 1259
ID ADH48030 standard; DNA; 37507 BP.
DE Clone FS3-135 DNA sequence SEQ ID NO:2.
FN EPI386966-A1.
PD 04-FEB-2004.
PA (LIBR-) LIBRAGEN.
Percent Similarity: 40.00%
Best Local Similarity: 31.25%
Query Match: 6.44%
Conservative: 14
Mismatch: 61
Indels: 35
RESULT 1260
ID AAD54230 standard; DNA; 50543 BP.
DE Streptomyces amfibiosporus lactimidomycin DNA.
FN WO200288176-A2.
PD 07-NOV-2002.
PA (ECOP-) ECOPIA BIOSCIENCES INC.
Percent Similarity: 39.06%
Best Local Similarity: 26.18%
Query Match: 6.44%
Conservative: 30
Mismatch: 90
Indels: 55
RESULT 1261
ID AAC55842 standard; DNA; 53500 BP.
DE Complete nucleotide sequence of the mitomycin biosynthetic genes.
FN WO200053737-A2.
PD 14-SEP-2000.
PA (MINU) UNIV MINNESOTA.
PA (SHER/) SHERMAN D H.
PA (MAOY/) MAO Y.
PA (VARO/) VAROGLU M.
PA (HEMM/) HE M.
PA (SHEL/) SHELTON P C.
Percent Similarity: 34.74%
Best Local Similarity: 25.96%
Query Match: 6.44%
Conservative: 25
Mismatch: 121
Indels: 65
RESULT 1262
ID ADE10261 standard; DNA; 53500 BP.
DE S. lavendulae mitomycin biosynthetic genes complete sequence.
FN US2003134398-A1.

PD 17-JUL-2003.
PA (SHER/) SHERMAN D H. 17-JUL-2003.
PA (MAOY/) MAO Y.
PA (VARO/) VAROGLU M.
PA (HEMM/) HE M.
PA (SHEL/) SHELTON P. 34.74%
Percent Similarity: 25.96%
Best Local Similarity: 25.96%
Query Match: 6.44%
Conservative: 25
Mismatches: 121
Indels: 65

RESULT 1263
ID AAF28545 standard; DNA; 62909 BP.
DE Genomic fragment #32.
PN WO200078968-A2.
PD 28-DEC-2000.
PA (INCY-) INCYTE GENOMICS INC.
Percent Similarity: 44.26%
Best Local Similarity: 27.87%
Query Match: 6.44%
Conservative: 20
Mismatches: 53
Indels: 15

RESULT 1264
ID AC45150 standard; DNA; 96649 BP.
DE Human NAC nucleotide sequence SEQ ID NO:10.
PN WO2003024988-A1.
PD 27-MAR-2003.
PA (ISIS-) ISIS PHARM INC.
Percent Similarity: 33.33%
Best Local Similarity: 22.92%
Query Match: 6.44%
Conservative: 30
Mismatches: 101
Indels: 92

RESULT 1265
ID ABD07574 standard; DNA; 822 BP.
DE Pseudomonas aeruginosa polynucleotide #6178.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Percent Similarity: 36.59%
Best Local Similarity: 26.48%
Query Match: 6.40%
Conservative: 29
Mismatches: 105
Indels: 78

RESULT 1266
ID AAN70355 standard; cDNA to mRNA; 909 BP.
DE Sequence encoding AA sequence (III) of a polypeptide having human
DE haematopoietic cell growth potentiating factor (HCGFF) activity.
PN EP232707-A.
PD 19-AUG-1987.
PA (AJIN) AJINOMOTO KK.
Percent Similarity: 38.58%
Best Local Similarity: 27.17%
Query Match: 6.40%
Conservative: 29
Mismatches: 94
Indels: 63

RESULT 1269
ID ADC26975 standard; DNA; 942 BP.
DE Sorangium cellulosum tmbA gene cluster ORF 3 DNA.
PN US2003054547-A1.
PD 20-MAR-2003.
PA (JULI/) JULIEN B.
Percent Similarity: 40.50%
Best Local Similarity: 27.50%
Query Match: 6.40%
Conservative: 26
Mismatches: 73
Indels: 48

RESULT 1270
ID ADU39859 standard; cDNA; 1030 BP.
DE Plant cDNA #859.
PN US2004016025-A1.
PD 22-JAN-2004.
PA (BUDW/) BUDWORTH P.
PA (MOUG/) MOUGHAMER T.
PA (BRIG/) BRIGGS S P.
PA (COOP/) COOPER B.
PA (GLAZ/) GLAZEBROOK J.
Conservative: 25
Mismatches: 112
Indels: 107

PA (GOFF/) GOFF S A.
PA (KATA/) KATAGIRI F.
PA (KREP/) KREPS J.
PA (PROV/) PROVART N.
PA (RICK/) RICKE D.
PA (ZHUT/) ZHU T. 34.15%
Percent Similarity: 24.39%
Best Local Similarity: 24.39%
Query Match: 6.40%
Conservative: 28
Mismatches: 83
Indels: 106

RESULT 1271
ID AAC74893 standard; cDNA; 1119 BP.
DE Human ORF448 polynucleotide sequence SEQ ID NO:895.
PN WO200058473-A2.
PD 05-OCT-2000.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 37.75%
Best Local Similarity: 26.51%
Query Match: 6.40%
Conservative: 28
Mismatches: 86
Indels: 69

RESULT 1272
ID ABD08503 standard; DNA; 1221 BP.
DE Pseudomonas aeruginosa polynucleotide #7107.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Percent Similarity: 36.12%
Best Local Similarity: 24.08%
Query Match: 6.40%
Conservative: 36
Mismatches: 101
Indels: 90

RESULT 1273
ID ADI21915 standard; cDNA; 1368 BP.
DE Novel human protein cDNA #174.
PN WO2003025148-A2.
PD 27-MAR-2003.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 35.80%
Best Local Similarity: 26.46%
Query Match: 6.40%
Conservative: 24
Mismatches: 104
Indels: 61

RESULT 1274
ID ABD10627 standard; DNA; 1488 BP.
DE Pseudomonas aeruginosa polynucleotide #9231.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Percent Similarity: 34.20%
Best Local Similarity: 26.94%
Query Match: 6.40%
Conservative: 14
Mismatches: 60
Indels: 67

RESULT 1275
ID ABT19078 standard; DNA; 1581 BP.
DE Aspergillus fumigatus essential gene #1436.
PN WO200286030-A2.
PD 31-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Percent Similarity: 33.47%
Best Local Similarity: 21.37%
Query Match: 6.40%
Conservative: 30
Mismatches: 83
Indels: 82

RESULT 1276
ID AAQ2784 standard; cDNA; 1906 BP.
DE Mullerian inhibiting substance cDNA.
PN US5427780-A.
PD 27-JUN-1995.
PA (BIOI) BIOGEN INC.
PA (GENO) GEN HOSPITAL CORP.
Percent Similarity: 32.41%
Best Local Similarity: 24.69%
Query Match: 6.40%
Conservative: 25
Mismatches: 112
Indels: 107

RESULT 1277
ID ABD10214 standard; DNA; 2019 BP.
DE Pseudomonas aeruginosa polynucleotide #8818.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Percent Similarity: 34.20%
Best Local Similarity: 26.94%
Query Match: 6.40%
Conservative: 14
Mismatches: 60
Indels: 67

RESULT 1278
ID ABD08834 standard; DNA; 2094 BP.
DE Pseudomonas aeruginosa polynucleotide #7438.
PN US651795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Percent Similarity: 36.86%
Best Local Similarity: 24.13%
Query Match: 6.40%
Conservative: 30
Mismatch: 92
Indels: 57
RESULT 1279
ID ADG91050 standard; DNA; 2120 BP.
DE Hepatic specific nucleic acid encoding sequence #239.
PN WO2003066877-A2.
PD 14-AUG-2003.
PA (DIAD-) DIADEXUS INC.
Percent Similarity: 42.75%
Best Local Similarity: 29.71%
Query Match: 6.40%
Conservative: 36
Mismatch: 85
Indels: 74
RESULT 1280
ID AA120576 standard; DNA; 2144 BP.
DE Probe #10509 for gene expression analysis in human cervical cell sample.
PN WO200157278-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Percent Similarity: 30.69%
Best Local Similarity: 26.35%
Query Match: 6.40%
Conservative: 12
Mismatch: 87
Indels: 105
RESULT 1281
ID ABA65620 standard; DNA; 2144 BP.
DE Human foetal liver single exon nucleic acid probe #13925.
PN WO200157277-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Percent Similarity: 30.69%
Best Local Similarity: 26.35%
Query Match: 6.40%
Conservative: 12
Mismatch: 87
Indels: 105
RESULT 1282
ID AA145786 standard; DNA; 2144 BP.
DE Probe #14472 used to measure gene expression in human placenta sample.
PN WO200157272-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Percent Similarity: 30.69%
Best Local Similarity: 26.35%
Query Match: 6.40%
Conservative: 12
Mismatch: 87
Indels: 105
RESULT 1283
ID ABA47725 standard; DNA; 2144 BP.
DE Human breast cell single exon nucleic acid probe #6420.
PN WO200157271-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Percent Similarity: 30.69%
Best Local Similarity: 26.35%
Query Match: 6.40%
Conservative: 12
Mismatch: 87
Indels: 105
RESULT 1284
ID ABA32707 standard; DNA; 2144 BP.
DE Probe #11173 for gene expression analysis in human heart cell sample.
PN WO200157274-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Percent Similarity: 30.69%
Best Local Similarity: 26.35%
Query Match: 6.40%
Conservative: 12
Mismatch: 87
Indels: 105
RESULT 1285
ID AA39770 standard; DNA; 2144 BP.
DE Human bone marrow expressed single exon probe SEQ ID NO: 14327.
PN WO200157276-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Percent Similarity: 30.69%
Best Local Similarity: 26.35%
Query Match: 6.40%
Conservative: 12
Mismatch: 87
Indels: 105
RESULT 1286
ID ABA42329 standard; DNA; 2463 BP.

ID AAK14023 standard; DNA; 2144 BP.
DE Human brain expressed single exon probe SEQ ID NO: 14014.
PN WO200157275-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Percent Similarity: 30.69%
Best Local Similarity: 26.35%
Query Match: 6.40%
Conservative: 12
Mismatch: 87
Indels: 105
RESULT 1287
ID ABS39357 standard; DNA; 2144 BP.
DE Human liver single exon probe, SEQ ID No 14347.
PN WO200157273-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Percent Similarity: 30.69%
Best Local Similarity: 26.35%
Query Match: 6.40%
Conservative: 12
Mismatch: 87
Indels: 105
RESULT 1288
ID AA106275 standard; DNA; 2144 BP.
DE Probe #6286 used to measure gene expression in human breast sample.
PN WO200157270-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Percent Similarity: 30.69%
Best Local Similarity: 26.35%
Query Match: 6.40%
Conservative: 12
Mismatch: 87
Indels: 105
RESULT 1289
ID ABS13864 standard; DNA; 2144 BP.
DE Human genome-derived single exon probe ORF from lung SEQ ID No 13855.
PN WO200186003-A2.
PD 15-NOV-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Percent Similarity: 30.69%
Best Local Similarity: 26.35%
Query Match: 6.40%
Conservative: 12
Mismatch: 87
Indels: 105
RESULT 1290
ID AA161256 standard; DNA; 2174 BP.
DE Human polynucleotide SEQ ID No 5245.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 30.69%
Best Local Similarity: 26.35%
Query Match: 6.40%
Conservative: 12
Mismatch: 87
Indels: 105
RESULT 1291
ID ADG91053 standard; DNA; 2280 BP.
DE Hepatic specific nucleic acid encoding sequence #242.
PN WO2003066877-A2.
PD 14-AUG-2003.
PA (DIAD-) DIADEXUS INC.
Percent Similarity: 42.75%
Best Local Similarity: 29.71%
Query Match: 6.40%
Conservative: 36
Mismatch: 85
Indels: 74
RESULT 1292
ID ADG91055 standard; DNA; 2321 BP.
DE Hepatic specific nucleic acid encoding sequence #244.
PN WO2003066877-A2.
PD 14-AUG-2003.
PA (DIAD-) DIADEXUS INC.
Percent Similarity: 42.75%
Best Local Similarity: 29.71%
Query Match: 6.40%
Conservative: 36
Mismatch: 85
Indels: 74
RESULT 1293
ID ADG91049 standard; DNA; 2457 BP.
DE Hepatic specific nucleic acid encoding sequence #238.
PN WO2003066877-A2.
PD 14-AUG-2003.
PA (DIAD-) DIADEXUS INC.
Percent Similarity: 42.75%
Best Local Similarity: 29.71%
Query Match: 6.40%
Conservative: 36
Mismatch: 85
Indels: 74
RESULT 1294
ID ACA42329 standard; DNA; 2463 BP.

DE Prokaryotic essential gene #23986.
 PN WO200277193-A2.
 PD 03-OCT-2002.
 PA (ELIT-) ELITRA PHARM INC.
 Percent Similarity: 23
 Best Local Similarity: 33.65%
 Mismatches: 117
 Indels: 94
 Query Match:
 RESULT 1295
 ID ADG91048 standard; DNA; 2489 BP.
 DE Hepatic specific nucleic acid encoding sequence #237.
 PN WO2003066877-A2.
 PD 14-AUG-2003.
 PA (DIAD-) DIADEXUS INC.
 Percent Similarity: 36
 Best Local Similarity: 42.75%
 Mismatches: 85
 Indels: 74
 Query Match:
 RESULT 1296
 ID ADG91047 standard; DNA; 2520 BP.
 DE Hepatic specific nucleic acid encoding sequence #236.
 PN WO2003066877-A2.
 PD 14-AUG-2003.
 PA (DIAD-) DIADEXUS INC.
 Percent Similarity: 36
 Best Local Similarity: 42.75%
 Mismatches: 85
 Indels: 74
 Query Match:
 RESULT 1297
 ID ADG91054 standard; DNA; 2641 BP.
 DE Hepatic specific nucleic acid encoding sequence #243.
 PN WO2003066877-A2.
 PD 14-AUG-2003.
 PA (DIAD-) DIADEXUS INC.
 Percent Similarity: 36
 Best Local Similarity: 42.75%
 Mismatches: 85
 Indels: 74
 Query Match:
 RESULT 1298
 ID ABD17161 standard; DNA; 2814 BP.
 DE Pseudomonas aeruginosa polynucleotide #15765.
 PN US6551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Percent Similarity: 23
 Best Local Similarity: 33.65%
 Mismatches: 117
 Indels: 94
 Query Match:
 RESULT 1299
 ID ABD08894 standard; DNA; 3012 BP.
 DE Pseudomonas aeruginosa polynucleotide #7498.
 PN US6551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Percent Similarity: 30
 Best Local Similarity: 36.86%
 Mismatches: 92
 Indels: 57
 Query Match:
 RESULT 1300
 ID ACC77568 standard; DNA; 3026 BP.
 DE Thermus aquaticus mutant DNA polymerase encoding DNA.
 PN WO2003025132-A2.
 PD 27-MAR-2003.
 PA (INVI-) INVITROGEN CORP.
 Percent Similarity: 42
 Best Local Similarity: 39.31%
 Mismatches: 99
 Indels: 79
 Query Match:
 RESULT 1301
 ID ACC77580 standard; DNA; 3026 BP.
 DE Thermus aquaticus mutant DNA polymerase encoding DNA.
 PN WO2003025132-A2.
 PD 27-MAR-2003.
 PA (INVI-) INVITROGEN CORP.
 Percent Similarity: 42
 Best Local Similarity: 39.31%
 Mismatches: 99
 Indels: 79
 Query Match:
 RESULT 1302
 ID ACC77561 standard; DNA; 3026 BP.
 DE Thermus aquaticus mutant DNA polymerase encoding DNA.

PN WO2003025132-A2.
 PD 27-MAR-2003.
 PA (INVI-) INVITROGEN CORP.
 Percent Similarity: 43
 Best Local Similarity: 42.09%
 Mismatches: 109
 Indels: 53
 Query Match:
 RESULT 1303
 ID ACC77598 standard; DNA; 3026 BP.
 DE Thermus aquaticus mutant DNA polymerase encoding DNA.
 PN WO2003025132-A2.
 PD 27-MAR-2003.
 PA (INVI-) INVITROGEN CORP.
 Percent Similarity: 40
 Best Local Similarity: 38.62%
 Mismatches: 101
 Indels: 79
 Query Match:
 RESULT 1304
 ID ACC77839 standard; DNA; 3026 BP.
 DE Thermus aquaticus mutant DNA polymerase encoding DNA.
 PN WO2003025132-A2.
 PD 27-MAR-2003.
 PA (INVI-) INVITROGEN CORP.
 Percent Similarity: 43
 Best Local Similarity: 39.31%
 Mismatches: 99
 Indels: 79
 Query Match:
 RESULT 1305
 ID ACC77780 standard; DNA; 3026 BP.
 DE Thermus aquaticus mutant DNA polymerase encoding DNA.
 PN WO2003025132-A2.
 PD 27-MAR-2003.
 PA (INVI-) INVITROGEN CORP.
 Percent Similarity: 39
 Best Local Similarity: 38.62%
 Mismatches: 101
 Indels: 79
 Query Match:
 RESULT 1306
 ID ACC77777 standard; DNA; 3026 BP.
 DE Thermus aquaticus mutant DNA polymerase encoding DNA.
 PN WO2003025132-A2.
 PD 27-MAR-2003.
 PA (INVI-) INVITROGEN CORP.
 Percent Similarity: 39
 Best Local Similarity: 38.62%
 Mismatches: 101
 Indels: 79
 Query Match:
 RESULT 1307
 ID ABD17264 standard; DNA; 3357 BP.
 DE Pseudomonas aeruginosa polynucleotide #15868.
 PN US6551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Percent Similarity: 23
 Best Local Similarity: 33.65%
 Mismatches: 117
 Indels: 94
 Query Match:
 RESULT 1308
 ID ADL45191 standard; DNA; 3574 BP.
 DE Human ovarian cancer DNA marker #19081.
 PN WO200170979-A2.
 PD 27-SEP-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Percent Similarity: 28
 Best Local Similarity: 36.09%
 Mismatches: 73
 Indels: 74
 Query Match:
 RESULT 1309
 ID AAX87412 standard; cDNA; 3607 BP.
 DE Hepatocellular carcinoma marker gene L4 cDNA.
 PN WO9939200-A1.
 PD 05-AUG-1999.
 PA (UNJJE-) UNIV JEFFERSON THOMAS.
 Percent Similarity: 12
 Best Local Similarity: 30.69%
 Mismatches: 87
 Indels: 105
 Query Match:
 RESULT 1310
 ID AAI59470 standard; cDNA; 3613 BP.
 DE Human polynucleotide SEQ ID NO 1673.
 PN WO200153312-A1.

Percent Similarity: 37.59% Conservative: 37
 Best Local Similarity: 23.58% Mismatches: 97
 Query Match: 6.37% Indels: 69
 RESULT 1327
 ID ABA21155 standard; DNA; 1695 BP.
 DE Human nervous system related polynucleotide SEQ ID NO 13486.
 PN WO200159063-A2.
 PD 16-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Percent Similarity: 32.98% Conservative: 10
 Best Local Similarity: 27.66% Mismatches: 92
 Query Match: 6.37% Indels: 34
 RESULT 1328
 ID AAG30164 standard; DNA; 1695 BP.
 DE Human lung antigen genomic DNA #234.
 PN WO200155303-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Percent Similarity: 32.98% Conservative: 10
 Best Local Similarity: 27.66% Mismatches: 92
 Query Match: 6.37% Indels: 34
 RESULT 1329
 ID ADB33501 standard; DNA; 1695 BP.
 DE Human novel lung related polypeptide DNA SEQ ID NO 428.
 PN US2003054368-A1.
 PD 20-MAR-2003.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Percent Similarity: 32.98% Conservative: 10
 Best Local Similarity: 27.66% Mismatches: 92
 Query Match: 6.37% Indels: 34
 RESULT 1330
 ID ABD10477 standard; DNA; 1944 BP.
 DE Pseudomonas aeruginosa polynucleotide #9081.
 PN US6551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Percent Similarity: 37.59% Conservative: 37
 Best Local Similarity: 23.68% Mismatches: 97
 Query Match: 6.37% Indels: 69
 RESULT 1331
 ID ADB63664 standard; cDNA; 2315 BP.
 DE Human cDNA encoding clone THYM20130470.
 PN EP1308459-A2.
 PD 07-MAY-2003.
 PA (HELI-) HELIX RES INST.
 Percent Similarity: 35.16% Conservative: 23
 Best Local Similarity: 26.17% Mismatches: 102
 Query Match: 6.37% Indels: 64
 RESULT 1332
 ID AAH18701 standard; cDNA; 2551 BP.
 DE Human cDNA sequence SEQ ID NO:18968.
 PN EP1074617-A2.
 PD 07-FEB-2001.
 PA (HELI-) HELIX RES INST.
 Percent Similarity: 42.86% Conservative: 32
 Best Local Similarity: 25.93% Mismatches: 76
 Query Match: 6.37% Indels: 32
 RESULT 1333
 ID ACA89902 standard; cDNA; 2637 BP.
 DE Gene differentially regulated in cardiovascular disease #23.
 PN WO2003031650-A2.
 PD 17-APR-2003.
 PA (FARB) BAYER AG.
 Percent Similarity: 33.98% Conservative: 28
 Best Local Similarity: 23.17% Mismatches: 95
 Query Match: 6.37% Indels: 77
 RESULT 1334
 ID ACC77944 standard; DNA; 3221 BP.
 DE Thermus thermophilus mutant DNA polymerase encoding DNA.
 PN WO2003025132-A2.
 PD 27-MAR-2003.
 PA (INVI-) INVITROGEN CORP.

Percent Similarity: 36.30% Conservative: 33
 Best Local Similarity: 25.00% Mismatches: 114
 Query Match: 6.37% Indels: 74
 RESULT 1335
 ID ACC77941 standard; DNA; 3221 BP.
 DE Thermus thermophilus mutant DNA polymerase encoding DNA.
 PN WO2003025132-A2.
 PD 27-MAR-2003.
 PA (INVI-) INVITROGEN CORP.
 Percent Similarity: 36.30% Conservative: 33
 Best Local Similarity: 25.00% Mismatches: 114
 Query Match: 6.37% Indels: 74
 RESULT 1336
 ID ACC77948 standard; DNA; 3221 BP.
 DE Thermus thermophilus mutant DNA polymerase encoding DNA.
 PN WO2003025132-A2.
 PD 27-MAR-2003.
 PA (INVI-) INVITROGEN CORP.
 Percent Similarity: 36.30% Conservative: 33
 Best Local Similarity: 25.00% Mismatches: 114
 Query Match: 6.37% Indels: 74
 RESULT 1337
 ID ACC77956 standard; DNA; 3221 BP.
 DE Thermus thermophilus mutant DNA polymerase encoding DNA.
 PN WO2003025132-A2.
 PD 27-MAR-2003.
 PA (INVI-) INVITROGEN CORP.
 Percent Similarity: 36.30% Conservative: 33
 Best Local Similarity: 25.00% Mismatches: 114
 Query Match: 6.37% Indels: 74
 RESULT 1338
 ID ACC77947 standard; DNA; 3221 BP.
 DE Thermus thermophilus mutant DNA polymerase encoding DNA.
 PN WO2003025132-A2.
 PD 27-MAR-2003.
 PA (INVI-) INVITROGEN CORP.
 Percent Similarity: 36.30% Conservative: 33
 Best Local Similarity: 25.00% Mismatches: 114
 Query Match: 6.37% Indels: 74
 RESULT 1339
 ID ACF79531 standard; cDNA; 4035 BP.
 DE Human E-cadherin repressed clone 1a (hECRepla) cDNA.
 PN WO2003070759-A2.
 PD 28-AUG-2003.
 PA (VLAA-) VLAAms INTERUNIVERSITAIR INST BIOTECHNOG.
 Percent Similarity: 32.98% Conservative: 10
 Best Local Similarity: 27.66% Mismatches: 92
 Query Match: 6.37% Indels: 34
 RESULT 1340
 ID AAD02722 standard; cDNA; 6792 BP.
 DE Human ATP binding cassette2 (ABC2) transporter protein cDNA.
 PN WO200114414-A2.
 PD 01-MAR-2001.
 PA (ACTI-) ACTIVEPASS PHARM INC.
 Percent Similarity: 37.44% Conservative: 24
 Best Local Similarity: 26.07% Mismatches: 92
 Query Match: 6.37% Indels: 40
 RESULT 1341
 ID AAL61173 standard; DNA; 9975 BP.
 DE Actinosynema pretiosum polyketide synthase (PKS) gene #4.
 PN WO2003045312-A2.
 PD 05-JUN-2003.
 PA (UNIW) UNIV WASHINGTON.
 Percent Similarity: 30.61% Conservative: 19
 Best Local Similarity: 24.15% Mismatches: 97
 Query Match: 6.37% Indels: 108
 RESULT 1342
 ID AAF80047 standard; DNA; 13591 BP.
 DE Nucleotide sequence of odorant binding polypeptide OBP1b gene.
 PN WO200112806-A2.
 PD 22-FEB-2001.
 PA (UYAU-) UNIV AUVERGNE.
 PD 27-MAR-2003.
 PA (PITI-) PITIOT G.

Percent Similarity: 35.79% Conservative: 29
 Best Local Similarity: 25.61% Mismatches: 104
 Query Match: 6.37% Indels: 79
 RESULT 1343
 ID ABL66291 standard; DNA; 14800 BP.
 DE Lung cancer related gene sequence SEQ ID NO:4628.
 PN WO200194629-A2.
 PD 13-DEC-2001.
 PA (AVAL-) AVALON PHARM.
 Percent Similarity: 36.07% Conservative: 24
 Best Local Similarity: 26.23% Mismatches: 95
 Query Match: 6.37% Indels: 61
 RESULT 1344
 ID ADP13447 standard; DNA; 14800 BP.
 DE Renal cell carcinoma differentially expressed gene #183.
 PN WO2004048933-A2.
 PD 10-JUN-2004.
 PA (AMHP) WYETH.
 PA (TWIN) TWINE N C.
 PA (BURC) BURCZYNSKI M E.
 PA (TREP) TREPICCHIO W L.
 PA (DORN) DORNER A.
 PA (STOV) STOVER J A.
 PA (SLON) SLONI D K.
 Percent Similarity: 36.07% Conservative: 24
 Best Local Similarity: 26.23% Mismatches: 95
 Query Match: 6.37% Indels: 61
 RESULT 1345
 ID AAV49654 standard; DNA; 29598 BP.
 DE Human SC2 DNA.
 PN WO9830687-A2.
 PD 16-JUL-1998.
 PA (DEKR-) DEUT KRESFORSCHUNGSZENTRUM.
 Percent Similarity: 32.40% Conservative: 15
 Best Local Similarity: 26.40% Mismatches: 77
 Query Match: 6.37% Indels: 92
 RESULT 1346
 ID AAK78219 standard; DNA; 47090 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:33031.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Percent Similarity: 37.06% Conservative: 9
 Best Local Similarity: 31.76% Mismatches: 54
 Query Match: 6.37% Indels: 53
 RESULT 1347
 ID AAK68725 standard; DNA; 47090 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:23537.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Percent Similarity: 37.06% Conservative: 9
 Best Local Similarity: 31.76% Mismatches: 54
 Query Match: 6.37% Indels: 53
 RESULT 1348
 ID ABL69213 standard; DNA; 145831 BP.
 DE Prostate cancer related gene sequence SEQ ID NO:7550.
 PN WO200194629-A2.
 PD 13-DEC-2001.
 PA (AVAL-) AVALON PHARM.
 Percent Similarity: 37.21% Conservative: 13
 Best Local Similarity: 29.65% Mismatches: 60
 Query Match: 6.37% Indels: 49
 RESULT 1349
 ID ABL69213 standard; DNA; 145831 BP.
 DE Prostate cancer related gene sequence SEQ ID NO:7550.
 PN WO200194629-A2.
 PD 13-DEC-2001.
 PA (AVAL-) AVALON PHARM.
 Percent Similarity: 37.06% Conservative: 9
 Best Local Similarity: 31.76% Mismatches: 54
 Query Match: 6.37% Indels: 53
 RESULT 1350
 ID ABL69213 standard; DNA; 145831 BP.
 DE Prostate cancer related gene sequence SEQ ID NO:7550.
 PN WO200194629-A2.
 PD 13-DEC-2001.
 PA (AVAL-) AVALON PHARM.
 Percent Similarity: 37.06% Conservative: 9
 Best Local Similarity: 31.76% Mismatches: 54
 Query Match: 6.37% Indels: 53
 RESULT 1351
 ID ABL66806 standard; DNA; 145831 BP.

DE Lung cancer related gene sequence SEQ ID NO:5143.
 PN WO200194629-A2.
 PD 13-DEC-2001.
 PA (AVAL-) AVALON PHARM.
 Percent Similarity: 37.06% Conservative: 9
 Best Local Similarity: 31.76% Mismatches: 54
 Query Match: 6.37% Indels: 53
 RESULT 1352
 ID ABL68588 standard; DNA; 145831 BP.
 DE Kidney cancer related gene sequence SEQ ID NO:6925.
 PN WO200194629-A2.
 PD 13-DEC-2001.
 PA (AVAL-) AVALON PHARM.
 Percent Similarity: 37.06% Conservative: 9
 Best Local Similarity: 31.76% Mismatches: 54
 Query Match: 6.37% Indels: 53
 RESULT 1353
 ID ABL62309 standard; DNA; 145831 BP.
 DE Colon adenocarcinoma related gene sequence SEQ ID NO:646.
 PN WO200194629-A2.
 PD 13-DEC-2001.
 PA (AVAL-) AVALON PHARM.
 Percent Similarity: 37.06% Conservative: 9
 Best Local Similarity: 31.76% Mismatches: 54
 Query Match: 6.37% Indels: 53
 RESULT 1354
 ID ABT10149 standard; cDNA; 145831 BP.
 DE Human breast cancer associated coding sequence SEQ ID NO: 283.
 PN WO200259271-A2.
 PD 01-AUG-2002.
 PA (GENE-) GENE LOGIC INC.
 Percent Similarity: 37.06% Conservative: 9
 Best Local Similarity: 31.76% Mismatches: 54
 Query Match: 6.37% Indels: 53
 RESULT 1355
 ID ABD08598 standard; DNA; 666 BP.
 DE Pseudomonas aeruginosa polynucleotide #7202.
 PN US6551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Percent Similarity: 36.75% Conservative: 30
 Best Local Similarity: 23.93% Mismatches: 91
 Query Match: 6.33% Indels: 57
 RESULT 1356
 ID ADF02355 standard; DNA; 798 BP.
 DE Bacterial polynucleotide #2640.
 PN US6605709-B1.
 PD 12-AUG-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Percent Similarity: 44.96% Conservative: 20
 Best Local Similarity: 29.46% Mismatches: 53
 Query Match: 6.33% Indels: 18
 RESULT 1357
 ID ADH76894 standard; DNA; 1023 BP.
 DE Partial human SOX18 coding DNA.
 PN US2002142415-A1.
 PD 03-OCT-2002.
 PA (KOOP/) KOOPMAN P A.
 PA (MUSC/) MUSCAT G E O.
 Percent Similarity: 32.92% Conservative: 22
 Best Local Similarity: 23.87% Mismatches: 84
 Query Match: 6.33% Indels: 79
 RESULT 1358
 ID ABK42735 standard; DNA; 1081 BP.
 DE Genomic sequence #634 encoding novel human connective tissue polypeptide.
 PN WO200155343-A1.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Percent Similarity: 39.74% Conservative: 38
 Best Local Similarity: 27.36% Mismatches: 100
 Query Match: 6.33% Indels: 87
 RESULT 1359
 ID AAS36751 standard; DNA; 1081 BP.

DE Human cardiovascular system antigen genomic DNA SEQ ID No 2251.
PN WO200155321-A2.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 39.74%
Best Local Similarity: 27.36%
Query Match: 6.33%
Conservative: 38
Mismatches: 100
Indels: 87
RESULT 1360
ID ADB60891 standard; DNA; 1081 BP.
DE Connective tissue related genomic DNA #634.
PN US2003054375-A1.
PD 20-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 39.74%
Best Local Similarity: 27.36%
Query Match: 6.33%
Conservative: 38
Mismatches: 100
Indels: 87
RESULT 1361
ID ADB47445 standard; DNA; 1081 BP.
DE Human cardiovascular system related genomic DNA #1011.
PN US2003059908-A1.
PD 27-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 39.74%
Best Local Similarity: 27.36%
Query Match: 6.33%
Conservative: 38
Mismatches: 100
Indels: 87
RESULT 1362
ID ADH76899 standard; DNA; 1155 BP.
DE Human SOX18 coding DNA.
PN US2002142415-A1.
PD 03-OCT-2002.
PA (MUSC/) MUSCAT G E O.
Percent Similarity: 32.92%
Best Local Similarity: 23.87%
Query Match: 6.33%
Conservative: 22
Mismatches: 84
Indels: 79
RESULT 1363
ID AAS54093 standard; DNA; 1305 BP.
DE Pseudomonas aeruginosa DNA for cellular proliferation protein #224.
PN WO200170955-A2.
PD 27-SEP-2001.
PA (ELIT-) ELITRA PHARM INC.
Percent Similarity: 40.98%
Best Local Similarity: 27.80%
Query Match: 6.33%
Conservative: 27
Mismatches: 90
Indels: 31
RESULT 1364
ID ACA42238 standard; DNA; 1305 BP.
DE Prokaryotic essential gene #23895.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Percent Similarity: 40.98%
Best Local Similarity: 27.80%
Query Match: 6.33%
Conservative: 27
Mismatches: 90
Indels: 31
RESULT 1365
ID ADN95131 standard; cDNA; 1339 BP.
DE Human Sox18 cDNA sequence SeqID53.
PN WO2003080640-A1.
PD 02-OCT-2003.
PA (LUDW-) LUDWIG INST CANCER RES.
Percent Similarity: 32.92%
Best Local Similarity: 23.87%
Query Match: 6.33%
Conservative: 22
Mismatches: 84
Indels: 79
RESULT 1366
ID ADH76892 standard; cDNA; 1421 BP.
DE Partial human SOX18 cDNA.
PN US2002142415-A1.
PD 03-OCT-2002.
PA (KOOP/) KOOPMAN P A.
Percent Similarity: 32.92%
Best Local Similarity: 23.87%
Query Match: 6.33%
Conservative: 22
Mismatches: 84
Indels: 79
RESULT 1367
ID ACA98969 standard; cDNA; 1729 BP.
DE cDNA encoding human nucleic acid-associated protein (NAAP) #50.
PN WO2003023003-A2.
PD 20-MAR-2003.
PA (INCY-) INCYTE GENOMICS INC.
Percent Similarity: 37.37%
Best Local Similarity: 28.11%
Query Match: 6.33%
Conservative: 26
Mismatches: 97
Indels: 80
RESULT 1368
ID ABS73866 standard; cDNA; 1755 BP.
DE Human cDNA encoding NAAP6, incyte 2294975CB1.
PN WO200274913-A2.
PD 26-SEP-2002.
PA (INCY-) INCYTE GENOMICS INC.
Percent Similarity: 32.92%
Best Local Similarity: 23.87%
Query Match: 6.33%
Conservative: 22
Mismatches: 84
Indels: 79
RESULT 1369
ID ABK35373 standard; cDNA; 1872 BP.
DE Human cDNA encoding secreted protein #511.
PN WO200177288-A2.
PD 18-OCT-2001.
PA (GEMY) GENETICS INST INC.
Percent Similarity: 36.69%
Best Local Similarity: 26.61%
Query Match: 6.33%
Conservative: 25
Mismatches: 90
Indels: 67
RESULT 1370
ID ADH76895 standard; DNA; 1919 BP.
DE Partial human SOX18 genomic DNA.
PN US2002142415-A1.
PD 03-OCT-2002.
PA (KOOP/) KOOPMAN P A.
Percent Similarity: 32.92%
Best Local Similarity: 23.87%
Query Match: 6.33%
Conservative: 22
Mismatches: 84
Indels: 79
RESULT 1371
ID ADB62907 standard; cDNA; 2135 BP.
DE Human cDNA encoding clone PLACE60064180.
PN EPI308459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.
Percent Similarity: 35.80%
Best Local Similarity: 25.29%
Query Match: 6.33%
Conservative: 27
Mismatches: 97
Indels: 68
RESULT 1372
ID ADQ24453 standard; DNA; 2221 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 7273.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Percent Similarity: 36.18%
Best Local Similarity: 26.42%
Query Match: 6.33%
Conservative: 24
Mismatches: 94
Indels: 63
RESULT 1373
ID ACA5288 standard; DNA; 2265 BP.
DE Prokaryotic essential gene #26945.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Percent Similarity: 39.02%
Best Local Similarity: 28.05%
Query Match: 6.33%
Conservative: 18
Mismatches: 46
Indels: 55
RESULT 1374
ID ACA51088 standard; DNA; 2373 BP.
DE Prokaryotic essential gene #32745.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Percent Similarity: 36.80%
Best Local Similarity: 28.57%
Query Match: 6.33%
Conservative: 19
Mismatches: 91

Query Match: 6.33% Indels: 57
 RESULT 1375
 ID ADB63375 standard; cDNA; 2442 BP.
 DE Human cDNA encoding clone TESTI20104090.
 PN EP1308459-A2.
 PD 07-MAY-2003.
 PA (HELI-) HELIX RES INST.
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.
 Percent Similarity: 36.69%
 Best Local Similarity: 26.61%
 Query Match: 6.33%
 RESULT 1376
 ID AAQ80749 standard; DNA; 2505 BP.
 DE T. aquaticus DNA-polymerase.
 PN WO9429482-A1.
 PD 22-DEC-1994.
 PA (THIR-) THIRD WAVE TECHNOLOGIES INC.
 Percent Similarity: 41.16%
 Best Local Similarity: 25.99%
 Query Match: 6.33%
 RESULT 1377
 ID ABO61045 standard; cDNA; 2620 BP.
 DE TEA domain family member 2 encoding sequence.
 PN WO200231111-A2.
 PD 18-APR-2002.
 PA (HYSE-) HYSEQ INC.
 Percent Similarity: 36.69%
 Best Local Similarity: 26.61%
 Query Match: 6.33%
 RESULT 1378
 ID AC47695 standard; DNA; 2694 BP.
 DE Thermus sp. X-1 DNA polymerase (TX1 DNA polymerase)-encoding gene.
 PN KR2002067092-A.
 PD 22-AUG-2002.
 PA (KWON/) KWON S T.
 PA (SUPE-) SUPER BIO CO LTD.
 Percent Similarity: 39.81%
 Best Local Similarity: 26.54%
 Query Match: 6.33%
 RESULT 1379
 ID ACCT7670 standard; DNA; 3026 BP.
 DE Thermus aquaticus mutant DNA polymerase encoding DNA.
 PN WO2003025132-A2.
 PD 27-MAR-2003.
 PA (INVI-) INVITROGEN CORP.
 Percent Similarity: 38.36%
 Best Local Similarity: 26.03%
 Query Match: 6.33%
 RESULT 1380
 ID ACCT7631 standard; DNA; 3026 BP.
 DE Thermus aquaticus mutant DNA polymerase encoding DNA.
 PN WO2003025132-A2.
 PD 27-MAR-2003.
 PA (INVI-) INVITROGEN CORP.
 Percent Similarity: 39.31%
 Best Local Similarity: 24.48%
 Query Match: 6.33%
 RESULT 1381
 ID ACCT7835 standard; DNA; 3026 BP.
 DE Thermus aquaticus mutant DNA polymerase encoding DNA.
 PN WO2003025132-A2.
 PD 27-MAR-2003.
 PA (INVI-) INVITROGEN CORP.
 Percent Similarity: 39.31%
 Best Local Similarity: 24.48%
 Query Match: 6.33%
 RESULT 1382
 ID ACCT7667 standard; DNA; 3026 BP.
 DE Thermus aquaticus mutant DNA polymerase encoding DNA.
 PN WO2003025132-A2.
 PD 27-MAR-2003.
 PA (INVI-) INVITROGEN CORP.
 Percent Similarity: 38.62%
 Best Local Similarity: 26.61%
 Query Match: 6.33%
 RESULT 1383
 ID ACCT7844 standard; DNA; 3026 BP.
 DE Thermus aquaticus mutant DNA polymerase encoding DNA.
 PN WO2003025132-A2.
 PD 27-MAR-2003.
 PA (INVI-) INVITROGEN CORP.
 Percent Similarity: 39.31%
 Best Local Similarity: 24.48%
 Query Match: 6.33%
 RESULT 1384
 ID AAQ10324 standard; cDNA; 3697 BP.
 DE Human Natriuretic Peptide Receptor B.
 PN WO9100292-A.
 PD 10-JAN-1991.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 34.72%
 Best Local Similarity: 27.08%
 Query Match: 6.33%
 RESULT 1385
 ID AAK52426 standard; cDNA; 5553 BP.
 DE Human polynucleotide SEQ ID NO 971.
 PN WO200457150-A2.
 PD 09-AUG-2001.
 PA (HYSE-) HYSEQ INC.
 Percent Similarity: 31.97%
 Best Local Similarity: 21.93%
 Query Match: 6.33%
 RESULT 1386
 ID ABT43729 standard; cDNA; 5987 BP.
 DE Molecule for disease detection and treatment (MDT)-37 cDNA sequence.
 PN WO2003052049-A2.
 PD 26-JUN-2003.
 PA (INCY-) INCYTE GENOMICS INC.
 Percent Similarity: 31.97%
 Best Local Similarity: 21.93%
 Query Match: 6.33%
 RESULT 1387
 ID AAJ59145 standard; DNA; 7178 BP.
 DE DNA encoding a peptide synthetase unit-PKS module.
 PN EPI026248-A2.
 PD 09-AUG-2000.
 PA (UYRA-) UNIV RAMOT APPLIED RES & IND DEV LTD.
 Percent Similarity: 36.97%
 Best Local Similarity: 23.53%
 Query Match: 6.33%
 RESULT 1388
 ID ADQ20518 standard; DNA; 7296 BP.
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 3338.
 PN WO2004048938-A2.
 PD 10-JUN-2004.
 PA (PROT-) PROTEIN DESIGN LABS INC.
 Percent Similarity: 31.97%
 Best Local Similarity: 21.93%
 Query Match: 6.33%
 RESULT 1389
 ID ADJ75976 standard; DNA; 7943 BP.
 DE Marker gene SEQ ID NO:1228.
 PN EPI394274-A2.
 PD 03-MAR-2004.
 PA (GENO-) GENOX RES INC.
 Percent Similarity: 30.21%
 Best Local Similarity: 22.98%
 Query Match: 6.33%
 RESULT 1390
 ID AAX60096 standard; DNA; 17091 BP.
 DE Acetobacter xylinum JCM7664 cellulose synthase gene.
 PN JP11127867-A.
 PD 18-MAY-1999.
 PA (TOEP) TOKYO ELECTRIC POWER CO INC.
 Percent Similarity: 39.13%
 Best Local Similarity: 27.27%
 Query Match: 6.33%

Best Local Similarity: 24.48%
 Query Match: 6.33%
 RESULT 1383
 ID ACCT7844 standard; DNA; 3026 BP.
 DE Thermus aquaticus mutant DNA polymerase encoding DNA.
 PN WO2003025132-A2.
 PD 27-MAR-2003.
 PA (INVI-) INVITROGEN CORP.
 Percent Similarity: 39.31%
 Best Local Similarity: 24.48%
 Query Match: 6.33%
 RESULT 1384
 ID AAQ10324 standard; cDNA; 3697 BP.
 DE Human Natriuretic Peptide Receptor B.
 PN WO9100292-A.
 PD 10-JAN-1991.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 34.72%
 Best Local Similarity: 27.08%
 Query Match: 6.33%
 RESULT 1385
 ID AAK52426 standard; cDNA; 5553 BP.
 DE Human polynucleotide SEQ ID NO 971.
 PN WO200457150-A2.
 PD 09-AUG-2001.
 PA (HYSE-) HYSEQ INC.
 Percent Similarity: 31.97%
 Best Local Similarity: 21.93%
 Query Match: 6.33%
 RESULT 1386
 ID ABT43729 standard; cDNA; 5987 BP.
 DE Molecule for disease detection and treatment (MDT)-37 cDNA sequence.
 PN WO2003052049-A2.
 PD 26-JUN-2003.
 PA (INCY-) INCYTE GENOMICS INC.
 Percent Similarity: 31.97%
 Best Local Similarity: 21.93%
 Query Match: 6.33%
 RESULT 1387
 ID AAJ59145 standard; DNA; 7178 BP.
 DE DNA encoding a peptide synthetase unit-PKS module.
 PN EPI026248-A2.
 PD 09-AUG-2000.
 PA (UYRA-) UNIV RAMOT APPLIED RES & IND DEV LTD.
 Percent Similarity: 36.97%
 Best Local Similarity: 23.53%
 Query Match: 6.33%
 RESULT 1388
 ID ADQ20518 standard; DNA; 7296 BP.
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 3338.
 PN WO2004048938-A2.
 PD 10-JUN-2004.
 PA (PROT-) PROTEIN DESIGN LABS INC.
 Percent Similarity: 31.97%
 Best Local Similarity: 21.93%
 Query Match: 6.33%
 RESULT 1389
 ID ADJ75976 standard; DNA; 7943 BP.
 DE Marker gene SEQ ID NO:1228.
 PN EPI394274-A2.
 PD 03-MAR-2004.
 PA (GENO-) GENOX RES INC.
 Percent Similarity: 30.21%
 Best Local Similarity: 22.98%
 Query Match: 6.33%
 RESULT 1390
 ID AAX60096 standard; DNA; 17091 BP.
 DE Acetobacter xylinum JCM7664 cellulose synthase gene.
 PN JP11127867-A.
 PD 18-MAY-1999.
 PA (TOEP) TOKYO ELECTRIC POWER CO INC.
 Percent Similarity: 39.13%
 Best Local Similarity: 27.27%
 Query Match: 6.33%

Query Match: 6.33% Indels: 62
 RESULT 1391
 ID AAS59514 standard; DNA; 21567 BP.
 DE Propionibacterium acnes immunogenic protein encoding DNA #9.
 PN WO2000161581-A2.
 PD 01-NOV-2001.
 PA (CORI-) CORIXA CORP.
 Percent Similarity: 39.46%
 Best Local Similarity: 27.80%
 Conservatives: 26
 Mismatches: 83
 Indels: 54
 Query Match: 6.33%
 RESULT 1392
 ID ACF64443 standard; DNA; 21567 BP.
 DE Propionibacterium acnes DNA contig sequence #9.
 PN WO2003033515-A1.
 PD 24-APR-2003.
 PA (CORI-) CORIXA CORP.
 Percent Similarity: 39.46%
 Best Local Similarity: 27.80%
 Conservatives: 26
 Mismatches: 83
 Indels: 54
 Query Match: 6.33%
 RESULT 1393
 ID ACF04818 standard; DNA; 51855 BP.
 DE Melithiazol biosynthetic gene cluster.
 PN WO2003080828-A2.
 PD 02-OCT-2003.
 PA (GBFB) GBF GES BIOTECH FORSCHUNG GMBH.
 Percent Similarity: 37.29%
 Best Local Similarity: 27.12%
 Conservatives: 24
 Mismatches: 92
 Indels: 56
 Query Match: 6.33%
 RESULT 1394
 ID AAM58471 standard; DNA; 58857 BP.
 DE Nucleotide sequence of the bleomycin (BLM) gene cluster ORFs 8-30.
 PN WO200040704-A1.
 PD 13-JUL-2000.
 PA (REGC) UNIV CALIFORNIA.
 Percent Similarity: 34.26%
 Best Local Similarity: 26.29%
 Conservatives: 20
 Mismatches: 88
 Indels: 77
 Query Match: 6.33%
 RESULT 1395
 ID ABX04971 standard; DNA; 103599 BP.
 DE S. cinamonensis monensin type I polyketide synthase gene cluster.
 PN WO200168867-A1.
 PD 20-SEP-2001.
 PA (BIOT-) BIOTICA TECHNOLOGY LTD.
 Percent Similarity: 37.50%
 Best Local Similarity: 24.50%
 Conservatives: 26
 Mismatches: 79
 Indels: 49
 Query Match: 6.33%
 RESULT 1396
 ID ABQ88139 standard; DNA; 103747 BP.
 DE Human osteoblast differentiation related cDNA SEQ ID NO 46.
 PN WO200250301-A2.
 PD 27-JUN-2002.
 PA (GENE-) GENE LOGIC INC.
 Percent Similarity: 33.81%
 Best Local Similarity: 23.38%
 Conservatives: 29
 Mismatches: 101
 Indels: 84
 Query Match: 6.33%
 RESULT 1397
 ID AAV20458 standard; DNA; 534720 BP.
 DE Rhizobium species plasmid pNGR234.
 PN WO20004033445-A2.
 PD 22-APR-2004.
 PA (ZYMO) ZYMOGENETICS INC.
 Percent Similarity: 34.35%
 Best Local Similarity: 25.22%
 Conservatives: 21
 Mismatches: 79
 Indels: 72
 Query Match: 6.29%
 RESULT 1400
 ID AAN81032 standard; cDNA; 909 BP.
 DE cDNA encoding a polypeptide having human haematopoietic cell growth DE potentiating factor (HCGPF) activity.
 PN EP274560-A.
 PD 20-JUL-1988.
 PA (AJIN) AJINOMOTO KK.
 Percent Similarity: 38.34%
 Best Local Similarity: 26.09%
 Conservatives: 31
 Mismatches: 94
 Indels: 63
 Query Match: 6.29%
 RESULT 1402
 ID ABK35605 standard; DNA; 1056 BP.
 DE Gene encoding novel human secreted or membrane-associated protein #24.
 PN WO200204600-A2.
 PD 17-JAN-2002.
 PA (SMIK) SMITHKLINE BEECHAM CORP.
 Percent Similarity: 34.27%
 Best Local Similarity: 26.61%
 Conservatives: 19
 Mismatches: 85
 Indels: 78
 Query Match: 6.29%
 RESULT 1403
 ID ABJ02649 standard; cDNA; 1128 BP.
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 2429.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Percent Similarity: 38.16%
 Best Local Similarity: 27.30%
 Conservatives: 33
 Mismatches: 102
 Indels: 86
 Query Match: 6.29%
 RESULT 1404
 ID ADP98700 standard; DNA; 1137 BP.
 DE C. albicans specific gene, orf6.1285, DNA sequence.
 PN WO20004056965-A2.
 PD 08-JUL-2004.
 PA (ELIT-) ELITRA PHARM INC.
 Percent Similarity: 37.58%
 Best Local Similarity: 21.82%
 Conservatives: 26
 Mismatches: 68
 Indels: 35
 Query Match: 6.29%
 RESULT 1405
 ID AAF83684 standard; DNA; 1161 BP.
 DE Short form of motilin receptor, GPR-38B isoform encoding DNA.
 PN WO200138355-A2.
 PD 31-MAY-2001.
 PA (ZYMO) ZYMOGENETICS INC.
 Percent Similarity: 34.35%
 Best Local Similarity: 25.22%
 Conservatives: 21
 Mismatches: 79
 Indels: 72
 Query Match: 6.29%
 RESULT 1406
 ID ADN11762 standard; cDNA; 1161 BP.
 DE Human motilin receptor GPR-38B coding sequence.
 PN WO20004033445-A2.
 PD 22-APR-2004.
 PA (ZYMO) ZYMOGENETICS INC.
 Percent Similarity: 34.35%
 Best Local Similarity: 25.22%
 Conservatives: 21
 Mismatches: 79
 Indels: 72
 Query Match: 6.29%
 RESULT 1407
 ID ACA44039 standard; DNA; 1176 BP.
 DE Prokaryotic essential gene #25696.
 PN WO200277183-A2.
 PD 03-OCT-2002.
 PA (ELIT-) ELITRA PHARM INC.
 Percent Similarity: 35.38%
 Best Local Similarity: 24.23%
 Conservatives: 29
 Mismatches: 78

Percent Similarity: 37.22%
 Best Local Similarity: 23.31%
 Conservatives: 37
 Mismatches: 116
 Indels: 51
 Query Match: 6.33%
 RESULT 1400
 ID AAN81032 standard; cDNA; 909 BP.
 DE cDNA encoding a polypeptide having human haematopoietic cell growth DE potentiating factor (HCGPF) activity.
 PN EP274560-A.
 PD 20-JUL-1988.
 PA (AJIN) AJINOMOTO KK.
 Percent Similarity: 38.34%
 Best Local Similarity: 26.09%
 Conservatives: 31
 Mismatches: 94
 Indels: 63
 Query Match: 6.29%
 RESULT 1402
 ID ABK35605 standard; DNA; 1056 BP.
 DE Gene encoding novel human secreted or membrane-associated protein #24.
 PN WO200204600-A2.
 PD 17-JAN-2002.
 PA (SMIK) SMITHKLINE BEECHAM CORP.
 Percent Similarity: 34.27%
 Best Local Similarity: 26.61%
 Conservatives: 19
 Mismatches: 85
 Indels: 78
 Query Match: 6.29%
 RESULT 1403
 ID ABJ02649 standard; cDNA; 1128 BP.
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 2429.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Percent Similarity: 38.16%
 Best Local Similarity: 27.30%
 Conservatives: 33
 Mismatches: 102
 Indels: 86
 Query Match: 6.29%
 RESULT 1404
 ID ADP98700 standard; DNA; 1137 BP.
 DE C. albicans specific gene, orf6.1285, DNA sequence.
 PN WO20004056965-A2.
 PD 08-JUL-2004.
 PA (ELIT-) ELITRA PHARM INC.
 Percent Similarity: 37.58%
 Best Local Similarity: 21.82%
 Conservatives: 26
 Mismatches: 68
 Indels: 35
 Query Match: 6.29%
 RESULT 1405
 ID AAF83684 standard; DNA; 1161 BP.
 DE Short form of motilin receptor, GPR-38B isoform encoding DNA.
 PN WO200138355-A2.
 PD 31-MAY-2001.
 PA (ZYMO) ZYMOGENETICS INC.
 Percent Similarity: 34.35%
 Best Local Similarity: 25.22%
 Conservatives: 21
 Mismatches: 79
 Indels: 72
 Query Match: 6.29%
 RESULT 1406
 ID ADN11762 standard; cDNA; 1161 BP.
 DE Human motilin receptor GPR-38B coding sequence.
 PN WO20004033445-A2.
 PD 22-APR-2004.
 PA (ZYMO) ZYMOGENETICS INC.
 Percent Similarity: 34.35%
 Best Local Similarity: 25.22%
 Conservatives: 21
 Mismatches: 79
 Indels: 72
 Query Match: 6.29%
 RESULT 1407
 ID ACA44039 standard; DNA; 1176 BP.
 DE Prokaryotic essential gene #25696.
 PN WO200277183-A2.
 PD 03-OCT-2002.
 PA (ELIT-) ELITRA PHARM INC.
 Percent Similarity: 35.38%
 Best Local Similarity: 24.23%
 Conservatives: 29
 Mismatches: 78

Query Match: 6.29% Indels: 91
 RESULT 1408
 ID ADA83986 standard; DNA; 1186 BP.
 DE Human CDKSR2 gene.
 PN WO2002103028-A2.
 PD 27-DEC-2002.
 PA (BIOM-) BIOMEDICAL CENT.
 Percent Similarity: 38.5%
 Best Local Similarity: 27.14%
 Query Match: 6.29%
 RESULT 1409
 ID ABD07713 standard; DNA; 1260 BP.
 DE Pseudomonas aeruginosa polynucleotide #6317.
 PN US6551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Percent Similarity: 30.26%
 Best Local Similarity: 22.51%
 Query Match: 6.29%
 RESULT 1410
 ID AA245404 standard; cDNA; 1390 BP.
 DE cDNA encoding the motilin receptor splice variant MTL-R1B.
 PN WO9964436-A1.
 PD 16-DEC-1999.
 PA (MERI) MERCK & CO INC.
 Percent Similarity: 34.35%
 Best Local Similarity: 25.22%
 Query Match: 6.29%
 RESULT 1411
 ID ABD10868 standard; DNA; 1524 BP.
 DE Pseudomonas aeruginosa polynucleotide #9472.
 PN US6551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Percent Similarity: 35.86%
 Best Local Similarity: 27.24%
 Query Match: 6.29%
 RESULT 1412
 ID ABL26243 standard; DNA; 1863 BP.
 DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 30202.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Percent Similarity: 37.74%
 Best Local Similarity: 28.40%
 Query Match: 6.29%
 RESULT 1413
 ID AAA46116 standard; cDNA; 2040 BP.
 DE Human G protein coupled receptor hGPR38 (V297K) cDNA SEQ ID NO:129.
 PN WO200022131-A2.
 PD 20-APR-2000.
 PA (AREN-) ARENA PHARM INC.
 Percent Similarity: 34.35%
 Best Local Similarity: 25.22%
 Query Match: 6.29%
 RESULT 1414
 ID ADG86512 standard; DNA; 2040 BP.
 DE Human orphan GPCR-associated DNA #1.
 PN US2003229216-A1.
 PD 11-DEC-2003.
 PA (CHEN/) CHEN R.
 PA (LIAM/) LIAM C W.
 PA (LOWI/) LOWITZ K.
 PA (CHAL/) CHALMERS D T.
 PA (BEHA/) BEHAN D P.
 Percent Similarity: 34.35%
 Best Local Similarity: 25.22%
 Query Match: 6.29%
 RESULT 1415
 ID ADG86490 standard; cDNA; 2040 BP.
 DE Human hGPR38 V297K mutant cDNA.
 PN US2003229216-A1.
 PD 11-DEC-2003.

PA (CHEN/) CHEN R.
 PA (LIAM/) LIAM C W.
 PA (LOWI/) LOWITZ K.
 PA (CHAL/) CHALMERS D T.
 PA (BEHA/) BEHAN D P.
 Percent Similarity: 34.35%
 Best Local Similarity: 25.22%
 Query Match: 6.29%
 RESULT 1416
 ID ADP20283 standard; DNA; 2040 BP.
 DE Human GPCR GPR38 V297K mutant DNA.
 PN US2004110218-A1.
 PD 10-JUN-2004.
 PA (CHEN/) CHEN R.
 PA (LIAM/) LIAM C W.
 PA (LOWI/) LOWITZ K.
 PA (CHAL/) CHALMERS D T.
 PA (BEHA/) BEHAN D P.
 Percent Similarity: 34.35%
 Best Local Similarity: 25.22%
 Query Match: 6.29%
 RESULT 1417
 ID AAF61014 standard; DNA; 2397 BP.
 DE P. putida KT2440-associated DNA ORF04125.
 PN DE19935088-A1.
 PD 01-FEB-2001.
 PA (TIGR-) TIGR INST GENOMIC RES.
 PA (QUIA-) QUIAGEN GMBH.
 PA (GRFB) GES BIOTECHNOLOGISCHE FORSCHUNG MBH.
 PA (DKFZ-) DKFZ DEUT KREBSFORSCHUNGSZENTRUM.
 PA (MEDI-) MEDIZINISCHE HOCHSCHULE HANNOVER.
 Percent Similarity: 34.70%
 Best Local Similarity: 23.88%
 Query Match: 6.29%
 RESULT 1418
 ID ABD12695 standard; DNA; 2406 BP.
 DE Pseudomonas aeruginosa polynucleotide #11299.
 PN US6551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Percent Similarity: 35.12%
 Best Local Similarity: 27.32%
 Query Match: 6.29%
 RESULT 1419
 ID ADO00918 standard; cDNA; 2904 BP.
 DE Fruit fly AD-related cDNA CG14918.
 PN US2004067535-A1.
 PD 08-APR-2004.
 PA (LIFE-) LIFE SCI DEV CORP.
 Percent Similarity: 37.74%
 Best Local Similarity: 28.40%
 Query Match: 6.29%
 RESULT 1420
 ID AAL61203 standard; DNA; 3018 BP.
 DE Actinosynnema pretiosum cytochrome P450 gene.
 PN WO2003045312-A2.
 PD 05-JUN-2003.
 PA (UNIW) UNIV WASHINGTON.
 Percent Similarity: 34.46%
 Best Local Similarity: 26.22%
 Query Match: 6.29%
 RESULT 1421
 ID ACC77755 standard; DNA; 3026 BP.
 DE Thermus aquaticus mutant DNA polymerase encoding DNA.
 PN WO2003025132-A2.
 PD 27-MAR-2003.
 PA (INVI-) INVITROGEN CORP.
 Percent Similarity: 37.93%
 Best Local Similarity: 24.48%
 Query Match: 6.29%
 RESULT 1422
 ID AA245402 standard; DNA; 3066 BP.
 DE Genomic sequence of the motilin receptor gene including 5' UTR.

PN WO9964436-A1.
PA 16-DEC-1999.
PA (MERI) MERCK & CO INC.
Percent Similarity: 34.35%
Best Local Similarity: 24.35%
Query Match: 6.29%
Conservative: 21
Mismatches: 79
Indels: 72
RESULT 1423
ID ACC77957 standard; DNA; 3221 BP.
DE Thermus thermophilus mutant DNA polymerase encoding DNA.
PN WO2003025132-A2.
PD 27-MAR-2003.
PA (INVI-) INVITROGEN CORP.
Percent Similarity: 36.30%
Best Local Similarity: 25.00%
Query Match: 6.29%
Conservative: 33
Mismatches: 114
Indels: 74
RESULT 1424
ID ACC77946 standard; DNA; 3221 BP.
DE Thermus thermophilus mutant DNA polymerase encoding DNA.
PN WO2003025132-A2.
PD 27-MAR-2003.
PA (INVI-) INVITROGEN CORP.
Percent Similarity: 36.30%
Best Local Similarity: 25.00%
Query Match: 6.29%
Conservative: 33
Mismatches: 114
Indels: 74
RESULT 1425
ID AAX87773 standard; cDNA; 3358 BP.
DE Human mucin gene MUC 5AC cDNA.
PN WO9941270-A1.
PD 19-AUG-1999.
PA (RECC) UNIV CALIFORNIA.
Percent Similarity: 37.17%
Best Local Similarity: 28.32%
Query Match: 6.29%
Conservative: 20
Mismatches: 79
Indels: 64
RESULT 1426
ID ADJ60926 standard; DNA; 4157 BP.
DE Concatemer of PDB4A oligonucleotides.
PN WO2004011613-A2.
PD 05-FEB-2004.
PA (EPIG-) EPIGENESIS PHARM INC.
Percent Similarity: 41.40%
Best Local Similarity: 25.81%
Query Match: 6.29%
Conservative: 29
Mismatches: 72
Indels: 37
RESULT 1427
ID ADO46415 standard; DNA; 4167 BP.
DE Human oligonucleotide #1781.
PN US2004049022-A1.
PD 11-MAR-2004.
PA (NYCE/) NYCE J W.
PA (SAND/) SANDRASAGRA A.
PA (TANG/) TANG L.
PA (AGUI/) AGUILAR D.
PA (MILL/) MILLER S.
PA (SHAH/) SHAHABUDDIN S.
PA (LUHH/) LU H.
PA (CONG/) CONG H.
Percent Similarity: 41.40%
Best Local Similarity: 25.81%
Query Match: 6.29%
Conservative: 29
Mismatches: 72
Indels: 37
RESULT 1428
ID AAH48621 standard; DNA; 13055 BP.
DE Human fascin DNA fragment #1.
PN WO200151631-A2.
PD 19-JUL-2001.
PA (RESK/) RESKE-KUNZ A.
PA (ROSS/) ROSS X.
PA (ROSS/) ROSS R.
PA (BROS/) BROS M.
Percent Similarity: 32.54%
Best Local Similarity: 23.39%
Query Match: 6.29%
Conservative: 27
Mismatches: 92
Indels: 107
RESULT 1429
ID ABL12192 standard; cDNA; 15372 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 31058.

PN WO200171042-A2.
PA 27-SEP-2001.
PA (PEKE) PE CORP NY.
Percent Similarity: 36.24%
Best Local Similarity: 23.69%
Query Match: 6.29%
Conservative: 36
Mismatches: 84
Indels: 100
RESULT 1430
ID AAF87198 standard; DNA; 22735 BP.
DE Human ion3 coding sequence #2.
PN WO200144283-A2.
PD 21-JUN-2001.
PA (PHAA) PHARMACIA & UPJOHN CO.
Percent Similarity: 43.48%
Best Local Similarity: 29.81%
Query Match: 6.29%
Conservative: 22
Mismatches: 49
Indels: 42
RESULT 1431
ID AAQ10190 standard; DNA; 23666 BP.
DE Cephalosporin antibiotic biosynthetic genes.
PN JP02291274-A.
PD 03-DEC-1990.
PA (TAKE) TAKEDA CHEM IND LTD.
Percent Similarity: 35.80%
Best Local Similarity: 24.28%
Query Match: 6.29%
Conservative: 28
Mismatches: 90
Indels: 66
RESULT 1432
ID AAX24332 standard; DNA; 34446 BP.
DE Bovine adenovirus type 3 genome.
PN WO9859063-A2.
PD 30-DEC-1998.
PA (UYSA-) UNIV SASKATCHEWAN.
Percent Similarity: 33.46%
Best Local Similarity: 25.00%
Query Match: 6.29%
Conservative: 23
Mismatches: 78
Indels: 103
RESULT 1433
ID ABA92463 standard; DNA; 34446 BP.
DE Bovine adenovirus type 3 complete genomic DNA sequence SEQ ID NO:35.
PN US6319716-B1.
PD 20-NOV-2001.
PA (UYSA-) UNIV SASKATCHEWAN.
Percent Similarity: 33.46%
Best Local Similarity: 25.00%
Query Match: 6.29%
Conservative: 23
Mismatches: 78
Indels: 103
RESULT 1434
ID ABA97532 standard; DNA; 34446 BP.
DE Bovine adenovirus 3 genome.
PN WO200192547-A2.
PD 06-DEC-2001.
PA (UYSA-) UNIV SASKATCHEWAN.
Percent Similarity: 33.46%
Best Local Similarity: 25.00%
Query Match: 6.29%
Conservative: 23
Mismatches: 78
Indels: 103
RESULT 1435
ID ADO47033 standard; DNA; 48480 BP.
DE Human oligonucleotide #2399.
PN US2004049022-A1.
PD 11-MAR-2004.
PA (NYCE/) NYCE J W.
PA (SAND/) SANDRASAGRA A.
PA (TANG/) TANG L.
PA (AGUI/) AGUILAR D.
PA (MILL/) MILLER S.
PA (SHAH/) SHAHABUDDIN S.
PA (LUHH/) LU H.
PA (CONG/) CONG H.
Percent Similarity: 41.40%
Best Local Similarity: 25.81%
Query Match: 6.29%
Conservative: 29
Mismatches: 72
Indels: 37
RESULT 1436
ID ADJ61643 standard; DNA; 48765 BP.
DE Concatemer of all oligonucleotides of invention.
PN WO2004011613-A2.
PD 05-FEB-2004.
PA (EPIG-) EPIGENESIS PHARM INC.

Percent Similarity: 41.40% Conservative: 29
 Best Local Similarity: 25.83% Mismatches: 37
 Query Match: 6.29% Indels: 37
 RESULT 1437
 ID ABQ77491 standard; DNA; 67459 BP.
 DE S. aurantiaca DNA containing sti gene cluster.
 PN DE10128661-A1.
 PD 19-DEC-2002.
 PA (GBPB) GBS BIOTECHNOLOGISCHE FORSCHUNG MBH.
 Percent Similarity: 34.66% Conservative: 32
 Best Local Similarity: 23.10% Mismatches: 100
 Query Match: 6.29% Indels: 82
 RESULT 1438
 ID ADG70447 standard; DNA; 410846 BP.
 DE Human ANGB-CLLD8-CLLD7 hybrid gene.
 PN WO2003000727-A2.
 PD 03-JAN-2003.
 PA (ISIS-) ISIS INNOVATIONS LTD.
 Percent Similarity: 34.35% Conservative: 21
 Best Local Similarity: 25.23% Mismatches: 79
 Query Match: 6.29% Indels: 72
 RESULT 1439
 ID AB279565 standard; DNA; 410846 BP.
 DE CLLD8 and NY-REN-34 encoding DNA.
 PN WO200300296-A2.
 PD 03-JAN-2003.
 PA (ISIS-) ISIS INNOVATIONS LTD.
 Percent Similarity: 34.35% Conservative: 21
 Best Local Similarity: 25.23% Mismatches: 79
 Query Match: 6.29% Indels: 72
 RESULT 1440
 ID ABQ63083 standard; DNA; 314 BP.
 DE Mycobacterium tuberculosis BAC vector clone RV45T7.
 PN WO9954487-A2.
 PD 28-OCT-1999.
 PA (INSP) INST PASTEUR.
 Percent Similarity: 53.06% Conservative: 6
 Best Local Similarity: 40.83% Mismatches: 19
 Query Match: 6.25% Indels: 4
 RESULT 1441
 ID ADC75612 standard; DNA; 611 BP.
 DE DNA homologous to phytopathogen resistance-related cDNA - SEQ ID 536.
 PN WO2003020905-A2.
 PD 13-MAR-2003.
 PA (DOWC) DOW CHEM CO.
 Percent Similarity: 34.71% Conservative: 15
 Best Local Similarity: 25.88% Mismatches: 59
 Query Match: 6.25% Indels: 52
 RESULT 1442
 ID ADN37281 standard; cDNA; 633 BP.
 DE Wheat thaumatin-like protein encoding cDNA SEQ ID NO:25.
 PN WO2004035790-A1.
 PD 29-APR-2004.
 PA (MOLE-) MOLECULAR PLANT BREEDING NOMINERS LTD.
 Percent Similarity: 44.07% Conservative: 12
 Best Local Similarity: 33.90% Mismatches: 43
 Query Match: 6.25% Indels: 23
 RESULT 1443
 ID AAT12172 standard; cDNA; 971 BP.
 DE Partial pUG4-5-CDK-BP cDNA clone #121 encoding CDK4 binding protein.
 PN WO9533819-A2.
 PD 14-DEC-1995.
 PA (MITO-) MITOTIX INC.
 Percent Similarity: 35.19% Conservative: 19
 Best Local Similarity: 26.39% Mismatches: 85
 Query Match: 6.25% Indels: 55
 RESULT 1444
 ID AAA50562 standard; DNA; 1017 BP.
 DE DNA encoding BHV-1 truncated gD-bovine GnrH tetramer fusion.
 PN EP1035133-A2.
 PD 13-SEP-2000.
 PA (PFIZ) PFIZER PROD INC.

Percent Similarity: 37.97% Conservative: 27
 Best Local Similarity: 26.58% Mismatches: 93
 Query Match: 6.25% Indels: 55
 RESULT 1445
 ID AAA50560 standard; DNA; 1020 BP.
 DE DNA encoding BHV-1 truncated mature gD antigen.
 PN EP1035133-A2.
 PD 13-SEP-2000.
 PA (PFIZ) PFIZER PROD INC.
 Percent Similarity: 37.97% Conservative: 27
 Best Local Similarity: 26.58% Mismatches: 93
 Query Match: 6.25% Indels: 55
 RESULT 1446
 ID ACA40569 standard; DNA; 1032 BP.
 DE Prokaryotic essential gene #22226.
 PN WO200277183-A2.
 PD 03-OCT-2002.
 PA (ELIT-) ELITRA PHARM INC.
 Percent Similarity: 38.61% Conservative: 13
 Best Local Similarity: 30.38% Mismatches: 62
 Query Match: 6.25% Indels: 36
 RESULT 1447
 ID ABD17716 standard; DNA; 1065 BP.
 DE Pseudomonas aeruginosa polynucleotide #16320.
 PN US5551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Percent Similarity: 38.00% Conservative: 20
 Best Local Similarity: 28.00% Mismatches: 73
 Query Match: 6.25% Indels: 51
 RESULT 1448
 ID AAA50555 standard; DNA; 1079 BP.
 DE DNA encoding BHV-1 truncated gD antigen.
 PN EP1035133-A2.
 PD 13-SEP-2000.
 PA (PFIZ) PFIZER PROD INC.
 Percent Similarity: 37.97% Conservative: 27
 Best Local Similarity: 26.58% Mismatches: 93
 Query Match: 6.25% Indels: 55
 RESULT 1449
 ID AAA50564 standard; DNA; 1144 BP.
 DE DNA encoding BHV-1 truncated gD-bovine GnrH tetramer fusion.
 PN EP1035133-A2.
 PD 13-SEP-2000.
 PA (PFIZ) PFIZER PROD INC.
 Percent Similarity: 37.97% Conservative: 27
 Best Local Similarity: 26.58% Mismatches: 93
 Query Match: 6.25% Indels: 55
 RESULT 1450
 ID ACD20408 standard; DNA; 1144 BP.
 DE DNA encoding human NOV23 protein.
 PN WO200298917-A2.
 PD 12-DEC-2002.
 PA (CURA-) CURAGEN CORP.
 Percent Similarity: 37.30% Conservative: 22
 Best Local Similarity: 28.57% Mismatches: 75
 Query Match: 6.25% Indels: 84
 RESULT 1451
 ID AAA50559 standard; DNA; 1179 BP.
 DE DNA encoding bovine GnrH tetramer-truncated BHV-1 gD fusion.
 PN EP1035133-A2.
 PD 13-SEP-2000.
 PA (PFIZ) PFIZER PROD INC.
 Percent Similarity: 37.97% Conservative: 27
 Best Local Similarity: 26.58% Mismatches: 93
 Query Match: 6.25% Indels: 55
 RESULT 1452
 ID ABK64534 standard; DNA; 1238 BP.
 DE Human benign prostatic hyperplasia gene #429.
 PN WO200212440-A2.
 PD 14-FEB-2002.
 PA (GENE-) GENE LOGIC INC.
 PA (NISR) JAPAN TOBACCO INC.

Percent Similarity: 37.61% Conservative: 32
 Best Local Similarity: 23.93% Mismatches: 96
 Query Match: 6.25% Indels: 50
 RESULT 1453
 ID ACH00815 standard; DNA; 1238 BP.
 DE Human spermidine synthase coding sequence.
 PN WO2003075945-A2.
 PD 18-SEP-2003.
 PA (DSVE-) DVELOGEN ENTWICKLUNGSBIOLOGISCHE FORSCH.
 Percent Similarity: 37.61% Conservative: 32
 Best Local Similarity: 23.93% Mismatches: 96
 Query Match: 6.25% Indels: 50
 RESULT 1454
 ID AD019193 standard; cDNA; 1238 BP.
 DE Human PRO polynucleotide #64.
 PN WO2004043361-A2.
 PD 27-MAY-2004.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 37.61% Conservative: 32
 Best Local Similarity: 23.93% Mismatches: 96
 Query Match: 6.25% Indels: 50
 RESULT 1455
 ID AA450556 standard; DNA; 1241 BP.
 DE DNA encoding BHV-1 truncated gD-bovine GnRH tetramer fusion.
 PN EP1035133-A2.
 PD 13-SEP-2000.
 PA (PFIZ) PFIZER PROD INC.
 Percent Similarity: 37.97% Conservative: 27
 Best Local Similarity: 26.58% Mismatches: 93
 Query Match: 6.25% Indels: 55
 RESULT 1456
 ID AA450549 standard; DNA; 1265 BP.
 DE DNA encoding bovine herpesvirus type 1 gD antigen.
 PN EP1035133-A2.
 PD 13-SEP-2000.
 PA (PFIZ) PFIZER PROD INC.
 Percent Similarity: 37.97% Conservative: 27
 Best Local Similarity: 26.58% Mismatches: 93
 Query Match: 6.25% Indels: 55
 RESULT 1457
 ID AA450563 standard; DNA; 1272 BP.
 DE DNA encoding GnRH tetramer-BHV-1 truncated gD-GnRH tetramer fusion.
 PN EP1035133-A2.
 PD 13-SEP-2000.
 PA (PFIZ) PFIZER PROD INC.
 Percent Similarity: 37.97% Conservative: 27
 Best Local Similarity: 26.58% Mismatches: 93
 Query Match: 6.25% Indels: 55
 RESULT 1458
 ID AA450551 standard; DNA; 1279 BP.
 DE DNA encoding BHV-1 truncated gD antigen-6His fusion.
 PN EP1035133-A2.
 PD 13-SEP-2000.
 PA (PFIZ) PFIZER PROD INC.
 Percent Similarity: 37.97% Conservative: 27
 Best Local Similarity: 26.58% Mismatches: 93
 Query Match: 6.25% Indels: 55
 RESULT 1459
 ID AAV73326 standard; DNA; 1290 BP.
 DE Human CD18 pseudogene clone 6 DNA.
 PN DE19716346-C1.
 PD 19-NOV-1998.
 PA (WAGE/) WAGENER C.
 Percent Similarity: 32.55% Conservative: 22
 Best Local Similarity: 23.92% Mismatches: 80
 Query Match: 6.25% Indels: 93
 RESULT 1460
 ID ABD17357 standard; DNA; 1332 BP.
 DE Pseudomonas aeruginosa polynucleotide #15961.
 PN US6551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Percent Similarity: 38.00% Conservative: 20

Best Local Similarity: 28.00% Mismatches: 73
 Query Match: 6.25% Indels: 51
 RESULT 1461
 ID ABD17940 standard; DNA; 1341 BP.
 DE Pseudomonas aeruginosa polynucleotide #16544.
 PN US6551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Percent Similarity: 37.35% Conservative: 23
 Best Local Similarity: 28.11% Mismatches: 88
 Query Match: 6.25% Indels: 69
 RESULT 1462
 ID AA450553 standard; DNA; 1360 BP.
 DE DNA encoding BHV-1 truncated gD-bovine GnRH tetramer fusion.
 PN EP1035133-A2.
 PD 13-SEP-2000.
 PA (PFIZ) PFIZER PROD INC.
 Percent Similarity: 37.97% Conservative: 27
 Best Local Similarity: 26.58% Mismatches: 93
 Query Match: 6.25% Indels: 55
 RESULT 1463
 ID AA450552 standard; DNA; 1360 BP.
 DE DNA encoding bovine GnRH tetramer-truncated BHV-1 gD fusion.
 PN EP1035133-A2.
 PD 13-SEP-2000.
 PA (PFIZ) PFIZER PROD INC.
 Percent Similarity: 37.97% Conservative: 27
 Best Local Similarity: 26.58% Mismatches: 93
 Query Match: 6.25% Indels: 55
 RESULT 1464
 ID AAQ42687 standard; DNA; 1405 BP.
 DE Sequence encoding a recombinant subunit antigen comprising a truncated DE bovine herpesvirus type 1 (BHV-1) giv glycoprotein.
 PN WO9311792-A1.
 PD 24-JUN-1993.
 PA (UYSA-) UNIV SASKATCHEWAN.
 Percent Similarity: 37.97% Conservative: 27
 Best Local Similarity: 26.58% Mismatches: 93
 Query Match: 6.25% Indels: 55
 RESULT 1465
 ID AAQ48251 standard; DNA; 1405 BP.
 DE Bovine herpesvirus type I giv gene.
 PN CA2057387-A.
 PD 12-JUN-1993.
 PA (VETE-) VETERINARY INFECTIOUS DISEASE.
 Percent Similarity: 37.97% Conservative: 27
 Best Local Similarity: 26.58% Mismatches: 93
 Query Match: 6.25% Indels: 55
 RESULT 1466
 ID AAQ94354 standard; DNA; 1405 BP.
 DE BHV1 giv glycoprotein genomic DNA.
 PN US5462734-A.
 PD 31-OCT-1995.
 PA (WISC) WISCONSIN ALUMNI RES FOUND.
 Percent Similarity: 37.97% Conservative: 27
 Best Local Similarity: 26.58% Mismatches: 93
 Query Match: 6.25% Indels: 55
 RESULT 1467
 ID AAV62389 standard; DNA; 1405 BP.
 DE Bovine herpes virus type-1 glycoprotein IV (BHV-1-gD) encoding DNA.
 PN EP873752-A2.
 PD 28-OCT-1998.
 PA (PFIZ) PFIZER INC.
 Percent Similarity: 37.97% Conservative: 27
 Best Local Similarity: 26.58% Mismatches: 93
 Query Match: 6.25% Indels: 55
 RESULT 1468
 ID AA450550 standard; DNA; 1405 BP.
 DE DNA encoding bovine herpesvirus type 1 gD antigen.
 PN EP1035133-A2.
 PD 13-SEP-2000.

PA (PFIZ) PRIZER PROD INC.
Percent Similarity: 37.97%
Best Local Similarity: 26.58%
Query Match: 6.25%
RESULT 1469
ID AAA50554 standard; DNA; 1441 BP.
DE DNA encoding GnRH tetramer-BHV-1 truncated gp-GnRH tetramer fusion.
PN EP1035133-A2.
PD 13-SEP-2000.
PA (PFIZ) PRIZER PROD INC.
Percent Similarity: 37.97%
Best Local Similarity: 26.58%
Query Match: 6.25%
RESULT 1470
ID ADQ23266 standard; DNA; 1737 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 6086.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Percent Similarity: 32.58%
Best Local Similarity: 23.22%
Query Match: 6.25%
RESULT 1471
ID AAQ98947 standard; DNA; 1785 BP.
DE bg11 insert encoding a B-G subregion fragment of fowl MHC.
PN US545670-A.
PD 19-SEP-1995.
PA (CITY) CITY OF HOPE.
Percent Similarity: 40.31%
Best Local Similarity: 26.18%
Query Match: 6.25%
RESULT 1472
ID AAD03976 standard; cDNA; 1785 BP.
DE Chicken bg11 cDNA clone.
PN US6218106-B1.
PD 17-APR-2001.
PA (CITY) CITY OF HOPE.
Percent Similarity: 40.31%
Best Local Similarity: 26.18%
Query Match: 6.25%
RESULT 1473
ID ACA51944 standard; DNA; 1935 BP.
DE Prokaryotic essential gene #33601.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Percent Similarity: 39.77%
Best Local Similarity: 25.00%
Query Match: 6.25%
RESULT 1474
ID AAH17684 standard; cDNA; 1948 BP.
DE Human cDNA sequence SEQ ID NO:17259.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Percent Similarity: 35.32%
Best Local Similarity: 25.00%
Query Match: 6.25%
RESULT 1475
ID ACA42420 standard; DNA; 1995 BP.
DE Prokaryotic essential gene #24077.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Percent Similarity: 39.53%
Best Local Similarity: 24.51%
Query Match: 6.25%
RESULT 1476
ID ABD03241 standard; DNA; 2055 BP.
DE Pseudomonas aeruginosa polynucleotide #1845.
PN US5551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.

Percent Similarity: 31.18%
Best Local Similarity: 22.65%
Query Match: 6.25%
RESULT 1477
ID ABD02794 standard; DNA; 2067 BP.
DE Pseudomonas aeruginosa polynucleotide #1398.
PN US5551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Percent Similarity: 39.53%
Best Local Similarity: 24.51%
Query Match: 6.25%
RESULT 1478
ID ABD02605 standard; DNA; 2100 BP.
DE Pseudomonas aeruginosa polynucleotide #1209.
PN US5551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Percent Similarity: 39.53%
Best Local Similarity: 24.51%
Query Match: 6.25%
RESULT 1479
ID AAF60839 standard; DNA; 2122 BP.
DE Pseudomonas sp export system associated DNA ORF02378a.
PN DE19935105-A1.
PD 01-FEB-2001.
PA (TIGR-) TIGR INST GENOMIC RES.
PA (QUIA-) QUIAGEN GMBH.
PA (GRFB) GES BIOTECHNOLOGISCHE FORSCHUNG MBH.
PA (DFEZ-) DFEZ DEUT KREBSFORSCHUNGSZENTRUM.
PA (MEDI-) MEDIZINISCHE HOCHSCHULE HANNOVER.
Percent Similarity: 38.20%
Best Local Similarity: 25.09%
Query Match: 6.25%
RESULT 1480
ID ADN95102 standard; DNA; 2225 BP.
DE Human LEC gene sequence SeqID24.
PN WO2003080640-A1.
PD 02-OCT-2003.
PA (LUDW-) LUDWIG INST CANCER RES.
PA (LICN) LICENTIA LTD.
Percent Similarity: 35.32%
Best Local Similarity: 25.00%
Query Match: 6.25%
RESULT 1481
ID ADK17423 standard; cDNA; 2367 BP.
DE Murine disrupted-in-schizophrenia 1 (Disc 1) splice variant cDNA.
PN WO2003098995-A2.
PD 04-DEC-2003.
PA (MERI) MERCK & CO INC.
Percent Similarity: 36.06%
Best Local Similarity: 24.54%
Query Match: 6.25%
RESULT 1482
ID ADM01554 standard; cDNA; 2406 BP.
DE Human cDNA of the invention SEQ ID NO:239.
PN EPI347046-A1.
PD 24-SEP-2003.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Percent Similarity: 35.32%
Best Local Similarity: 25.00%
Query Match: 6.25%
RESULT 1483
ID ADM02518 standard; cDNA; 2489 BP.
DE Human cDNA of the invention SEQ ID NO:1203.
PN EPI347046-A1.
PD 24-SEP-2003.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Percent Similarity: 34.76%
Best Local Similarity: 19.74%
Query Match: 6.25%
RESULT 1484
ID ADK17421 standard; cDNA; 2556 BP.

DE cDNA encoding murine disrupted-in-schizophrenia 1 (Disc 1) protein.
PN WO200309995-A2.
PD 04-DEC-2003.
PA (MERI) MERCK & CO INC.
Percent Similarity: 36.06%
Best Local Similarity: 24.54%
Query Match: 6.25%
Conservative: 31
Mismatch: 79
Indels: 93
RESULT 1485
ID ABK92062 standard; DNA; 2995 BP.
DE DNA encoding novel UNC5 receptor-like protein.
PN WO200229058-A2.
PD 11-APR-2002.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 35.32%
Best Local Similarity: 25.00%
Query Match: 6.25%
Conservative: 26
Mismatch: 101
Indels: 63
RESULT 1486
ID AC77578 standard; DNA; 3026 BP.
DE Thermus aquaticus mutant DNA polymerase encoding DNA.
PN WO2003025132-A2.
PD 27-MAR-2003.
PA (INVI-) INVITROGEN CORP.
Percent Similarity: 39.31%
Best Local Similarity: 24.83%
Query Match: 6.25%
Conservative: 42
Mismatch: 99
Indels: 79
RESULT 1487
ID AC77757 standard; DNA; 3026 BP.
DE Thermus aquaticus mutant DNA polymerase encoding DNA.
PN WO2003025132-A2.
PD 27-MAR-2003.
PA (INVI-) INVITROGEN CORP.
Percent Similarity: 39.31%
Best Local Similarity: 24.83%
Query Match: 6.25%
Conservative: 39
Mismatch: 103
Indels: 79
RESULT 1488
ID AC77625 standard; DNA; 3026 BP.
DE Thermus aquaticus mutant DNA polymerase encoding DNA.
PN WO2003025132-A2.
PD 27-MAR-2003.
PA (INVI-) INVITROGEN CORP.
Percent Similarity: 39.31%
Best Local Similarity: 24.48%
Query Match: 6.25%
Conservative: 43
Mismatch: 99
Indels: 79
RESULT 1489
ID AC77702 standard; DNA; 3026 BP.
DE Thermus aquaticus mutant DNA polymerase encoding DNA.
PN WO2003025132-A2.
PD 27-MAR-2003.
PA (INVI-) INVITROGEN CORP.
Percent Similarity: 38.97%
Best Local Similarity: 24.83%
Query Match: 6.25%
Conservative: 41
Mismatch: 100
Indels: 79
RESULT 1490
ID AC77768 standard; DNA; 3026 BP.
DE Thermus aquaticus mutant DNA polymerase encoding DNA.
PN WO2003025132-A2.
PD 27-MAR-2003.
PA (INVI-) INVITROGEN CORP.
Percent Similarity: 37.93%
Best Local Similarity: 24.48%
Query Match: 6.25%
Conservative: 39
Mismatch: 103
Indels: 79
RESULT 1491
ID AC77851 standard; DNA; 3026 BP.
DE Thermus aquaticus mutant DNA polymerase encoding DNA.
PN WO2003025132-A2.
PD 27-MAR-2003.
PA (INVI-) INVITROGEN CORP.
Percent Similarity: 39.31%
Best Local Similarity: 24.48%
Query Match: 6.25%
Conservative: 43
Mismatch: 99
Indels: 79
RESULT 1492
ID AC77629 standard; DNA; 3026 BP.
DE Thermus aquaticus mutant DNA polymerase encoding DNA.
PN WO2003025132-A2.
PD 27-MAR-2003.
PA (INVI-) INVITROGEN CORP.
Percent Similarity: 39.31%
Best Local Similarity: 24.48%
Query Match: 6.25%
Conservative: 43
Mismatch: 99
Indels: 79
RESULT 1493
ID AC77759 standard; DNA; 3026 BP.
DE Thermus aquaticus mutant DNA polymerase encoding DNA.
PN WO2003025132-A2.
PD 27-MAR-2003.
PA (INVI-) INVITROGEN CORP.
Percent Similarity: 37.93%
Best Local Similarity: 24.48%
Query Match: 6.25%
Conservative: 39
Mismatch: 103
Indels: 79
RESULT 1494
ID AC77576 standard; DNA; 3026 BP.
DE Thermus aquaticus mutant DNA polymerase encoding DNA.
PN WO2003025132-A2.
PD 27-MAR-2003.
PA (INVI-) INVITROGEN CORP.
Percent Similarity: 39.31%
Best Local Similarity: 24.83%
Query Match: 6.25%
Conservative: 42
Mismatch: 99
Indels: 79
RESULT 1495
ID AC77703 standard; DNA; 3026 BP.
DE Thermus aquaticus mutant DNA polymerase encoding DNA.
PN WO2003025132-A2.
PD 27-MAR-2003.
PA (INVI-) INVITROGEN CORP.
Percent Similarity: 38.97%
Best Local Similarity: 24.83%
Query Match: 6.25%
Conservative: 41
Mismatch: 100
Indels: 79
RESULT 1496
ID AC77861 standard; DNA; 3026 BP.
DE Thermus aquaticus mutant DNA polymerase encoding DNA.
PN WO2003025132-A2.
PD 27-MAR-2003.
PA (INVI-) INVITROGEN CORP.
Percent Similarity: 39.31%
Best Local Similarity: 24.48%
Query Match: 6.25%
Conservative: 43
Mismatch: 99
Indels: 79
RESULT 1497
ID AC77766 standard; DNA; 3026 BP.
DE Thermus aquaticus mutant DNA polymerase encoding DNA.
PN WO2003025132-A2.
PD 27-MAR-2003.
PA (INVI-) INVITROGEN CORP.
Percent Similarity: 37.93%
Best Local Similarity: 24.48%
Query Match: 6.25%
Conservative: 39
Mismatch: 103
Indels: 79
RESULT 1498
ID AAA51260 standard; cDNA; 3121 BP.
DE Human DNA encoding PRO539, a Costal-2 homologue.
PN WO200036102-A2.
PD 22-JUN-2000.
PA (GETH) GENENTECH INC.
Percent Similarity: 34.16%
Best Local Similarity: 25.25%
Query Match: 6.25%
Conservative: 18
Mismatch: 65
Indels: 68
RESULT 1499
ID ABS68384 standard; cDNA; 3121 BP.
DE Human cDNA encoding secreted protein PRO539.
PN US2002098506-A1.
PD 25-JUL-2002.
PA (GETH) GENENTECH INC.
Percent Similarity: 34.16%
Best Local Similarity: 25.25%
Query Match: 6.25%
Conservative: 18
Mismatch: 65
Indels: 68
RESULT 1500
ID ABS67452 standard; cDNA; 3121 BP.
DE cDNA encoding novel human secreted protein #2.
PN US2002098505-A1.

PD 25-JUL-2002.
PA (GETH) GENENTECH INC.
Percent Similarity: 34.16%
Best Local Similarity: 25.25%
Query Match: 6.25%
Conservative: 18
Mismatches: 65
Indels: 68

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 12, 2005, 15:13:22 ; Search time 114 Seconds
(without alignment)
6166.405 Million cell updates/sec

Perfect score: 989
Sequence: 1 gcggccgcgagtcgaga.....caaaaaaaaaaaaaaaaaa 989

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database : Issued Patents NA:*
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4: /cgm2_6/ptodata/1/ina/6B COMB.seq:*
5: /cgm2_6/ptodata/1/ina/PTCUS COMB.seq:*
6: /cgm2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	189	19.1	846	4	US-09-252-991A-3196
2	161.8	16.4	953	4	US-09-452-239-45
3	159.2	16.1	1049	4	US-09-452-239-43
4	158.6	16.0	997	4	US-09-452-239-13
5	157.2	15.9	1078	4	US-09-452-239-41
6	155.6	15.7	1018	4	US-09-452-239-35
7	154	15.6	891	4	US-09-452-239-1
8	153	15.5	77536	4	US-09-410-551B-1
9	153	15.5	77536	4	US-09-940-316B-1
10	148	15.0	1118	4	US-09-452-239-37
11	148	15.0	1146	4	US-09-452-239-3
12	144.4	14.6	1057	4	US-09-452-239-5
13	140.6	14.2	1058	4	US-09-452-239-11
14	126	12.7	923	4	US-09-452-239-7
15	122.8	12.4	1810	1	US-07-708-866A-1
16	122.8	12.4	1810	1	US-07-708-866A-2
17	96.8	9.8	1012	4	US-09-615-192A-94
18	96.8	9.8	1012	4	US-09-169-789-94
19	96.8	9.8	1026	2	US-08-713-000-6
20	96.8	9.8	1026	2	US-08-975-316-6
21	96.8	9.8	1026	3	US-09-211-710-6
22	96.8	9.8	1026	4	US-09-615-192A-6
23	96.8	9.8	1026	4	US-09-169-789-6
24	93.4	9.4	675	4	US-09-489-039A-6750
25	88	8.9	931	4	US-09-452-239-17
26	87.8	8.9	534	4	US-09-452-239-47
27	85.6	8.7	962	4	US-09-452-239-23
28	85.6	8.7	1023	4	US-09-452-239-25

29	82.8	8.4	1258	1	US-08-335-518-1	Sequence 1, Appli
30	82.8	8.4	1258	3	US-08-988-054-1	Sequence 1, Appli
31	79.2	8.0	980	4	US-09-452-239-21	Sequence 21, Appli
32	76.2	7.7	760	2	US-08-975-316-25	Sequence 25, Appli
33	76.2	7.7	760	4	US-09-615-192A-25	Sequence 25, Appli
34	76.2	7.7	760	4	US-09-169-789-25	Sequence 25, Appli
35	74.4	7.5	929	4	US-09-452-239-19	Sequence 19, Appli
36	73.2	7.4	870	4	US-09-453-323-2	Sequence 2, Appli
37	70	7.1	811	4	US-09-453-323-3	Sequence 3, Appli
38	66.8	6.8	1074	2	US-08-975-316-54	Sequence 54, Appli
39	66.8	6.8	1074	4	US-09-615-192A-54	Sequence 54, Appli
40	66.8	6.8	1074	4	US-09-169-789-54	Sequence 54, Appli
41	66.8	6.8	1075	2	US-08-975-316-55	Sequence 55, Appli
42	66.8	6.8	1075	4	US-09-615-192A-55	Sequence 55, Appli
43	66.8	6.8	1075	4	US-09-169-789-55	Sequence 55, Appli
44	66.2	6.7	912	4	US-09-452-239-27	Sequence 27, Appli
45	64.8	6.6	967	4	US-09-453-323-5	Sequence 5, Appli
46	64.4	6.5	143	4	US-09-513-999C-15362	Sequence 15362, A
47	64.2	6.5	600	4	US-09-452-239-39	Sequence 39, Appli
48	63.6	6.4	510	4	US-09-452-239-9	Sequence 9, Appli
49	62.8	6.3	4403765	3	US-09-103-840A-2	Sequence 2, Appli
50	62.8	6.3	4411529	3	US-09-103-840A-1	Sequence 1, Appli
51	62.4	6.3	4403765	3	US-09-103-840A-2	Sequence 2, Appli
52	62.4	6.3	4411529	3	US-09-103-840A-1	Sequence 1, Appli
53	61.6	6.2	845	4	US-09-453-323-4	Sequence 4, Appli
54	60.8	6.1	1578	1	US-08-681-129-1	Sequence 1, Appli
55	60	6.1	982	4	US-09-452-239-31	Sequence 31, Appli
56	59.6	6.0	399	4	US-09-615-192A-194	Sequence 194, App
57	58.4	5.9	1288	1	US-08-440-856A-9	Sequence 9, Appli
58	57	5.8	11219	1	US-07-642-734C-1	Sequence 1, Appli
59	57	5.8	11219	3	US-08-439-009A-1	Sequence 1, Appli
60	57	5.8	38494	4	US-08-311-731A-24	Sequence 24, Appli
61	57	5.8	38675	4	US-08-311-731A-135	Sequence 135, App
62	56.8	5.7	1182	3	US-09-385-028-19	Sequence 19, Appli
63	56.8	5.7	1182	4	US-09-726-614-19	Sequence 19, Appli
64	56.8	5.7	1182	4	US-09-385-040-19	Sequence 19, Appli
65	56.8	5.7	11604	3	US-09-385-028-13	Sequence 13, Appli
66	56.8	5.7	11604	4	US-09-726-614-13	Sequence 13, Appli
67	56.8	5.7	11604	4	US-09-385-040-13	Sequence 13, Appli
68	56.8	5.7	15079	3	US-09-385-028-1	Sequence 1, Appli
69	56.8	5.7	15079	4	US-09-726-614-1	Sequence 1, Appli
70	56.8	5.7	15120	4	US-09-385-040-1	Sequence 1, Appli
71	56.8	5.7	22976	4	US-09-269-939A-19	Sequence 19, Appli
72	56.2	5.7	2793	1	US-08-209-747-1	Sequence 1, Appli
73	56.2	5.7	2793	1	US-08-458-298-1	Sequence 1, Appli
74	56	5.7	1098	4	US-09-252-991A-14407	Sequence 14407, A
75	56	5.7	1566	4	US-09-252-991A-14264	Sequence 14264, A
76	56	5.7	1908	4	US-09-252-991A-14353	Sequence 14353, A
77	56	5.7	2109	4	US-09-370-838-153	Sequence 153, App
78	56	5.7	2109	4	US-09-854-133-153	Sequence 153, App
79	56	5.7	4257	2	US-08-690-473-1	Sequence 1, Appli
80	56	5.7	4257	3	US-09-259-821A-1	Sequence 1, Appli
81	56	5.7	4257	3	US-08-843-659-1	Sequence 1, Appli
82	56	5.7	4257	4	US-08-825-288A-1	Sequence 1, Appli
83	56	5.7	12001	1	US-08-458-588A-11	Sequence 11, Appli
84	55.8	5.6	1926	4	US-09-249-565A-2	Sequence 2, Appli
85	55.8	5.6	1926	4	US-09-410-399-3	Sequence 3, Appli
86	55.8	5.6	2580	3	US-09-050-863-2	Sequence 2, Appli
87	55.8	5.6	2580	3	US-09-359-081-2	Sequence 2, Appli
88	55.8	5.6	5452	2	US-09-130-114-1	Sequence 1, Appli
89	55.8	5.6	8705	4	US-09-647-344A-14	Sequence 14, Appli
90	55.8	5.6	9551	2	US-08-056-200-93	Sequence 93, Appli
91	55.8	5.6	9551	2	US-08-800-644-93	Sequence 93, Appli
92	55.8	5.6	9600	3	US-08-910-647-1	Sequence 1, Appli
93	55.8	5.6	9600	4	US-09-620-925-1	Sequence 1, Appli
94	55.8	5.6	10596	1	US-07-884-811-15	Sequence 15, Appli
95	55.8	5.6	10596	1	US-07-885-971-15	Sequence 15, Appli
96	55.8	5.6	10596	1	US-08-087-783A-15	Sequence 15, Appli
97	55.8	5.6	10596	2	US-08-194-088B-15	Sequence 15, Appli
98	55.8	5.6	10596	2	US-08-194-087-15	Sequence 15, Appli
99	55.8	5.6	10596	5	PCT-US93-04548-15	Sequence 15, Appli
100	55.8	5.6	16080	4	US-09-724-566A-48	Sequence 48, Appli
101	55.4	5.6	774	4	US-09-252-991A-965	Sequence 965, Ap

102	55.4	5.6	3033	4	US-09-724-797-81	Sequence 81, Appl	c 175	49.8	5.0	3411	4	US-09-252-991A-14823	Sequence 14823, A
103	55	5.6	2559	4	US-09-657-013-40	Sequence 40, Appl	c 176	49.6	5.0	678	4	US-09-252-991A-2221	Sequence 2221, Ap
104	54.8	5.5	594	4	US-09-615-192A-105	Sequence 105, App	c 177	49.6	5.0	753	4	US-09-252-991A-2382	Sequence 2382, Ap
105	54.8	5.5	594	4	US-09-163-789-105	Sequence 105, App	c 178	49.6	5.0	2814	4	US-09-252-991A-2537	Sequence 2537, App
106	54.8	5.5	607	2	US-08-975-316-23	Sequence 23, Appl	c 179	49.4	5.0	1419	4	US-09-252-991A-152	Sequence 152, App
107	54.8	5.5	607	4	US-09-615-192A-23	Sequence 23, Appl	c 180	49.4	5.0	1692	4	US-09-252-991A-157	Sequence 157, App
108	54.8	5.5	607	4	US-09-163-789-23	Sequence 23, Appl	c 181	49.4	5.0	1698	4	US-09-252-991A-186	Sequence 186, App
109	54.6	5.5	1308	4	US-08-937-067-18	Sequence 18, Appl	c 182	49.4	5.0	2214	3	US-08-864-038A-1	Sequence 1, Appl
110	54.6	5.5	2830	2	US-09-010-928B-1	Sequence 1, Appl	c 183	49.4	5.0	2745	1	US-08-363-255-13	Sequence 13, Appl
c 111	54	5.5	4530	4	US-09-793-451-881	Sequence 881, App	c 184	49.4	5.0	2745	1	US-08-363-255-13	Sequence 2, Appl
112	53.8	5.4	2082	4	US-09-818-780-67	Sequence 67, Appl	c 185	49.4	5.0	3331	3	US-08-864-038A-2	Sequence 2, Appl
113	53.8	5.4	44377	2	US-08-804-227C-7	Sequence 7, Appl	c 186	49.4	5.0	3331	3	US-08-864-038A-4	Sequence 4, Appl
114	53.8	5.4	44377	2	US-08-804-198-1	Sequence 1, Appl	c 187	49.4	5.0	3489	2	US-08-728-323A-1	Sequence 1, Appl
115	53.8	5.4	114793	4	US-10-148-806-3	Sequence 3, Appl	c 188	49.4	5.0	3489	3	US-09-298-568-1	Sequence 1, Appl
c 116	53.4	5.4	2248	3	US-09-345-214-20	Sequence 20, Appl	c 189	49.4	5.0	3489	3	US-09-410-399-1	Sequence 1, Appl
c 117	53.4	5.4	2248	3	US-09-743-980-20	Sequence 20, Appl	c 190	49.4	5.0	3489	4	US-09-894-273-1	Sequence 20, Appl
118	53.4	5.4	2338	1	US-08-425-069-1	Sequence 1, Appl	c 191	49.4	5.0	32207	2	US-08-770-379-20	Sequence 20, Appl
119	53.4	5.4	2338	1	US-08-317-844B-1	Sequence 1, Appl	c 192	49.4	5.0	32207	3	US-08-757-669A-20	Sequence 20, Appl
c 120	53	5.4	632	4	US-09-221-017B-655	Sequence 655, App	c 193	49.4	5.0	789	4	US-09-230-371A-20	Sequence 15913, A
c 121	52.8	5.3	1236	1	US-08-440-856A-1	Sequence 1, Appl	c 194	49.2	5.0	789	4	US-09-252-991A-11852	Sequence 11852, A
c 122	52.6	5.3	2561	4	US-09-616-289-48	Sequence 48, Appl	c 195	49.2	5.0	888	4	US-09-252-991A-16512	Sequence 16512, A
123	52.4	5.3	3978	3	US-08-728-214-1	Sequence 41, Appl	c 196	49.2	5.0	1221	4	US-09-252-991A-11531	Sequence 11531, A
124	52.4	5.3	5640	4	US-09-620-312D-41	Sequence 41, Appl	c 197	49.2	5.0	1263	4	US-09-252-991A-13467	Sequence 13467, A
c 125	52	5.3	1248	4	US-09-252-991A-1681	Sequence 1681, Ap	c 198	49.2	5.0	1263	4	US-09-252-991A-13658	Sequence 13658, A
126	52	5.3	1302	4	US-09-252-991A-1437	Sequence 1437, Ap	c 199	49.2	5.0	1521	4	US-09-252-991A-15778	Sequence 15778, A
127	52	5.3	1956	4	US-09-252-991A-1494	Sequence 1494, Ap	c 200	49.2	5.0	1521	4	US-09-252-991A-15778	Sequence 15778, A
128	51.8	5.2	498	4	US-09-252-991A-10389	Sequence 10389, A	c 201	49.2	5.0	1569	4	US-09-252-991A-15857	Sequence 15857, A
c 129	51.8	5.2	561	4	US-09-252-991A-10580	Sequence 10580, A	c 202	49.2	5.0	2400	4	US-09-252-991A-15857	Sequence 15857, A
c 130	51.8	5.2	1053	4	US-09-252-991A-10684	Sequence 10684, A	c 203	49.2	5.0	3318	3	US-09-252-991A-15991	Sequence 15991, A
c 131	51.8	5.2	1233	4	US-09-252-991A-3104	Sequence 3104, Ap	c 204	49.2	5.0	3318	3	US-09-531-589-3	Sequence 3, Appl
c 132	51.8	5.2	1386	4	US-09-252-991A-2867	Sequence 2867, Ap	c 205	49	5.0	399	4	US-09-615-192A-193	Sequence 193, App
c 133	51.8	5.2	1926	4	US-09-249-585A-4	Sequence 4, Appl	c 206	49	5.0	843	4	US-09-724-797-33	Sequence 33, Appl
c 134	51.8	5.2	1931	2	US-09-130-114-2	Sequence 2, Appl	c 207	49	5.0	1355	3	US-08-415-655-14	Sequence 14, Appl
c 135	51.8	5.2	2075	4	US-09-087-031E-2	Sequence 2, Appl	c 208	49	5.0	1614	4	US-09-616-289-45	Sequence 45, Appl
136	51.8	5.2	2075	4	US-09-546-043-1	Sequence 1, Appl	c 209	49	5.0	12425	4	US-09-616-289-50	Sequence 50, Appl
c 137	51.8	5.2	2715	4	US-09-514-885-2	Sequence 2, Appl	c 210	49	5.0	77536	4	US-09-410-551B-1	Sequence 1, Appl
c 138	51.6	5.2	1311	4	US-09-252-991A-14065	Sequence 14065, A	c 211	49	5.0	77536	4	US-09-940-316B-1	Sequence 1, Appl
c 139	51.6	5.2	2850	4	US-09-252-991A-14205	Sequence 591, App	c 212	48.8	4.9	852	4	US-09-252-991A-7607	Sequence 7607, Ap
140	51.4	5.2	7847	4	US-09-799-451-591	Sequence 5, Appl	c 213	48.8	4.9	1083	4	US-09-252-991A-8817	Sequence 8817, Ap
141	51.2	5.2	2277	1	US-08-676-967-5	Sequence 5, Appl	c 214	48.8	4.9	1227	4	US-09-252-991A-9232	Sequence 9232, Ap
142	51.2	5.2	2277	2	US-08-676-967-5	Sequence 5, Appl	c 215	48.8	4.9	1296	4	US-09-252-991A-9150	Sequence 9150, Ap
143	51.2	5.2	2277	2	US-09-098-487-5	Sequence 5, Appl	c 216	48.8	4.9	2232	4	US-09-252-991A-11756	Sequence 11756, A
144	51	5.2	501	4	US-09-252-991A-11947	Sequence 11947, A	c 217	48.8	4.9	2274	4	US-09-252-991A-11609	Sequence 11609, A
145	51	5.2	1500	4	US-09-252-991A-11907	Sequence 11907, A	c 218	48.8	4.9	2613	4	US-09-252-991A-11836	Sequence 11836, A
146	51	5.2	2561	4	US-09-616-289-48	Sequence 48, Appl	c 219	48.8	4.9	2715	4	US-09-252-991A-8715	Sequence 8715, Ap
147	51	5.2	8438	1	US-07-945-283-1	Sequence 1, Appl	c 220	48.6	4.9	528	4	US-09-452-239-33	Sequence 33, Appl
c 148	50.8	5.1	741	4	US-09-724-797-73	Sequence 73, Appl	c 221	48.6	4.9	1320	4	US-09-724-797-85	Sequence 85, Appl
149	50.8	5.1	1155	3	US-08-818-112-12	Sequence 12, Appl	c 222	48.6	4.9	1479	1	US-08-644-271-31	Sequence 31, Appl
150	50.8	5.1	1155	3	US-08-818-111-12	Sequence 12, Appl	c 223	48.6	4.9	1479	4	US-09-077-955-35	Sequence 35, Appl
151	50.8	5.1	1155	3	US-09-056-556-12	Sequence 12, Appl	c 224	48.6	4.9	1575	4	US-09-252-991A-11212	Sequence 11212, A
152	50.8	5.1	1155	4	US-09-072-596-12	Sequence 12, Appl	c 225	48.6	4.9	1620	4	US-09-252-991A-11146	Sequence 11146, A
153	50.8	5.1	1155	4	US-09-072-967-12	Sequence 12, Appl	c 226	48.6	4.9	2040	2	US-08-533-669A-5	Sequence 5, Appl
154	50.6	5.1	508	4	US-09-452-239-15	Sequence 15, Appl	c 227	48.6	4.9	2040	3	US-09-183-861-5	Sequence 5, Appl
155	50.4	5.1	23673	3	US-09-773-816-1	Sequence 1, Appl	c 228	48.6	4.9	2040	3	US-09-022-765-5	Sequence 5, Appl
c 156	50.2	5.1	864	4	US-09-252-991A-10932	Sequence 10932, A	c 229	48.6	4.9	2040	4	US-09-551-974A-5	Sequence 5, Appl
c 157	50.2	5.1	2211	4	US-09-252-991A-11256	Sequence 11256, A	c 230	48.6	4.9	2040	4	US-09-563-501A-5	Sequence 5, Appl
158	50.2	5.1	2289	4	US-09-252-991A-10995	Sequence 10995, A	c 231	48.6	4.9	2040	4	US-09-639-206A-5	Sequence 5, Appl
159	50.2	5.1	4826	4	US-09-772-304A-1	Sequence 1, Appl	c 232	48.6	4.9	2040	4	US-09-874-923-5	Sequence 5, Appl
c 160	50	5.1	888	4	US-09-311-021-155	Sequence 155, App	c 233	48.6	4.9	2040	4	US-08-798-841-5	Sequence 5, Appl
161	50	5.1	13842	3	US-09-105-537-30	Sequence 30, Appl	c 234	48.6	4.9	2472	3	US-09-252-991A-11043	Sequence 11043, A
162	50	5.1	36778	3	US-09-105-537-5	Sequence 5, Appl	c 235	48.6	4.9	2712	3	US-09-025-691-4	Sequence 4, Appl
163	50	5.1	38506	3	US-09-320-808-19	Sequence 19, Appl	c 236	48.4	4.9	562	2	US-08-975-316-53	Sequence 53, Appl
164	50	5.1	38506	4	US-09-141-908-1	Sequence 1, Appl	c 237	48.4	4.9	562	4	US-09-615-192A-53	Sequence 53, Appl
165	50	5.1	38506	4	US-09-657-440-19	Sequence 19, Appl	c 238	48.4	4.9	756	1	US-09-169-789-53	Sequence 53, Appl
c 166	50	5.1	229354	4	US-09-765-400-64	Sequence 64, Appl	c 239	48.4	4.9	822	4	US-08-642-255-50	Sequence 50, Appl
c 167	50	5.1	229354	4	US-09-705-400-64	Sequence 64, Appl	c 240	48.2	4.9	920	4	US-09-252-991A-11707	Sequence 11707, A
168	49.8	5.0	3003	4	US-09-252-991A-14790	Sequence 14790, A	c 241	48.2	4.9	1035	1	US-09-620-312D-132	Sequence 132, App
169	49.8	5.0	3113	4	US-09-894-998A-52	Sequence 52, Appl	c 242	48.2	4.9	1035	3	US-07-601-094-30	Sequence 30, Appl
170	49.8	5.0	3132	4	US-09-252-991A-14540	Sequence 14540, A	c 243	48.2	4.9	1035	3	US-08-012-711A-3	Sequence 30, Appl
171	49.8	5.0	3147	2	US-08-781-802-7	Sequence 7, Appl	c 244	48.2	4.9	1910	1	US-09-593-711A-3	Sequence 3, Appl
172	49.8	5.0	3147	3	US-08-694-078-7	Sequence 7, Appl	c 245	48.2	4.9	1914	1	US-07-601-094-1	Sequence 1, Appl
173	49.8	5.0	3147	3	US-09-058-260-7	Sequence 7, Appl	c 246	48.2	4.9	1914	1	US-08-012-735-1	Sequence 1, Appl
174	49.8	5.0	3345	4	US-09-894-998A-49	Sequence 49, Appl	c 247	48.2	4.9	2009	4	US-09-646-403-1	Sequence 1, Appl

248	48.2	4.9	2023	4	US-09-491-522-6	Sequence 6, Appli	321	47.4	4.8	50937	3	US-09-428-517-1	Sequence 1, Appli
249	48.2	4.9	2034	4	US-09-646-403-2	Sequence 2, Appli	c 322	47.4	4.8	50937	3	US-09-428-517-1	Sequence 1, Appli
250	48.2	4.9	2450	4	US-09-491-522-2	Sequence 2, Appli	c 323	47.2	4.8	714	4	US-09-252-991A-16021	Sequence 16021, A
c 251	48.2	4.9	3350	4	US-09-894-998A-48	Sequence 48, Appli	324	47.2	4.8	888	3	US-08-765-907A-2	Sequence 2, Appli
c 252	48.2	4.9	6692	4	US-09-491-522-1	Sequence 1, Appli	325	47.2	4.8	999	4	US-09-252-991A-970	Sequence 970, App
c 253	48	4.9	465	4	US-09-252-991A-2233	Sequence 2233, Ap	326	47.2	4.8	1110	4	US-09-252-991A-1014	Sequence 1014, Ap
c 254	48	4.9	822	4	US-09-252-991A-7080	Sequence 7080, Ap	327	47.2	4.8	1194	4	US-09-724-797-25	Sequence 25, Appl
c 255	48	4.9	852	4	US-09-252-991A-4447	Sequence 2447, Ap	c 328	47.2	4.8	1275	4	US-09-252-991A-1080	Sequence 1080, Ap
256	48	4.9	1071	4	US-09-252-991A-1635	Sequence 1635, Ap	329	47.2	4.8	1347	4	US-09-724-797-43	Sequence 43, Appl
257	48	4.9	1128	4	US-09-622-439-1	Sequence 1, Appli	330	47.2	4.8	1944	4	US-09-252-991A-16245	Sequence 16245, A
258	48	4.9	1359	4	US-09-252-991A-2528	Sequence 2528, Ap	331	47.2	4.8	2133	4	US-09-252-991A-5907	Sequence 5907, Ap
c 259	48	4.9	1473	4	US-09-252-991A-2391	Sequence 2391, Ap	332	47.2	4.8	2312	4	US-09-475-515-84	Sequence 84, Appl
c 260	48	4.9	1695	4	US-09-252-991A-1686	Sequence 1686, Ap	333	47.2	4.8	2808	4	US-09-252-991A-16466	Sequence 16466, A
c 261	48	4.9	1740	4	US-09-252-991A-1492	Sequence 1492, Ap	c 334	47.2	4.8	2862	4	US-09-252-991A-10659	Sequence 10659, A
c 262	48	4.9	1806	4	US-09-252-991A-1534	Sequence 1534, Ap	c 335	47.2	4.8	2888	3	US-08-765-907A-1	Sequence 1, Appli
c 263	48	4.9	1929	4	US-09-252-991A-1017	Sequence 1017, Ap	336	47.2	4.8	3110	4	US-09-252-991A-10414	Sequence 10414, A
c 264	48	4.9	1947	4	US-09-252-991A-7111	Sequence 7111, Ap	337	47.2	4.8	3111	4	US-09-252-991A-10504	Sequence 10504, A
c 265	48	4.9	2253	4	US-09-252-991A-7191	Sequence 7191, Ap	338	47.2	4.8	3135	4	US-09-252-991A-5922	Sequence 5922, Ap
c 266	48	4.9	2409	4	US-09-252-991A-7253	Sequence 7253, Ap	339	47.2	4.8	4319	4	US-09-252-991A-5922	Sequence 6, Appli
c 267	48	4.9	2490	4	US-09-252-991A-7447	Sequence 7447, Ap	340	47.2	4.8	11220	3	US-09-105-537-32	Sequence 32, Appl
c 268	48	4.9	3529	3	US-09-144-085-3	Sequence 3, Appli	c 341	47	4.8	441	4	US-09-252-991A-14658	Sequence 14658, A
c 269	47.8	4.8	309	4	US-09-252-991A-6725	Sequence 6725, Ap	342	47	4.8	758	4	US-09-902-331B-5	Sequence 5, Appli
c 270	47.8	4.8	801	4	US-09-252-991A-15941	Sequence 15941, A	c 343	47	4.8	1260	4	US-09-252-991A-14526	Sequence 14526, A
c 271	47.8	4.8	819	4	US-09-252-991A-14581	Sequence 14581, A	c 344	47	4.8	1260	4	US-09-252-991A-14838	Sequence 14838, A
c 272	47.8	4.8	966	4	US-09-252-991A-6895	Sequence 6895, Ap	c 345	47	4.8	1320	2	US-08-461-775-8	Sequence 8, Appli
c 273	47.8	4.8	1218	4	US-09-252-991A-16453	Sequence 16453, A	c 346	47	4.8	1320	3	US-09-031-606-8	Sequence 8, Appli
c 274	47.8	4.8	1485	4	US-09-252-991A-6815	Sequence 6815, Ap	347	47	4.8	1416	3	US-08-911-853-3	Sequence 3, Appli
c 275	47.8	4.8	1509	4	US-09-252-991A-6930	Sequence 6930, Ap	348	47	4.8	1416	3	US-09-479-409-3	Sequence 3, Appli
c 276	47.8	4.8	1771	2	US-08-533-669A-7	Sequence 7, Appli	349	47	4.8	1416	3	US-09-479-453-3	Sequence 3, Appli
c 277	47.8	4.8	1771	2	US-08-511-872-1	Sequence 1, Appli	c 350	47	4.8	1620	2	US-08-461-775-10	Sequence 10, Appl
c 278	47.8	4.8	1771	3	US-09-183-861-7	Sequence 7, Appli	c 351	47	4.8	1620	3	US-09-031-606-10	Sequence 10, Appl
c 279	47.8	4.8	1771	3	US-09-022-765-7	Sequence 7, Appli	352	47	4.8	1707	4	US-09-724-797-15	Sequence 15, Appl
c 280	47.8	4.8	1771	4	US-09-551-974A-7	Sequence 7, Appli	353	47	4.8	4377	3	US-08-911-853-28	Sequence 28, Appl
c 281	47.8	4.8	1771	4	US-09-565-501A-7	Sequence 7, Appli	354	47	4.8	4377	3	US-09-479-409-28	Sequence 28, Appl
c 282	47.8	4.8	1771	4	US-09-639-206A-7	Sequence 7, Appli	355	47	4.8	4377	3	US-09-479-453-28	Sequence 28, Appl
c 283	47.8	4.8	1771	4	US-09-874-923-7	Sequence 7, Appli	356	47	4.8	80161	3	US-03-036-987A-1	Sequence 1, Appli
c 284	47.8	4.8	1771	4	US-08-798-841-7	Sequence 7, Appli	357	47	4.8	80161	3	US-09-370-700-1	Sequence 1, Appli
c 285	47.8	4.8	1962	4	US-09-252-991A-16037	Sequence 16037, A	358	47	4.8	80161	3	US-09-603-207-1	Sequence 1, Appli
c 286	47.8	4.8	2526	4	US-09-252-991A-16563	Sequence 16563, A	359	46.8	4.7	296	4	US-09-615-192A-195	Sequence 195, App
c 287	47.8	4.8	3126	4	US-09-252-991A-9066	Sequence 9066, Ap	360	46.8	4.7	792	4	US-09-252-991A-4971	Sequence 4971, Ap
c 288	47.8	4.8	4524	2	US-08-845-998-7	Sequence 7, Appli	361	46.8	4.7	801	2	US-08-770-379-16	Sequence 16, Appl
c 289	47.8	4.8	4524	3	US-09-206-537-7	Sequence 7, Appli	362	46.8	4.7	801	3	US-08-757-669A-16	Sequence 16, Appl
c 290	47.8	4.8	4524	3	US-09-430-854-7	Sequence 7, Appli	363	46.8	4.7	801	3	US-09-298-568-3	Sequence 3, Appli
c 291	47.8	4.8	5121	4	US-09-252-991A-15189	Sequence 15189, A	364	46.8	4.7	801	3	US-09-230-371A-16	Sequence 16, Appl
c 292	47.8	4.8	71989	3	US-09-252-991A-14931	Sequence 14931, A	365	46.8	4.7	801	4	US-09-894-273-3	Sequence 3, Appli
c 293	47.8	4.8	71989	3	US-09-443-501A-2	Sequence 2, Appli	366	46.8	4.7	801	4	US-09-252-991A-4955	Sequence 4955, Ap
c 294	47.6	4.8	930	4	US-09-252-991A-15663	Sequence 15663, A	367	46.8	4.7	1131	4	US-09-252-991A-4994	Sequence 4994, Ap
c 295	47.6	4.8	1248	4	US-09-252-991A-2635	Sequence 2635, Ap	368	46.8	4.7	1215	4	US-09-252-991A-4994	Sequence 4994, Ap
c 296	47.6	4.8	1278	4	US-09-252-991A-3896	Sequence 3896, Ap	c 369	46.8	4.7	3171	4	US-09-252-991A-7591	Sequence 7591, Ap
c 297	47.6	4.8	1971	4	US-09-252-991A-2197	Sequence 2197, Ap	370	46.8	4.7	3210	4	US-09-252-991A-7962	Sequence 7962, Ap
c 298	47.6	4.8	1977	4	US-09-252-991A-3924	Sequence 3924, Ap	371	46.6	4.7	270	4	US-09-252-991A-14378	Sequence 14378, A
c 299	47.6	4.8	2091	4	US-09-252-991A-4016	Sequence 4016, Ap	c 372	46.6	4.7	489	4	US-09-252-991A-452	Sequence 452, App
c 300	47.6	4.8	2211	4	US-09-252-991A-2477	Sequence 2477, Ap	c 373	46.6	4.7	777	4	US-09-252-991A-12568	Sequence 12568, A
c 301	47.6	4.8	2305	4	US-09-475-515-80	Sequence 80, Appl	374	46.6	4.7	786	4	US-09-252-991A-13239	Sequence 13239, A
c 302	47.6	4.8	2306	4	US-09-475-515-82	Sequence 82, Appl	c 375	46.6	4.7	981	4	US-09-252-991A-431	Sequence 431, App
c 303	47.6	4.8	2481	4	US-09-894-998A-35	Sequence 35, Appli	376	46.6	4.7	981	4	US-09-252-991A-10487	Sequence 10487, A
c 304	47.6	4.8	9960	3	US-08-822-586-46	Sequence 46, Appl	377	46.6	4.7	1062	4	US-09-252-991A-6751	Sequence 6751, Ap
c 305	47.4	4.8	9818	4	US-09-252-991A-8762	Sequence 8762, Ap	378	46.6	4.7	1380	4	US-09-252-991A-3550	Sequence 3550, Ap
c 306	47.4	4.8	948	4	US-09-252-991A-9192	Sequence 9192, Ap	c 379	46.6	4.7	1530	4	US-09-252-991A-6874	Sequence 6874, Ap
c 307	47.4	4.8	954	4	US-09-252-991A-5807	Sequence 5807, Ap	380	46.6	4.7	1947	4	US-09-252-991A-3557	Sequence 3557, Ap
c 308	47.4	4.8	1116	4	US-09-252-991A-10924	Sequence 10924, A	381	46.6	4.7	2325	4	US-09-252-991A-12916	Sequence 12916, A
c 309	47.4	4.8	1149	4	US-09-252-991A-8983	Sequence 8983, Ap	c 382	46.6	4.7	7419	4	US-09-252-991A-481	Sequence 481, App
c 310	47.4	4.8	1209	4	US-09-252-991A-11138	Sequence 11138, A	383	46.6	4.7	7449	4	US-09-252-991A-396	Sequence 396, App
c 311	47.4	4.8	1248	4	US-09-724-797-23	Sequence 23, Appl	c 384	46.4	4.7	981	4	US-09-252-991A-14299	Sequence 14299, A
c 312	47.4	4.8	1251	4	US-09-252-991A-5844	Sequence 5844, Ap	385	46.4	4.7	1072	3	US-09-088-549-2	Sequence 2, Appli
c 313	47.4	4.8	1650	4	US-09-252-991A-3338	Sequence 3338, Ap	386	46.4	4.7	1263	4	US-09-252-991A-14349	Sequence 14349, A
c 314	47.4	4.8	1869	4	US-09-252-991A-3231	Sequence 3231, Ap	387	46.4	4.7	2235	4	US-09-252-991A-14374	Sequence 14374, A
c 315	47.4	4.8	1881	4	US-09-252-991A-11264	Sequence 11264, A	c 388	46.2	4.7	432	1	US-08-642-255-48	Sequence 48, Appl
c 316	47.4	4.8	1986	4	US-09-252-991A-5767	Sequence 5767, Ap	389	46.2	4.7	1362	4	US-09-724-797-31	Sequence 31, Appl
c 317	47.4	4.8	2283	4	US-09-252-991A-3298	Sequence 3298, Ap	390	46.2	4.7	1509	4	US-09-724-797-89	Sequence 89, Appl
c 318	47.4	4.8	2583	4	US-09-252-991A-9110	Sequence 9110, Ap	391	46.2	4.7	3102	4	US-09-252-991A-4429	Sequence 4429, Ap
c 319	47.4	4.8	2634	1	US-08-196-218-31	Sequence 31, Appl	392	46.2	4.7	30001	2	US-08-125-468-1	Sequence 1, Appli
c 320	47.4	4.8	2634	1	US-08-681-953-31	Sequence 31, Appl	393	46.2	4.7	30001	2	US-08-474-933-1	Sequence 1, Appli

C 394	46.2	4.7	53500	4	US-09-266-965-76	Sequence 76, Appl	467	45.4	4.6	1449	4	US-09-252-991A-3558	Sequence 3558, Ap
C 395	46	4.7	606	4	US-09-252-991A-2567	Sequence 2567, Ap	468	45.4	4.6	1548	2	US-08-762-106-5	Sequence 5, Appl
C 396	46	4.7	606	4	US-09-252-991A-9531	Sequence 9531, Ap	469	45.4	4.6	1548	3	US-09-320-774-5	Sequence 5, Appl
C 397	46	4.7	906	4	US-09-252-991A-1329	Sequence 1329, Ap	470	45.4	4.6	1572	2	US-09-252-991A-3270	Sequence 3270, Ap
C 398	46	4.7	1023	4	US-09-252-991A-1283	Sequence 1283, Ap	471	45.4	4.6	1581	2	US-08-762-106-6	Sequence 6, Appl
C 399	46	4.7	1024	1	US-07-975-526-3	Sequence 3, Appl	472	45.4	4.6	1581	3	US-09-320-774-6	Sequence 6, Appl
C 400	46	4.7	1044	3	US-07-974-409C-425	Sequence 425, App	473	45.4	4.6	1698	4	US-09-252-991A-3551	Sequence 3551, Ap
C 401	46	4.7	1070	4	US-09-252-991A-7892	Sequence 7892, Ap	474	45.4	4.6	1698	1	US-07-918-023-1	Sequence 1, Appl
C 402	46	4.7	1080	4	US-09-252-991A-1187	Sequence 1187, Ap	475	45.4	4.6	1965	2	US-09-252-991A-3234	Sequence 9, Appl
C 403	46	4.7	1112	3	US-09-434-288-9	Sequence 9, Appl	476	45.4	4.6	2167	3	US-09-031-606-9	Sequence 9, Appl
C 404	46	4.7	1266	4	US-09-252-991A-10804	Sequence 10804, A	477	45.4	4.6	2167	3	US-09-252-991A-3536	Sequence 3536, Ap
C 405	46	4.7	1275	4	US-09-252-991A-2484	Sequence 2484, A	478	45.4	4.6	2196	4	US-09-252-991A-3413	Sequence 3413, Ap
C 406	46	4.7	1371	4	US-09-252-991A-9717	Sequence 9717, Ap	479	45.4	4.6	2325	4	US-09-252-991A-3413	Sequence 1, Appl
C 407	46	4.7	1383	4	US-09-252-991A-2350	Sequence 2350, Ap	480	45.4	4.6	2571	4	US-09-984-880-1	Sequence 1, Appl
C 408	46	4.7	1443	4	US-09-252-991A-10228	Sequence 10228, A	481	45.4	4.6	2571	4	US-10-277-032-1	Sequence 11, Appl
C 409	46	4.7	1818	4	US-09-252-991A-10345	Sequence 10345, A	482	45.4	4.6	2668	2	US-08-461-775-11	Sequence 11, Appl
C 410	46	4.7	1935	4	US-09-620-312D-236	Sequence 236, App	483	45.4	4.6	2668	3	US-09-031-606-11	Sequence 9, Appl
C 411	46	4.7	2400	1	US-08-967-513-1	Sequence 1, Appl	484	45.4	4.6	2668	4	US-09-031-606-11	Sequence 9, Appl
C 412	46	4.7	2400	2	US-08-687-645B-1	Sequence 1, Appl	485	45.4	4.6	357	3	US-08-556-978B-83	Sequence 8, Appl
C 413	46	4.7	17612	3	US-08-911-853-29	Sequence 29, Appl	486	45.2	4.6	447	4	US-09-252-991A-4677	Sequence 4677, Ap
C 414	46	4.7	17612	3	US-09-479-453-29	Sequence 29, Appl	487	45.2	4.6	504	4	US-09-252-991A-4720	Sequence 4720, Ap
C 415	46	4.7	17612	3	US-09-479-453-29	Sequence 29, Appl	488	45.2	4.6	522	4	US-09-252-991A-12264	Sequence 12264, A
C 416	45.8	4.6	657	4	US-09-252-991A-4833	Sequence 4833, Ap	489	45.2	4.6	702	4	US-09-252-991A-4703	Sequence 4703, Ap
C 417	45.8	4.6	774	3	US-08-956-307B-11	Sequence 11, Appl	490	45.2	4.6	807	4	US-09-252-991A-12392	Sequence 12392, A
C 418	45.8	4.6	778	3	US-08-956-307B-11	Sequence 11, Appl	491	45.2	4.6	888	4	US-09-252-991A-7041	Sequence 7041, Ap
C 419	45.8	4.6	1245	4	US-09-252-991A-13463	Sequence 13463, A	492	45.2	4.6	897	4	US-09-252-991A-8854	Sequence 8854, Ap
C 420	45.8	4.6	1401	4	US-09-252-991A-4911	Sequence 4911, Ap	493	45.2	4.6	1026	4	US-09-252-991A-12295	Sequence 12295, A
C 421	45.8	4.6	1569	4	US-09-252-991A-13880	Sequence 13880, A	494	45.2	4.6	1095	4	US-09-252-991A-6626	Sequence 6626, Ap
C 422	45.8	4.6	2259	4	US-09-252-991A-13556	Sequence 13556, A	495	45.2	4.6	1419	4	US-09-252-991A-10421	Sequence 10421, A
C 423	45.8	4.6	5661	3	US-08-938-105-2	Sequence 2, Appl	496	45.2	4.6	1602	4	US-09-252-991A-6639	Sequence 6639, Ap
C 424	45.8	4.6	43280	2	US-08-804-227C-1	Sequence 1, Appl	497	45.2	4.6	1695	4	US-09-252-991A-6578	Sequence 6578, Ap
C 425	45.6	4.6	900	4	US-09-252-991A-14108	Sequence 14108, A	498	45.2	4.6	2363	4	US-09-818-780-22	Sequence 22, Appl
C 426	45.6	4.6	900	4	US-09-252-991A-1017	Sequence 1017, Ap	499	45.2	4.6	2376	4	US-09-252-991A-10741	Sequence 10741, A
C 427	45.6	4.6	924	4	US-09-252-991A-1483	Sequence 1483, Ap	500	45.2	4.6	2379	4	US-09-252-991A-9205	Sequence 9205, A
C 428	45.6	4.6	1035	4	US-09-252-991A-14017	Sequence 14017, A	501	45.2	4.6	2844	4	US-09-252-991A-4764	Sequence 4764, Ap
C 429	45.6	4.6	1200	4	US-09-787-292-4	Sequence 4, Appl	502	45.2	4.6	3084	4	US-09-252-991A-6639	Sequence 6639, Ap
C 430	45.6	4.6	1209	6	5352575-4	Patent No. 5352575	503	45.2	4.6	3273	4	US-09-252-991A-6578	Sequence 6578, Ap
C 431	45.6	4.6	1213	3	US-09-232-468A-7	Sequence 7, Appl	504	45.2	4.6	30001	2	US-08-474-933-1	Sequence 1, Appl
C 432	45.6	4.6	1213	4	US-09-784-984B-6	Sequence 6, Appl	505	45.2	4.6	30001	2	US-08-474-933-1	Sequence 1, Appl
C 433	45.6	4.6	1365	4	US-09-252-991A-14122	Sequence 14122, A	506	45	4.6	582	4	US-09-252-991A-6152	Sequence 6152, Ap
C 434	45.6	4.6	1458	4	US-09-252-991A-1112	Sequence 1112, Ap	507	45	4.6	820	3	US-09-150-900-48	Sequence 2, Appl
C 435	45.6	4.6	1461	4	US-09-252-991A-972	Sequence 972, App	508	45	4.6	1187	1	US-08-440-856A-2	Sequence 2, Appl
C 436	45.6	4.6	1505	1	US-07-915-246-1	Sequence 1, Appl	509	45	4.6	1377	4	US-09-585-173B-43	Sequence 43, Appl
C 437	45.6	4.6	1588	4	US-09-490-291-7	Sequence 7, Appl	510	45	4.6	1413	4	US-09-252-991A-6071	Sequence 6071, Ap
C 438	45.6	4.6	1663	4	US-09-398-522-108	Sequence 108, App	511	45	4.6	1491	4	US-09-252-991A-6228	Sequence 6228, Ap
C 439	45.6	4.6	1768	4	US-09-485-523-13	Sequence 13, Appl	512	45	4.6	1506	4	US-09-252-991A-6228	Sequence 6228, Ap
C 440	45.6	4.6	2124	4	US-09-266-965-44	Sequence 44, Appl	513	45	4.6	1690	4	US-09-620-312D-69	Sequence 69, Appl
C 441	45.6	4.6	2125	4	US-09-485-523-14	Sequence 14, Appl	514	45	4.6	3651	2	US-08-790-374-1	Sequence 1, Appl
C 442	45.6	4.6	2282	4	US-09-922-445-50	Sequence 50, Appl	515	45	4.6	7812	3	US-09-368-590-1	Sequence 1, Appl
C 443	45.6	4.6	3681	4	US-09-581-105-1	Sequence 1, Appl	516	45	4.6	23187	4	US-09-499-522-1	Sequence 1, Appl
C 444	45.6	4.6	4095	4	US-09-252-991A-10309	Sequence 10309, A	517	44.8	4.5	753	4	US-09-252-991A-6830	Sequence 6830, Ap
C 445	45.6	4.6	4233	4	US-09-551-974A-99	Sequence 99, Appl	518	44.8	4.5	783	4	US-09-252-991A-8452	Sequence 8452, A
C 446	45.6	4.6	4233	4	US-09-565-501A-99	Sequence 99, Appl	519	44.8	4.5	948	4	US-09-252-991A-14810	Sequence 14810, A
C 447	45.6	4.6	4233	4	US-09-639-206A-99	Sequence 99, Appl	520	44.8	4.5	1110	4	US-09-252-991A-14810	Sequence 8388, Ap
C 448	45.6	4.6	4233	4	US-09-874-923-99	Sequence 99, Appl	521	44.8	4.5	1131	4	US-09-252-991A-8388	Sequence 8388, Ap
C 449	45.6	4.6	4563	4	US-09-252-991A-930	Sequence 930, App	522	44.8	4.5	1162	2	US-09-252-991A-8486	Sequence 52, Appl
C 450	45.6	4.6	4917	4	US-09-551-974A-100	Sequence 100, App	523	44.8	4.5	1320	4	US-08-726-306A-52	Sequence 1, Appl
C 451	45.6	4.6	4917	4	US-09-565-501A-100	Sequence 100, App	524	44.8	4.5	1365	3	US-09-319-832-1	Sequence 1, Appl
C 452	45.6	4.6	4917	4	US-09-639-206A-100	Sequence 100, App	525	44.8	4.5	1428	4	US-09-252-991A-14802	Sequence 14802, A
C 453	45.6	4.6	4917	4	US-09-874-923-100	Sequence 100, App	526	44.8	4.5	1668	4	US-09-252-991A-14950	Sequence 14950, A
C 454	45.6	4.6	4929	4	US-09-551-974A-98	Sequence 98, Appl	527	44.8	4.5	1899	4	US-09-252-991A-6781	Sequence 7081, Ap
C 455	45.6	4.6	4929	4	US-09-565-501A-98	Sequence 98, Appl	528	44.8	4.5	2028	4	US-09-252-991A-7091	Sequence 7091, Ap
C 456	45.6	4.6	4929	4	US-09-639-206A-98	Sequence 98, Appl	529	44.8	4.5	2064	4	US-09-252-991A-9616	Sequence 9616, Ap
C 457	45.6	4.6	4929	4	US-09-874-923-98	Sequence 98, Appl	530	44.8	4.5	2235	4	US-09-252-991A-7032	Sequence 7032, Ap
C 458	45.4	4.6	468	4	US-09-252-991A-3528	Sequence 3528, Ap	531	44.8	4.5	3078	3	US-09-418-817-9	Sequence 9, Appl
C 459	45.4	4.6	538	1	US-10-095-946-13	Sequence 13, Appl	532	44.8	4.5	3162	4	US-09-252-991A-9569	Sequence 9569, Ap
C 460	45.4	4.6	538	3	US-09-183-959-13	Sequence 13, Appl	533	44.8	4.5	5064	4	US-09-774-528-224	Sequence 224, App
C 461	45.4	4.6	538	4	US-09-315-315-13	Sequence 13, Appl	534	44.8	4.5	6217	3	US-09-418-817-1	Sequence 1, Appl
C 462	45.4	4.6	845	4	US-09-347-650-1	Sequence 1, Appl	535	44.6	4.5	813	4	US-09-252-991A-5455	Sequence 5455, Ap
C 463	45.4	4.6	954	3	US-08-911-853-24	Sequence 24, Appl	536	44.6	4.5	837	4	US-09-252-991A-5983	Sequence 5983, Ap
C 464	45.4	4.6	954	3	US-09-479-409-24	Sequence 24, Appl	537	44.6	4.5	897	4	US-09-252-991A-8789	Sequence 8789, Ap
C 465	45.4	4.6	954	4	US-09-479-453-24	Sequence 24, Appl	538	44.6	4.5	1236	4	US-09-252-991A-8061	Sequence 8061, Ap
C 466	45.4	4.6	975	4	US-09-489-039A-791	Sequence 791, App	539	44.6	4.5	1272	4	US-09-252-991A-14082	Sequence 14082, A

540	44.6	4.5	1329	4	US-09-252-991A-14036	Sequence 14036, A	613	44.2	4.5	1740	4	US-09-252-991A-13753	Sequence 13753, A
c 541	44.6	4.5	1378	4	US-09-252-991A-9965	Sequence 9965, Ap	614	44.2	4.5	1835	4	US-09-417-704-2	Sequence 2, Appl
542	44.6	4.5	1587	4	US-09-252-991A-16504	Sequence 16504, A	c 615	44.2	4.5	1848	4	US-09-252-991A-15408	Sequence 15408, A
c 543	44.6	4.5	1620	4	US-09-252-991A-14186	Sequence 14186, A	c 616	44.2	4.5	2040	4	US-09-252-991A-12316	Sequence 12316, A
544	44.6	4.5	1623	4	US-09-252-991A-5431	Sequence 5431, Ap	617	44.2	4.5	2483	1	US-08-464-340A-3	Sequence 3, Appl
545	44.6	4.5	1656	4	US-10-140-002-239	Sequence 239, App	618	44.2	4.5	2483	5	PCT-US94-08449A-3	Sequence 3, Appl
546	44.6	4.5	2005	4	US-09-482-273-15	Sequence 15, Appl	619	44.2	4.5	2751	4	US-09-252-991A-14671	Sequence 14671, A
c 547	44.6	4.5	2070	4	US-09-252-991A-16098	Sequence 16098, A	c 620	44.2	4.5	2872	3	US-09-327-487A-2	Sequence 2, Appl
c 548	44.6	4.5	2154	4	US-09-252-991A-5458	Sequence 5458, Ap	c 621	44.2	4.5	3201	4	US-09-252-991A-14959	Sequence 14959, A
549	44.6	4.5	2163	4	US-09-252-991A-2047	Sequence 2047, Ap	c 622	44.2	4.5	3255	4	US-09-252-991A-10617	Sequence 10617, A
c 550	44.6	4.5	2556	4	US-09-252-991A-8202	Sequence 8202, Ap	623	44.2	4.5	3375	4	US-09-252-991A-10239	Sequence 10239, A
551	44.6	4.5	2664	4	US-09-482-273-83	Sequence 83, Appl	624	44.2	4.5	3402	4	US-09-252-991A-14791	Sequence 14791, A
552	44.6	4.5	3453	4	US-09-252-991A-8100	Sequence 8100, Ap	c 625	44.2	4.5	4689	3	US-09-105-537-34	Sequence 34, Appl
c 553	44.6	4.5	3546	4	US-09-252-991A-1909	Sequence 1909, Ap	c 626	44.2	4.5	13842	3	US-09-105-537-30	Sequence 30, Appl
554	44.6	4.5	3978	4	US-09-266-965-19	Sequence 19, Appl	c 627	44.2	4.5	20235	1	US-07-643-734C-3	Sequence 3, Appl
555	44.6	4.5	8931	3	US-09-028-934-28	Sequence 28, Appl	628	44.2	4.5	20235	3	US-08-439-009A-3	Sequence 3, Appl
556	44.6	4.5	12249	4	US-09-266-965-74	Sequence 74, Appl	c 629	44.2	4.5	3778	3	US-09-105-537-5	Sequence 5, Appl
557	44.6	4.5	18331	4	US-09-266-965-96	Sequence 96, Appl	c 630	44.2	4.5	3806	3	US-09-320-878-19	Sequence 19, Appl
c 558	44.4	4.5	465	4	US-09-252-991A-1459	Sequence 1459, Ap	c 631	44.2	4.5	38506	4	US-09-141-908-1	Sequence 1, Appl
c 559	44.4	4.5	720	4	US-09-252-991A-14268	Sequence 14268, A	c 632	44.2	4.5	38506	4	US-09-657-440-19	Sequence 19, Appl
c 560	44.4	4.5	756	4	US-09-252-991A-15229	Sequence 15229, A	c 633	44	4.4	426	4	US-09-252-991A-16285	Sequence 16285, A
c 561	44.4	4.5	819	4	US-09-252-991A-15235	Sequence 15235, A	c 634	44	4.4	426	4	US-09-252-991A-2270	Sequence 2270, Ap
c 562	44.4	4.5	1161	4	US-09-252-991A-10489	Sequence 10489, A	c 635	44	4.4	492	4	US-09-252-991A-4051	Sequence 4051, Ap
c 563	44.4	4.5	1161	4	US-09-252-991A-11607	Sequence 11607, A	c 636	44	4.4	897	3	US-09-434-288-6	Sequence 6, Appl
564	44.4	4.5	1305	4	US-09-252-991A-11762	Sequence 11762, A	c 637	44	4.4	948	4	US-09-252-991A-2569	Sequence 2569, Ap
565	44.4	4.5	1317	4	US-09-252-991A-3556	Sequence 3556, Ap	c 638	44	4.4	957	4	US-09-252-991A-5476	Sequence 5476, Ap
c 566	44.4	4.5	1512	4	US-09-252-991A-1551	Sequence 1551, Ap	c 639	44	4.4	981	4	US-09-252-991A-5453	Sequence 5453, Ap
c 567	44.4	4.5	1600	3	US-09-434-288-10	Sequence 10, Appl	c 640	44	4.4	1026	4	US-09-252-991A-2349	Sequence 2349, Ap
568	44.4	4.5	1677	4	US-09-252-991A-1616	Sequence 1616, Ap	c 641	44	4.4	1062	4	US-09-252-991A-16067	Sequence 16067, A
569	44.4	4.5	1731	2	US-08-466-583-1	Sequence 1, Appl	c 642	44	4.4	1110	4	US-09-252-991A-1858	Sequence 1858, Ap
570	44.4	4.5	1731	4	US-08-263-427-1	Sequence 1, Appl	c 643	44	4.4	1110	4	US-09-252-991A-8823	Sequence 8823, Ap
571	44.4	4.5	1731	5	PCT-US95-07820-1	Sequence 1, Appl	c 644	44	4.4	1116	4	US-09-252-991A-2104	Sequence 2104, Ap
572	44.4	4.5	1878	4	US-09-489-039A-2045	Sequence 2045, Ap	c 645	44	4.4	1126	3	US-08-949-155-5	Sequence 5, Appl
c 573	44.4	4.5	2073	4	US-09-252-991A-10279	Sequence 10279, A	c 646	44	4.4	1126	3	US-09-819-964-5	Sequence 5, Appl
574	44.4	4.5	2176	6	5320958-1	Patent No. 5320958	c 647	44	4.4	1152	4	US-09-252-991A-1791	Sequence 1791, Ap
575	44.4	4.5	2325	4	US-09-252-991A-218	Sequence 218, App	c 648	44	4.4	1333	3	US-09-372-422A-9	Sequence 9, Appl
576	44.4	4.5	2430	4	US-09-252-991A-15188	Sequence 15188, A	c 649	44	4.4	1683	4	US-09-252-991A-1126	Sequence 1126, A
577	44.4	4.5	2772	4	US-09-252-991A-10577	Sequence 10577, A	c 650	44	4.4	1734	4	US-09-252-991A-9061	Sequence 9061, Ap
c 578	44.4	4.5	2784	4	US-09-252-991A-194	Sequence 194, App	c 651	44	4.4	1908	4	US-09-252-991A-16529	Sequence 16529, A
579	44.4	4.5	2946	4	US-09-252-991A-227	Sequence 227, App	c 652	44	4.4	1926	4	US-09-249-585A-2	Sequence 2, Appl
c 580	44.4	4.5	3503	4	US-09-252-991A-14443	Sequence 14443, A	c 653	44	4.4	1926	4	US-09-410-399-3	Sequence 3, Appl
581	44.4	4.5	4267	3	US-08-948-155-51	Sequence 51, Appl	c 654	44	4.4	1974	4	US-08-252-991A-1111	Sequence 1111, A
582	44.4	4.5	4267	3	US-09-819-964-51	Sequence 51, Appl	c 655	44	4.4	2154	4	US-09-252-991A-9144	Sequence 9144, Ap
583	44.2	4.5	483	4	US-09-252-991A-15272	Sequence 15272, A	c 656	44	4.4	2159	3	US-08-286-870A-7	Sequence 7, Appl
584	44.2	4.5	594	4	US-09-252-991A-3950	Sequence 3950, Ap	c 657	44	4.4	2283	4	US-09-252-991A-10956	Sequence 10956, A
585	44.2	4.5	765	4	US-09-252-991A-3922	Sequence 3922, Ap	c 658	44	4.4	2580	3	US-09-050-863-2	Sequence 2, Appl
c 586	44.2	4.5	798	4	US-09-252-991A-9181	Sequence 9181, Ap	c 659	44	4.4	2580	3	US-09-359-081-2	Sequence 2, Appl
587	44.2	4.5	810	4	US-09-252-991A-3647	Sequence 3647, Ap	c 660	44	4.4	2721	6	5215881-2	Patent No. 5215881
588	44.2	4.5	837	4	US-09-252-991A-15324	Sequence 15324, A	c 661	44	4.4	4267	3	US-08-949-155-51	Sequence 51, Appl
589	44.2	4.5	879	4	US-09-252-991A-3602	Sequence 3602, Ap	c 662	44	4.4	4267	3	US-09-819-964-51	Sequence 51, Appl
590	44.2	4.5	903	4	US-09-252-991A-8894	Sequence 8894, Ap	c 663	44	4.4	4542	2	US-09-130-114-1	Sequence 1, Appl
591	44.2	4.5	975	4	US-09-252-991A-12244	Sequence 12244, A	c 664	44	4.4	7065	4	US-09-874-923-115	Sequence 115, App
c 592	44.2	4.5	999	4	US-09-252-991A-14326	Sequence 14326, A	c 665	44	4.4	8705	4	US-09-647-344A-14	Sequence 14, Appl
593	44.2	4.5	1018	1	US-08-444-083-6	Sequence 6, Appl	c 666	44	4.4	9600	3	US-08-910-647-1	Sequence 1, Appl
594	44.2	4.5	1018	1	US-08-286-304-6	Sequence 6, Appl	c 667	44	4.4	9600	4	US-09-620-925-1	Sequence 1, Appl
595	44.2	4.5	1018	1	US-08-442-745-6	Sequence 6, Appl	c 668	44	4.4	10596	1	US-07-884-811-15	Sequence 15, Appl
596	44.2	4.5	1018	1	US-08-443-129-6	Sequence 6, Appl	c 669	44	4.4	10596	1	US-07-885-971-15	Sequence 15, Appl
597	44.2	4.5	1018	1	US-08-443-129-6	Sequence 6, Appl	c 670	44	4.4	10596	1	US-08-087-783A-15	Sequence 15, Appl
598	44.2	4.5	1018	1	US-08-443-130-6	Sequence 6, Appl	c 671	44	4.4	10596	1	US-08-194-088B-15	Sequence 15, Appl
599	44.2	4.5	1018	3	US-08-898-911-6	Sequence 6, Appl	c 672	44	4.4	10596	2	US-08-194-087-15	Sequence 15, Appl
600	44.2	4.5	1018	5	PCT-US95-04467-6	Sequence 6, Appl	c 673	44	4.4	10596	5	PCT-US93-04648-15	Sequence 15, Appl
c 601	44.2	4.5	1116	4	US-09-252-991A-13384	Sequence 13384, A	c 674	44	4.4	16080	4	US-09-724-566A-48	Sequence 48, Appl
c 602	44.2	4.5	1194	4	US-09-252-991A-4021	Sequence 4021, Ap	c 675	44	4.4	47981	4	US-09-679-279-1	Sequence 1, Appl
c 603	44.2	4.5	1233	4	US-09-252-991A-15366	Sequence 15366, A	c 676	44	4.4	552	4	US-09-252-991A-3410	Sequence 3410, Ap
c 604	44.2	4.5	1257	4	US-09-252-991A-15464	Sequence 15464, A	c 677	44	4.4	618	4	US-09-252-991A-9002	Sequence 9002, Ap
605	44.2	4.5	1377	4	US-09-252-991A-13964	Sequence 13964, A	c 678	44	4.4	681	4	US-09-252-991A-3274	Sequence 3274, Ap
606	44.2	4.5	1518	4	US-09-252-991A-12104	Sequence 12104, A	c 679	44	4.4	696	4	US-09-252-991A-1248	Sequence 1248, Ap
607	44.2	4.5	1539	4	US-09-648-183-1	Sequence 1, Appl	c 680	44	4.4	723	4	US-09-252-991A-5281	Sequence 5281, Ap
c 608	44.2	4.5	1539	4	US-09-648-183-2	Sequence 2, Appl	c 681	44	4.4	741	4	US-09-252-991A-5345	Sequence 5345, Ap
c 609	44.2	4.5	1593	4	US-09-252-991A-14376	Sequence 14376, A	c 682	44	4.4	891	4	US-09-252-991A-13471	Sequence 13471, A
610	44.2	4.5	1614	4	US-09-252-991A-10453	Sequence 10453, A	c 683	44	4.4	954	4	US-09-252-991A-5307	Sequence 5307, Ap
c 611	44.2	4.5	1632	4	US-09-252-991A-3859	Sequence 3859, Ap	c 684	44	4.4	978	4	US-09-252-991A-5172	Sequence 5172, Ap
612	44.2	4.5	1716	4	US-09-252-991A-15268	Sequence 15268, A	c 685	44	4.4	993	4	US-09-252-991A-9006	Sequence 9006, Ap

C 686	43.8	4.4	993	4	US-09-252-991A-15615	Sequence 15615, A	C 764	43.4	4.4	674	3	US-09-543-106-1	Sequence 1, Appli
C 687	43.8	4.4	1008	4	US-09-252-991A-7377	Sequence 7377, Ap	C 765	43.4	4.4	753	4	US-09-252-991A-15657	Sequence 15657, A
C 688	43.8	4.4	1026	4	US-09-252-991A-12367	Sequence 12367, A	C 766	43.4	4.4	957	4	US-09-252-991A-3136	Sequence 3136, Ap
C 689	43.8	4.4	1047	4	US-09-252-991A-3327	Sequence 3327, Ap	C 767	43.4	4.4	1011	4	US-09-252-991A-4029	Sequence 4029, Ap
C 690	43.8	4.4	1098	4	US-09-252-991A-1354	Sequence 1354, Ap	C 768	43.4	4.4	1017	4	US-09-252-991A-3038	Sequence 3038, Ap
C 691	43.8	4.4	1098	4	US-09-252-991A-13766	Sequence 13766, A	C 769	43.4	4.4	1104	4	US-09-794-534-1	Sequence 1, Appli
C 692	43.8	4.4	1188	4	US-09-286-965-62	Sequence 62, Appl	C 770	43.4	4.4	1361	4	US-09-614-912-37	Sequence 37, Appl
C 693	43.8	4.4	1197	4	US-09-252-991A-5115	Sequence 5115, Ap	C 771	43.4	4.4	1425	4	US-09-252-991A-2830	Sequence 2830, Ap
C 694	43.8	4.4	1280	3	US-08-483-533-38	Sequence 38, Appl	C 772	43.4	4.4	1446	4	US-09-252-991A-3888	Sequence 3888, Ap
C 695	43.8	4.4	1356	4	US-09-283-471A-38	Sequence 38, Appl	C 773	43.4	4.4	1566	4	US-09-724-797-61	Sequence 61, Appl
C 696	43.8	4.4	1371	4	US-09-252-991A-11031	Sequence 11031, A	C 774	43.4	4.4	1581	4	US-09-252-991A-3962	Sequence 3962, Ap
C 697	43.8	4.4	1416	4	US-09-252-991A-5005	Sequence 5005, Ap	C 775	43.4	4.4	1614	4	US-09-616-283-45	Sequence 45, Appl
C 698	43.8	4.4	1431	4	US-09-252-991A-15670	Sequence 15670, A	C 776	43.4	4.4	1742	3	US-09-232-468A-1	Sequence 1, Appli
C 699	43.8	4.4	1521	4	US-09-724-797-87	Sequence 87, Appl	C 777	43.4	4.4	2742	4	US-09-784-984B-1	Sequence 1, Appli
C 700	43.8	4.4	1536	4	US-09-252-991A-15579	Sequence 15579, A	C 778	43.4	4.4	2943	4	US-09-252-991A-349	Sequence 349, App
C 701	43.8	4.4	1596	4	US-09-266-965-60	Sequence 60, Appl	C 779	43.4	4.4	3147	2	US-08-781-802-7	Sequence 7, Appli
C 702	43.8	4.4	1608	4	US-09-252-991A-11089	Sequence 11089, A	C 780	43.4	4.4	3147	3	US-08-694-078-7	Sequence 7, Appli
C 703	43.8	4.4	1608	4	US-09-252-991A-11665	Sequence 11665, A	C 781	43.4	4.4	3381	4	US-09-058-260-7	Sequence 1361, Ap
C 704	43.8	4.4	1608	4	US-09-252-991A-11769	Sequence 11769, A	C 782	43.4	4.4	3981	4	US-09-252-991A-1244	Sequence 1244, Ap
C 705	43.8	4.4	1761	4	US-09-252-991A-13674	Sequence 13674, A	C 783	43.4	4.4	4179	4	US-09-252-991A-11572	Sequence 11572, A
C 706	43.8	4.4	1761	4	US-09-252-991A-4120	Sequence 4120, Ap	C 784	43.4	4.4	4326	4	US-09-252-991A-11871	Sequence 11871, A
C 707	43.8	4.4	1800	4	US-09-252-991A-4085	Sequence 4085, Ap	C 785	43.4	4.4	4473	4	US-09-252-991A-11871	Sequence 11871, A
C 708	43.8	4.4	1802	4	US-09-535-315-22	Sequence 22, Appl	C 786	43.4	4.4	4897	6	5196515-7	Patent No. 5196516
C 709	43.8	4.4	1869	4	US-09-252-991A-15737	Sequence 15737, A	C 787	43.4	4.4	6854	3	US-09-194-905-7	Sequence 7, Appli
C 710	43.8	4.4	2067	4	US-09-252-991A-1398	Sequence 1398, Ap	C 788	43.4	4.4	7263	4	US-09-620-312D-55	Sequence 55, Appl
C 711	43.8	4.4	2100	4	US-09-252-991A-1209	Sequence 1209, Ap	C 789	43.4	4.4	12425	1	US-09-616-289-50	Sequence 50, Appl
C 712	43.8	4.4	2127	4	US-09-252-991A-8192								

837	43	4.3	342	4	US-09-252-991A-604	Sequence 604, App	C 910	42.8	4.3	1479	4	US-09-252-991A-7048	Sequence 7048, Ap
C 838	43	4.3	525	4	US-09-252-991A-2828	Sequence 2828, Ap	C 911	42.8	4.3	1611	4	US-09-252-991A-16550	Sequence 16550, A
C 839	43	4.3	714	4	US-09-252-991A-15925	Sequence 15925, A	C 912	42.8	4.3	1617	4	US-09-252-991A-16558	Sequence 16558, A
840	43	4.3	720	4	US-09-252-991A-74	Sequence 74, Appl	C 913	42.8	4.3	1721	1	US-08-241-766-3	Sequence 3, Appl1
841	43	4.3	780	4	US-09-252-991A-15799	Sequence 15799, A	C 914	42.8	4.3	1818	4	US-09-252-991A-8941	Sequence 8941, Ap
C 842	43	4.3	861	4	US-09-252-991A-13981	Sequence 13981, A	C 915	42.8	4.3	1836	4	US-09-252-991A-1026	Sequence 1026, Ap
C 843	43	4.3	1071	4	US-09-252-991A-14206	Sequence 14206, A	C 916	42.8	4.3	2003	1	US-08-036-555B-21	Sequence 21, Appl
844	43	4.3	1419	4	US-09-252-991A-10421	Sequence 10421, A	C 917	42.8	4.3	2003	1	US-08-463-569-21	Sequence 21, Appl
C 845	43	4.3	1419	4	US-09-252-991A-11636	Sequence 11636, A	C 918	42.8	4.3	2003	1	US-08-249-322A-21	Sequence 21, Appl
C 846	43	4.3	1419	4	US-09-252-991A-9286	Sequence 9286, Ap	C 919	42.8	4.3	2003	1	US-08-469-526A-21	Sequence 21, Appl
C 847	43	4.3	1509	4	US-09-252-991A-63	Sequence 63, Appl	C 920	42.8	4.3	2003	2	US-08-734-591A-21	Sequence 21, Appl
C 848	43	4.3	1587	4	US-09-252-991A-11720	Sequence 11720, A	C 921	42.8	4.3	2003	2	US-08-469-660-21	Sequence 21, Appl
C 849	43	4.3	1623	4	US-09-252-991A-538	Sequence 538, App	C 922	42.8	4.3	2003	3	US-08-341-018-71	Sequence 71, Appl
C 850	43	4.3	1695	4	US-09-252-991A-10319	Sequence 10319, A	C 923	42.8	4.3	2003	3	US-08-470-335-21	Sequence 21, Appl
C 851	43	4.3	1803	4	US-09-252-991A-15466	Sequence 15466, A	C 924	42.8	4.3	2003	3	US-08-735-021-21	Sequence 21, Appl
C 852	43	4.3	1818	4	US-09-731-166-3	Sequence 3, Appl1	C 925	42.8	4.3	2003	3	US-08-734-664A-21	Sequence 21, Appl
C 853	43	4.3	1845	4	US-09-614-034-188	Sequence 188, App	C 926	42.8	4.3	2003	3	US-08-470-339-21	Sequence 21, Appl
C 854	43	4.3	1890	4	US-09-252-991A-579	Sequence 579, App	C 927	42.8	4.3	2003	4	US-08-467-602-21	Sequence 21, Appl
C 855	43	4.3	1977	4	US-09-252-991A-9290	Sequence 9290, Ap	C 928	42.8	4.3	2003	4	US-08-411-295F-64	Sequence 64, Appl
C 856	43	4.3	1995	4	US-09-252-991A-9265	Sequence 9265, Ap	C 929	42.8	4.3	2003	5	PCT-US94-05083C-21	Sequence 21, Appl
C 857	43	4.3	2058	6	5212296-8	Patent No. 5212296	C 930	42.8	4.3	2046	5	PCT-US95-06846A-21	Sequence 21, Appl
C 858	43	4.3	2095	4	US-09-252-991A-15771	Sequence 15771, A	C 931	42.8	4.3	2046	5	US-09-490-291-3	Sequence 3, Appl1
C 859	43	4.3	2242	1	US-08-641-627A-37	Sequence 37, Appl	C 932	42.8	4.3	2076	4	US-09-490-291-5	Sequence 5, Appl1
C 860	43	4.3	2304	4	US-09-252-991A-11802	Sequence 11802, A	C 933	42.8	4.3	3051	1	US-08-241-766-10	Sequence 10, Appl
C 861	43	4.3	2310	4	US-09-252-991A-3040	Sequence 3040, Ap	C 934	42.8	4.3	3195	4	US-09-252-991A-937	Sequence 937, App
C 862	43	4.3	2376	4	US-09-252-991A-10741	Sequence 10741, A	C 935	42.8	4.3	4236	4	US-09-252-991A-7057	Sequence 7057, Ap
C 863	43	4.3	2376	4	US-09-252-991A-15323	Sequence 15323, A	C 936	42.8	4.3	4236	4	US-08-949-386-23	Sequence 23, Appl
C 864	43	4.3	2688	4	US-09-252-991A-14064	Sequence 14064, A	C 937	42.8	4.3	7791	3	US-08-450-562-23	Sequence 23, Appl
C 865	43	4.3	2686	4	US-09-252-991A-15370	Sequence 15370, A	C 938	42.8	4.3	7791	3	US-08-984-709A-23	Sequence 23, Appl
C 866	43	4.3	3794	4	US-09-192-434-1	Sequence 1, Appl1	C 939	42.8	4.3	7791	3	US-08-450-272-23	Sequence 23, Appl
C 867	43	4.3	3825	4	US-09-252-991A-3815	Sequence 3815, Ap	C 940	42.8	4.3	7791	3	US-08-450-272-23	Sequence 23, Appl
C 868	43	4.3	4059	2	US-08-485-139-1	Sequence 1, Appl1	C 941	42.8	4.3	7808	3	US-08-949-386-22	Sequence 22, Appl
C 869	43	4.3	4506	4	US-09-252-991A-3695	Sequence 3695, Ap	C 942	42.8	4.3	7808	3	US-08-450-562-22	Sequence 22, Appl
C 870	43	4.3	4800	3	US-09-106-638-1	Sequence 1, Appl1	C 943	42.8	4.3	7808	3	US-08-984-709A-22	Sequence 22, Appl
C 871	43	4.3	4800	3	US-08-941-445A-4	Sequence 4, Appl1	C 944	42.8	4.3	7808	3	US-08-450-272-22	Sequence 22, Appl
C 872	43	4.3	7527	4	US-09-252-991A-71	Sequence 71, Appl	C 945	42.8	4.3	7808	4	US-08-450-272-22	Sequence 22, Appl
C 873	42.8	4.3	426	4	US-09-252-991A-7105	Sequence 7105, Ap	C 946	42.8	4.3	10023	4	US-09-252-991A-6997	Sequence 6997, Ap
C 874	42.8	4.3	561	4	US-09-252-991A-7275	Sequence 7275, Ap	C 947	42.6	4.3	468	4	US-09-252-991A-16394	Sequence 16394, A
C 875	42.8	4.3	570	4	US-09-252-991A-3834	Sequence 3834, Ap	C 948	42.6	4.3	555	4	US-09-252-991A-16030	Sequence 16030, A
C 876	42.8	4.3	639	4	US-09-252-991A-1078	Sequence 1078, Ap	C 949	42.6	4.3	588	4	US-09-252-991A-1995	Sequence 1995, Ap
C 877	42.8	4.3	745	1	US-08-036-555B-163	Sequence 163, App	C 950	42.6	4.3	621	4	US-09-252-991A-3944	Sequence 3944, Ap
C 878	42.8	4.3	745	1	US-08-469-569-163	Sequence 163, App	C 951	42.6	4.3	624	4	US-09-252-991A-12492	Sequence 12492, A
C 879	42.8	4.3	745	1	US-08-249-322A-163	Sequence 163, App	C 952	42.6	4.3	690	4	US-09-252-991A-11336	Sequence 11336, A
C 880	42.8	4.3	745	1	US-08-469-526A-163	Sequence 163, App	C 953	42.6	4.3	693	4	US-09-252-991A-15166	Sequence 15166, A
C 881	42.8	4.3	745	2	US-08-734-591A-163	Sequence 163, App	C 954	42.6	4.3	747	4	US-09-252-991A-16349	Sequence 16349, A
C 882	42.8	4.3	745	2	US-08-469-660-163	Sequence 163, App	C 955	42.6	4.3	750	4	US-09-252-991A-12577	Sequence 12577, A
C 883	42.8	4.3	745	3	US-08-341-018-51	Sequence 51, Appl	C 956	42.6	4.3	771	4	US-09-252-991A-12986	Sequence 12986, A
C 884	42.8	4.3	745	3	US-08-470-335-163	Sequence 163, App	C 957	42.6	4.3	840	4	US-09-252-991A-7712	Sequence 7712, Ap
C 885	42.8	4.3	745	3	US-08-735-021-163	Sequence 163, App	C 958	42.6	4.3	912	4	US-09-252-991A-11313	Sequence 11313, A
C 886	42.8	4.3	745	3	US-08-734-664A-163	Sequence 163, App	C 959	42.6	4.3	1050	4	US-09-252-991A-12884	Sequence 12884, A
C 887	42.8	4.3	745	3	US-08-470-339-163	Sequence 163, App	C 960	42.6	4.3	1068	4	US-09-252-991A-16463	Sequence 16463, A
C 888	42.8	4.3	745	4	US-08-467-602-163	Sequence 163, App	C 961	42.6	4.3	1126	3	US-08-949-155-5	Sequence 5, Appl1
C 889	42.8	4.3	745	4	US-08-411-295F-44	Sequence 44, Appl	C 962	42.6	4.3	1126	3	US-09-819-964-5	Sequence 5, Appl1
C 890	42.8	4.3	745	5	PCT-US94-05083C-159	Sequence 159, App	C 963	42.6	4.3	1154	3	US-09-347-803-15	Sequence 15, Appl
C 891	42.8	4.3	745	5	PCT-US95-06846A-163	Sequence 163, App	C 964	42.6	4.3	1206	4	US-09-252-991A-519	Sequence 519, App
C 892	42.8	4.3	756	1	US-08-642-255-50	Sequence 50, Appl	C 965	42.6	4.3	1221	4	US-09-252-991A-7850	Sequence 7850, Ap
C 893	42.8	4.3	801	4	US-09-252-991A-16176	Sequence 16176, A	C 966	42.6	4.3	1227	4	US-09-252-991A-11278	Sequence 11278, A
C 894	42.8	4.3	801	4	US-09-252-991A-9143	Sequence 9143, Ap	C 967	42.6	4.3	1269	4	US-09-252-991A-12933	Sequence 12933, A
C 895	42.8	4.3	849	4	US-09-252-991A-3722	Sequence 3722, Ap	C 968	42.6	4.3	1281	4	US-09-252-991A-12551	Sequence 12551, A
C 896	42.8	4.3	873	4	US-09-252-991A-16052	Sequence 16052, A	C 969	42.6	4.3	1416	4	US-09-252-991A-2625	Sequence 2625, Ap
C 897	42.8	4.3	939	4	US-09-252-991A-16069	Sequence 16069, A	C 970	42.6	4.3	1446	4	US-09-252-991A-7937	Sequence 7937, Ap
C 898	42.8	4.3	1035	3	US-08-858-003-30	Sequence 30, Appl	C 971	42.6	4.3	1488	4	US-09-252-991A-8426	Sequence 8426, Ap
C 899	42.8	4.3	1035	3	US-09-078-166-30	Sequence 30, Appl	C 972	42.6	4.3	1503	3	US-09-463-702A-33	Sequence 33, Appl
C 900	42.8	4.3	1035	3	US-09-997-467-30	Sequence 30, Appl	C 973	42.6	4.3	1503	4	US-09-699-135-33	Sequence 33, Appl
C 901	42.8	4.3	1050	4	US-09-252-991A-8232	Sequence 8232, Ap	C 974	42.6	4.3	1509	4	US-09-252-991A-12165	Sequence 12165, A
C 902	42.8	4.3	1113	4	US-09-252-991A-7427	Sequence 7427, Ap	C 975	42.6	4.3	1551	4	US-09-252-991A-13148	Sequence 13148, A
C 903	42.8	4.3	1143	4	US-09-252-991A-1032	Sequence 1032, Ap	C 976	42.6	4.3	1569	4	US-09-252-991A-11892	Sequence 11892, A
C 904	42.8	4.3	1218	4	US-09-252-991A-7486	Sequence 7486, Ap	C 977	42.6	4.3	1584	4	US-09-252-991A-2288	Sequence 2288, Ap
C 905	42.8	4.3	1443	1	US-08-076-089-1	Sequence 1, Appl1	C 978	42.6	4.3	1662	4	US-09-252-991A-1413	Sequence 1413, Ap
C 906	42.8	4.3	1443	2	US-08-707-200-1	Sequence 1, Appl1	C 979	42.6	4.3	1662	4	US-09-252-991A-7894	Sequence 7894, Ap
C 907	42.8	4.3	1443	3	US-08-996-565-1	Sequence 1, Appl1	C 980	42.6	4.3	1692	4	US-09-252-991A-12425	Sequence 12425, A
C 908	42.8	4.3	1443	5	PCT-US93-05643-1	Sequence 1, Appl1	C 981	42.6	4.3	1767	4	US-09-252-991A-7614	Sequence 7614, Ap
C 909	42.8	4.3	1470	4	US-09-252-991A-7210	Sequence 7210, Ap	C 982	42.6	4.3	1899	4	US-09-252-991A-7664	Sequence 7664, Ap

c 983	42.6	4.3	1923	4	US-09-252-991A-3380	Sequence 3380, Ap	1056	42.6	4.3	4162	2	US-08-459-448A-26	Sequence 26, Appl
c 984	42.6	4.3	2049	4	US-09-252-991A-8348	Sequence 8348, Ap	1057	42.6	4.3	4162	3	US-08-459-595A-26	Sequence 26, Appl
c 985	42.6	4.3	2070	4	US-09-252-991A-15031	Sequence 15031, A	1058	42.6	4.3	4162	3	US-08-459-504B-26	Sequence 26, Appl
c 986	42.6	4.3	2181	4	US-09-252-991A-493	Sequence 493, App	1059	42.6	4.3	4162	3	US-08-459-444-26	Sequence 26, Appl
c 987	42.6	4.3	2186	2	US-08-878-546-9	Sequence 9, Appli	1060	42.6	4.3	4162	3	US-09-547-422-26	Sequence 26, Appl
c 988	42.6	4.3	2196	4	US-09-252-991A-609	Sequence 609, App	1061	42.6	4.3	4162	3	US-09-988-462-26	Sequence 26, Appl
c 989	42.6	4.3	2526	4	US-09-252-991A-12018	Sequence 12018, A	1062	42.6	4.3	4165	1	US-07-951-715A-26	Sequence 26, Appl
c 990	42.6	4.3	2724	4	US-09-252-991A-7543	Sequence 7543, Ap	1063	42.6	4.3	4269	4	US-09-799-451-363	Sequence 363, App
c 991	42.6	4.3	2742	3	US-09-233-468A-1	Sequence 1, Appli	1064	42.6	4.3	4897	6	5196516-7	Patent No. 5196516
c 992	42.6	4.3	2742	4	US-09-784-984B-1	Sequence 1, Appli	1065	42.6	4.3	5970	3	US-09-320-878-21	Sequence 21, Appl
c 993	42.6	4.3	2754	4	US-09-252-991A-1147	Sequence 1147, Ap	1066	42.6	4.3	5970	4	US-09-141-908-11	Sequence 11, Appl
c 994	42.6	4.3	3147	3	US-09-105-537-40	Sequence 40, Appl	1067	42.6	4.3	5970	4	US-09-657-440-21	Sequence 21, Appl
c 995	42.6	4.3	3187	4	US-09-252-991A-12797	Sequence 12797, A	1068	42.6	4.3	23673	3	US-09-773-816-1	Sequence 1, Appli
c 996	42.6	4.3	3627	4	US-09-252-991A-1324	Sequence 1324, Ap	1069	42.4	4.3	495	4	US-09-252-991A-10553	Sequence 10553, A
c 997	42.6	4.3	3627	4	US-09-793-594-3	Sequence 3, Appli	1070	42.4	4.3	546	4	US-09-252-991A-9911	Sequence 9911, A
c 998	42.6	4.3	3698	2	US-08-231-193A-43	Sequence 43, Appl	1071	42.4	4.3	561	4	US-09-252-991A-3862	Sequence 3862, Ap
c 999	42.6	4.3	3698	2	US-08-486-273A-43	Sequence 43, Appl	1072	42.4	4.3	657	3	US-09-527-345-3	Sequence 3, Appli
1000	42.6	4.3	3698	3	US-08-480-474-43	Sequence 43, Appl	1073	42.4	4.3	678	4	US-09-252-991A-8721	Sequence 8721, Ap
1001	42.6	4.3	3698	3	US-08-940-086A-43	Sequence 43, Appl	1074	42.4	4.3	792	4	US-09-818-780-31	Sequence 31, Appl
1002	42.6	4.3	3698	3	US-08-940-035A-43	Sequence 43, Appl	1075	42.4	4.3	810	4	US-09-252-991A-10034	Sequence 10034, A
1003	42.6	4.3	3698	3	US-08-935-105A-43	Sequence 43, Appl	1076	42.4	4.3	918	4	US-09-252-991A-16461	Sequence 16461, A
1004	42.6	4.3	3698	4	US-09-648-797-43	Sequence 43, Appl	1077	42.4	4.3	987	4	US-09-252-991A-10099	Sequence 10099, A
1005	42.6	4.3	3698	4	US-09-386-123-43	Sequence 43, Appl	1078	42.4	4.3	1005	4	US-09-252-991A-16346	Sequence 16346, A
1006	42.6	4.3	3850	3	US-09-463-702A-1	Sequence 1, Appli	1079	42.4	4.3	1026	4	US-09-252-991A-6481	Sequence 6481, Ap
1007	42.6	4.3	3850	4	US-09-699-135-1	Sequence 1, Appli	1080	42.4	4.3	1038	4	US-09-252-991A-9197	Sequence 9197, Ap
1008	42.6	4.3	4002	2	US-08-231-193A-53	Sequence 53, Appl	1081	42.4	4.3	1062	4	US-09-252-991A-6310	Sequence 6310, A
1009	42.6	4.3	4002	2	US-08-486-273A-53	Sequence 53, Appl	1082	42.4	4.3	1098	4	US-09-252-991A-16142	Sequence 16142, A
1010	42.6	4.3	4002	3	US-08-480-474-53	Sequence 53, Appl	1083	42.4	4.3	1137	4	US-09-724-797-53	Sequence 53, Appl
1011	42.6	4.3	4002	3	US-08-940-086A-53	Sequence 53, Appl	1084	42.4	4.3	1230	4	US-09-252-991A-5993	Sequence 5993, Ap
1012	42.6	4.3	4002	3	US-08-940-035A-53	Sequence 53, Appl	1085	42.4	4.3	1380	4	US-09-252-991A-3550	Sequence 3550, Ap
1013	42.6	4.3	4002	3	US-08-935-105A-53	Sequence 53, Appl	1086	42.4	4.3	1410	4	US-09-252-991A-8867	Sequence 8867, Ap
1014	42.6	4.3	4002	4	US-09-648-797-53	Sequence 53, Appl	1087	42.4	4.3	1546	3	US-09-383-318A-1	Sequence 1, Appli
1015	42.6	4.3	4002	4	US-09-386-123-53	Sequence 53, Appl	1088	42.4	4.3	1566	4	US-09-724-797-61	Sequence 61, Appl
1016	42.6	4.3	4017	2	US-08-231-193A-49	Sequence 49, Appl	1089	42.4	4.3	1902	4	US-09-252-991A-10005	Sequence 10005, A
1017	42.6	4.3	4017	2	US-08-486-273A-49	Sequence 49, Appl	1090	42.4	4.3	1919	4	US-09-614-912-175	Sequence 175, App
1018	42.6	4.3	4017	3	US-08-480-474-49	Sequence 49, Appl	1091	42.4	4.3	1947	4	US-09-252-991A-3557	Sequence 3557, Ap
1019	42.6	4.3	4017	3	US-08-940-086A-49	Sequence 49, Appl	1092	42.4	4.3	1983	4	US-09-252-991A-13314	Sequence 13314, A
1020	42.6	4.3	4017	3	US-08-940-035A-49	Sequence 49, Appl	1093	42.4	4.3	1992	4	US-09-252-991A-9693	Sequence 9693, Ap
1021	42.6	4.3	4017	3	US-08-935-105A-49	Sequence 49, Appl	1094	42.4	4.3	1998	4	US-09-252-991A-13154	Sequence 13154, A
1022	42.6	4.3	4017	4	US-09-648-797-49	Sequence 49, Appl	1095	42.4	4.3	2043	4	US-09-252-991A-12652	Sequence 12652, A
1023	42.6	4.3	4017	4	US-09-386-123-49	Sequence 49, Appl	1096	42.4	4.3	2067	4	US-09-252-991A-9114	Sequence 9114, Ap
1024	42.6	4.3	4053	2	US-08-231-193A-47	Sequence 47, Appl	1097	42.4	4.3	2376	4	US-09-976-594-496	Sequence 496, App
1025	42.6	4.3	4053	2	US-08-486-273A-47	Sequence 47, Appl	1098	42.4	4.3	2634	4	US-09-252-991A-9558	Sequence 9558, Ap
1026	42.6	4.3	4053	3	US-08-480-474-47	Sequence 47, Appl	1099	42.4	4.3	2658	4	US-09-252-991A-9558	Sequence 9558, Ap
1027	42.6	4.3	4053	3	US-08-940-086A-47	Sequence 47, Appl	1100	42.4	4.3	2799	4	US-09-252-991A-9604	Sequence 9604, Ap
1028	42.6	4.3	4053	3	US-08-940-035A-47	Sequence 47, Appl	1101	42.4	4.3	3241	3	US-09-434-288-11	Sequence 11, Appl
1029	42.6	4.3	4053	3	US-08-935-105A-47	Sequence 47, Appl	1102	42.4	4.3	4143	4	US-09-919-039-345	Sequence 345, App
1030	42.6	4.3	4053	4	US-09-648-797-47	Sequence 47, Appl	1103	42.4	4.3	4992	4	US-09-015-339-10	Sequence 10, Appl
1031	42.6	4.3	4053	4	US-09-386-123-47	Sequence 47, Appl	1104	42.4	4.3	55216	4	US-09-716-865-23	Sequence 23, Appl
1032	42.6	4.3	4068	2	US-08-231-193A-5	Sequence 5, Appli	1105	42.2	4.3	456	4	US-09-252-991A-6665	Sequence 6665, Ap
1033	42.6	4.3	4068	2	US-08-486-273A-5	Sequence 5, Appli	1106	42.2	4.3	564	4	US-09-252-991A-6557	Sequence 6557, Ap
1034	42.6	4.3	4068	3	US-08-480-474-5	Sequence 5, Appli	1107	42.2	4.3	609	4	US-09-252-991A-11904	Sequence 11904, A
1035	42.6	4.3	4068	3	US-08-940-086A-5	Sequence 5, Appli	1108	42.2	4.3	639	4	US-09-252-991A-6537	Sequence 6537, Ap
1036	42.6	4.3	4068	3	US-08-940-035A-5	Sequence 5, Appli	1109	42.2	4.3	672	4	US-09-252-991A-15696	Sequence 15696, A
1037	42.6	4.3	4068	4	US-08-935-105A-5	Sequence 5, Appli	1110	42.2	4.3	788	4	US-09-252-991A-14234	Sequence 14234, A
1038	42.6	4.3	4068	4	US-09-648-797-5	Sequence 5, Appli	1111	42.2	4.3	789	4	US-09-252-991A-9734	Sequence 9734, Ap
1039	42.6	4.3	4068	4	US-09-386-123-5	Sequence 5, Appli	1112	42.2	4.3	825	4	US-09-252-991A-7593	Sequence 7593, Ap
1040	42.6	4.3	4077	2	US-08-231-193A-51	Sequence 51, Appl	1113	42.2	4.3	861	4	US-09-252-991A-7540	Sequence 7540, Ap
1041	42.6	4.3	4077	2	US-08-486-273A-51	Sequence 51, Appl	1114	42.2	4.3	864	4	US-09-252-991A-5099	Sequence 5099, Ap
1042	42.6	4.3	4077	3	US-08-480-474-51	Sequence 51, Appl	1115	42.2	4.3	884	4	US-09-252-991A-15661	Sequence 15661, A
1043	42.6	4.3	4077	3	US-08-940-086A-51	Sequence 51, Appl	1116	42.2	4.3	882	4	US-09-252-991A-9535	Sequence 9535, Ap
1044	42.6	4.3	4077	3	US-08-940-035A-51	Sequence 51, Appl	1117	42.2	4.3	984	4	US-09-252-991A-5126	Sequence 5126, Ap
1045	42.6	4.3	4077	3	US-08-935-105A-51	Sequence 51, Appl	1118	42.2	4.3	996	4	US-09-252-991A-7732	Sequence 7732, Ap
1046	42.6	4.3	4077	4	US-09-648-797-51	Sequence 51, Appl	1119	42.2	4.3	996	4	US-09-252-991A-10775	Sequence 10775, A
1047	42.6	4.3	4077	4	US-09-386-123-51	Sequence 51, Appl	1120	42.2	4.3	1041	4	US-09-489-039A-6251	Sequence 6251, Ap
1048	42.6	4.3	4092	2	US-08-231-193A-45	Sequence 45, Appl	1121	42.2	4.3	1107	4	US-09-252-991A-14146	Sequence 14146, A
1049	42.6	4.3	4092	3	US-08-486-273A-45	Sequence 45, Appl	1122	42.2	4.3	1149	4	US-09-252-991A-5033	Sequence 5033, Ap
1050	42.6	4.3	4092	3	US-08-480-474-45	Sequence 45, Appl	1123	42.2	4.3	1176	4	US-09-252-991A-11843	Sequence 11843, A
1051	42.6	4.3	4092	3	US-08-940-086A-45	Sequence 45, Appl	1124	42.2	4.3	1194	4	US-09-252-991A-7454	Sequence 7454, Ap
1052	42.6	4.3	4092	3	US-08-940-035A-45	Sequence 45, Appl	1125	42.2	4.3	1236	4	US-09-252-991A-1087	Sequence 1087, Ap
1053	42.6	4.3	4092	3	US-08-935-105A-45	Sequence 45, Appl	1126	42.2	4.3	1245	4	US-09-252-991A-12071	Sequence 12071, A
1054	42.6	4.3	4092	4	US-09-648-797-45	Sequence 45, Appl	1127	42.2	4.3	1248	4	US-09-252-991A-8391	Sequence 8391, Ap
1055	42.6	4.3	4092	4	US-09-386-123-45	Sequence 45, Appl	1128	42.2	4.3	1266	4	US-09-252-991A-8926	Sequence 8926, Ap

c1130	42.2	4.3	1269	4	US-09-252-991A-14054	Sequence 14054, A	1202	42	4.2	1683	4	US-09-724-797-21	Sequence 21, Appl
c1131	42.2	4.3	1272	4	US-09-252-991A-10690	Sequence 10690, A	1203	42	4.2	1695	4	US-09-252-991A-6801	Sequence 6801, Ap
c1132	42.2	4.3	1281	3	US-09-105-537-19	Sequence 10590, A	1204	42	4.2	1930	3	US-08-987-367-1	Sequence 1, Appl
c1133	42.2	4.3	1323	4	US-09-252-991A-14169	Sequence 14169, A	c1205	42	4.2	2028	4	US-09-252-991A-11416	Sequence 11416, A
c1134	42.2	4.3	1422	4	US-09-252-991A-10550	Sequence 10550, A	1206	42	4.2	2689	3	US-09-105-537-34	Sequence 34, Appl
c1135	42.2	4.3	1428	4	US-09-252-991A-15727	Sequence 15727, A	1207	42	4.2	5331	4	US-09-453-956-1	Sequence 1, Appl
c1136	42.2	4.3	1485	4	US-09-252-991A-7612	Sequence 7612, Ap	c1208	42	4.2	5331	4	US-09-698-235-2	Sequence 2, Appl
c1137	42.2	4.3	1503	4	US-09-252-991A-8482	Sequence 8482, Ap	1209	41.8	4.2	534	4	US-09-252-991A-12543	Sequence 12543, A
c1138	42.2	4.3	1521	4	US-09-252-991A-13990	Sequence 13990, A	c1210	41.8	4.2	564	4	US-09-252-991A-12263	Sequence 12263, A
c1139	42.2	4.3	1554	4	US-09-252-991A-15262	Sequence 15262, A	c1211	41.8	4.2	573	4	US-09-252-991A-5674	Sequence 5674, Ap
c1140	42.2	4.3	1611	4	US-09-252-991A-6694	Sequence 6694, Ap	c1212	41.8	4.2	714	4	US-09-252-991A-11042	Sequence 11042, A
c1141	42.2	4.3	1645	4	US-09-620-312D-807	Sequence 807, Appl	1213	41.8	4.2	732	4	US-09-252-991A-12697	Sequence 12697, A
c1142	42.2	4.3	1671	4	US-09-252-991A-7673	Sequence 7673, Ap	c1214	41.8	4.2	759	4	US-09-252-991A-14329	Sequence 14329, A
c1143	42.2	4.3	1686	4	US-09-252-991A-9577	Sequence 9577, Ap	c1215	41.8	4.2	822	4	US-09-252-991A-4946	Sequence 4946, Ap
c1144	42.2	4.3	1716	4	US-09-252-991A-9577	Sequence 9577, Ap	1216	41.8	4.2	825	4	US-09-252-991A-3004	Sequence 3004, Ap
c1145	42.2	4.3	1734	4	US-09-252-991A-15356	Sequence 15356, A	c1217	41.8	4.2	867	4	US-09-252-991A-16236	Sequence 16236, A
c1146	42.2	4.3	1782	4	US-09-252-991A-14102	Sequence 14102, A	c1218	41.8	4.2	882	4	US-09-252-991A-5644	Sequence 5644, Ap
c1147	42.2	4.3	1788	4	US-09-252-991A-4632	Sequence 4632, Ap	1219	41.8	4.2	888	4	US-09-252-991A-16530	Sequence 16530, A
c1148	42.2	4.3	1791	1	US-08-399-646-3	Sequence 3, Appl	c1220	41.8	4.2	942	4	US-09-252-991A-10909	Sequence 10909, A
c1149	42.2	4.3	1791	1	US-08-607-321-3	Sequence 3, Appl	c1221	41.8	4.2	966	4	US-09-252-991A-8354	Sequence 8354, Ap
c1150	42.2	4.3	1791	2	US-08-961-240-3	Sequence 3, Appl	1222	41.8	4.2	1020	4	US-09-252-991A-5550	Sequence 5550, Ap
c1151	42.2	4.3	1839	4	US-09-252-991A-9156	Sequence 9156, Ap	1223	41.8	4.2	1092	4	US-09-252-991A-8481	Sequence 8481, Ap
c1152	42.2	4.3	1848	4	US-09-252-991A-9071	Sequence 9071, Ap	c1224	41.8	4.2	1125	4	US-09-252-991A-16066	Sequence 16066, A
c1153	42.2	4.3	1851	4	US-09-252-991A-9067	Sequence 9067, Ap	1225	41.8	4.2	1200	4	US-09-252-991A-8527	Sequence 8527, Ap
c1154	42.2	4.3	1947	4	US-09-252-991A-1048	Sequence 1048, Ap	1226	41.8	4.2	1248	4	US-09-252-991A-10656	Sequence 10656, A
c1155	42.2	4.3	1980	4	US-09-252-991A-8712	Sequence 8712, Ap	c1227	41.8	4.2	1257	4	US-09-489-039A-5712	Sequence 5712, Ap
c1156	42.2	4.3	2056	1	US-08-399-646-13	Sequence 13, Appl	1228	41.8	4.2	1260	4	US-09-252-991A-13265	Sequence 13265, A
c1157	42.2	4.3	2056	1	US-08-607-321-13	Sequence 13, Appl	1229	41.8	4.2	1263	4	US-09-252-991A-2546	Sequence 2546, Ap
c1158	42.2	4.3	2056	2	US-08-961-240-13	Sequence 13, Appl	c1231	41.8	4.2	1278	4	US-09-252-991A-11277	Sequence 11277, A
c1159	42.2	4.3	2056	2	US-08-605-501-13	Sequence 13, Appl	1232	41.8	4.2	1296	4	US-09-252-991A-12123	Sequence 12123, A
c1160	42.2	4.3	2103	4	US-09-252-991A-11773	Sequence 11773, A	1233	41.8	4.2	1326	4	US-09-252-991A-12394	Sequence 12394, A
c1161	42.2	4.3	2103	4	US-09-252-991A-13604	Sequence 13604, A	1234	41.8	4.2	1608	4	US-09-252-991A-9091	Sequence 9091, Ap
c1162	42.2	4.3	2126	4	US-08-789-354-1	Sequence 1, Appl	c1235	41.8	4.2	1626	4	US-09-252-991A-4561	Sequence 4561, Ap
c1163	42.2	4.3	2126	3	US-09-110-937-1	Sequence 1, Appl	1236	41.8	4.2	1665	4	US-09-252-991A-4934	Sequence 4934, Ap
c1164	42.2	4.3	2126	3	US-09-058-725B-1	Sequence 1, Appl	1237	41.8	4.2	1710	2	US-09-252-991A-9011	Sequence 9011, Ap
c1165	42.2	4.3	2126	3	US-09-232-857-1	Sequence 1, Appl	1238	41.8	4.2	1780	2	US-08-933-821-5	Sequence 5, Appl
c1166	42.2	4.3	2250	4	US-09-252-991A-4181	Sequence 4181, Ap	1239	41.8	4.2	1780	3	US-08-960-507-5	Sequence 5, Appl
c1167	42.2	4.3	2259	4	US-09-252-991A-13396	Sequence 13396, A	1240	41.8	4.2	1780	3	US-09-136-828-5	Sequence 5, Appl
c1168	42.2	4.3	2313	4	US-09-252-991A-11939	Sequence 11939, A	1241	41.8	4.2	1780	3	US-09-332-928A-5	Sequence 5, Appl
c1169	42.2	4.3	2361	4	US-09-252-991A-15781	Sequence 15781, A	1242	41.8	4.2	1780	4	US-09-136-801-5	Sequence 5, Appl
c1170	42.2	4.3	2577	4	US-09-252-991A-6607	Sequence 6607, Ap	1243	41.8	4.2	1780	4	US-09-333-929-5	Sequence 5, Appl
c1171	42.2	4.3	2640	4	US-09-252-991A-15419	Sequence 15419, A	1244	41.8	4.2	1780	4	US-09-333-077-5	Sequence 5, Appl
c1172	42.2	4.3	2679	4	US-09-252-991A-15623	Sequence 15623, A	1245	41.8	4.2	1780	4	US-09-202-088A-5	Sequence 5, Appl
c1173	42.2	4.3	2952	4	US-09-252-991A-5096	Sequence 5096, Ap	1246	41.8	4.2	1806	4	US-09-333-077-5	Sequence 5, Appl
c1174	42.2	4.3	3222	4	US-09-252-991A-13746	Sequence 13746, Ap	c1247	41.8	4.2	1920	4	US-09-252-991A-11213	Sequence 11213, Ap
c1175	42.2	4.3	4095	4	US-09-252-991A-10309	Sequence 10309, A	c1248	41.8	4.2	1944	4	US-09-252-991A-16245	Sequence 16245, A
c1176	42.2	4.3	4143	4	US-09-252-991A-9151	Sequence 9151, Ap	c1249	41.8	4.2	1956	4	US-09-724-797-57	Sequence 57, Appl
c1177	42.2	4.3	4212	4	US-09-252-991A-8929	Sequence 8929, Ap	1250	41.8	4.2	2031	4	US-09-252-991A-9572	Sequence 9572, Ap
c1178	42.2	4.3	4767	4	US-09-410-551B-28	Sequence 28, Appl	c1251	41.8	4.2	2064	1	US-08-343-428-1	Sequence 1, Appl
c1179	42.2	4.3	4767	4	US-09-940-316B-28	Sequence 28, Appl	1252	41.8	4.2	2079	4	US-09-252-991A-5584	Sequence 5584, Ap
c1180	42.2	4.3	4818	4	US-09-410-551B-32	Sequence 32, Appl	1253	41.8	4.2	2349	4	US-09-252-991A-4983	Sequence 4983, Ap
c1181	42.2	4.3	4818	4	US-09-940-316B-32	Sequence 32, Appl	1254	41.8	4.2	2367	4	US-09-252-991A-726	Sequence 726, App
c1182	42.2	4.3	13613	3	US-09-105-537-3	Sequence 3, Appl	c1255	41.8	4.2	2379	4	US-09-252-991A-686	Sequence 686, App
c1183	42.2	4.3	35300	4	US-09-266-965-76	Sequence 76, Appl	1256	41.8	4.2	2475	3	US-09-624-693A-20	Sequence 20, Appl
c1184	42.2	4.3	369	3	US-09-422-487-5	Sequence 5, Appl	1257	41.8	4.2	2499	4	US-09-252-991A-696	Sequence 696, App
c1185	42.2	4.3	369	3	US-09-378-088A-127	Sequence 127, App	c1258	41.8	4.2	2592	4	US-09-252-991A-9528	Sequence 9528, Ap
c1186	42.2	4.3	369	4	US-09-643-596B-127	Sequence 127, App	c1259	41.8	4.2	2808	4	US-09-252-991A-16466	Sequence 16466, A
c1187	42.2	4.3	432	4	US-09-252-991A-11821	Sequence 11821, A	c1260	41.8	4.2	3006	4	US-09-252-991A-9720	Sequence 9720, Ap
c1188	42.2	4.3	750	4	US-09-724-797-91	Sequence 91, Appl	1261	41.8	4.2	3387	4	US-09-194-640A-2	Sequence 2, Appl
c1189	42.2	4.3	816	4	US-09-252-991A-2684	Sequence 2684, Ap	1262	41.8	4.2	3678	4	US-09-252-991A-8447	Sequence 8447, Ap
c1190	42.2	4.3	918	4	US-09-252-991A-6846	Sequence 6846, Ap	1263	41.8	4.2	3868	3	US-09-357-070-1	Sequence 1, Appl
c1191	42.2	4.3	927	4	US-09-252-991A-15420	Sequence 15420, A	1264	41.8	4.2	4078	4	US-09-016-434-1152	Sequence 1152, Ap
c1192	42.2	4.3	1107	4	US-09-252-991A-2872	Sequence 2872, Ap	1265	41.8	4.2	4553	2	US-09-023-655-975	Sequence 975, App
c1193	42.2	4.3	1254	4	US-09-252-991A-11478	Sequence 11478, A	1266	41.8	4.2	4695	2	US-09-023-655-975	Sequence 975, App
c1194	42.2	4.3	1335	4	US-09-252-991A-2994	Sequence 2994, Ap	1267	41.8	4.2	4695	2	US-08-231-193A-57	Sequence 57, Appl
c1195	42.2	4.3	1386	4	US-09-252-991A-11563	Sequence 11563, A	1268	41.8	4.2	4695	3	US-08-486-273A-57	Sequence 57, Appl
c1196	42.2	4.3	1416	4	US-09-252-991A-11499	Sequence 11499, A	1269	41.8	4.2	4695	3	US-08-940-035A-57	Sequence 57, Appl
c1197	42.2	4.3	1431	4	US-09-252-991A-11886	Sequence 11886, A	1270	41.8	4.2	4695	3	US-08-935-105A-57	Sequence 57, Appl
c1198	42.2	4.3	1461	4	US-09-252-991A-15308	Sequence 15308, A	1271	41.8	4.2	4695	4	US-09-648-797-57	Sequence 57, Appl
c1199	42.2	4.3	1524	4	US-09-252-991A-11455	Sequence 11455, A	1272	41.8	4.2	4695	4	US-09-386-123-57	Sequence 57, Appl
c1200	42.2	4.3	1626	4	US-09-252-991A-3266	Sequence 3266, Ap	1273	41.8	4.2	5045	3	US-09-390-721-1	Sequence 1, Appl
c1201	42.2	4.3	1626	4	US-09-252-991A-3266	Sequence 3266, Ap	1274	41.8	4.2	5045	3	US-09-390-721-1	Sequence 1, Appl

1275	41.8	4.2	5045	4	US-09-713-893-1	Sequence 1, Appl	1348	41.6	4.2	4478	4	US-09-940-316B-16	Sequence 16, Appl
1276	41.8	4.2	5045	4	US-09-713-893-3	Sequence 3, Appl	1349	41.6	4.2	4547	4	US-09-410-551B-22	Sequence 22, Appl
1277	41.8	4.2	5220	2	US-08-777-405A-1	Sequence 1, Appl	1350	41.6	4.2	4547	4	US-09-940-316B-22	Sequence 22, Appl
1278	41.8	4.2	5220	2	US-08-777-871A-1	Sequence 1, Appl	1351	41.6	4.2	4571	4	US-09-410-551B-18	Sequence 18, Appl
1279	41.8	4.2	5220	2	US-09-225-951-1	Sequence 1, Appl	1352	41.6	4.2	4571	4	US-09-940-316B-18	Sequence 18, Appl
1280	41.8	4.2	5220	2	US-09-841-341-1	Sequence 1, Appl	1353	41.6	4.2	4571	4	US-09-940-316B-18	Sequence 18, Appl
1281	41.8	4.2	5220	4	US-10-027-591-1	Sequence 1, Appl	1354	41.4	4.2	8051	2	US-08-576-626A-2	Sequence 2, Appl
1282	41.8	4.2	15872	3	US-09-105-537-1	Sequence 1, Appl	1355	41.4	4.2	459	4	US-09-252-991A-14069	Sequence 14069, A
1283	41.8	4.2	15872	4	US-09-091-609-1	Sequence 1, Appl	1356	41.4	4.2	540	4	US-09-252-991A-9624	Sequence 9624, A
1284	41.8	4.2	15872	4	US-09-091-609-3	Sequence 3, Appl	1357	41.4	4.2	743	3	US-09-095-855-198	Sequence 198, App
1285	41.8	4.2	28958	1	US-08-258-261B-6	Sequence 6, Appl	1358	41.4	4.2	750	4	US-09-205-426-198	Sequence 198, App
1286	41.8	4.2	28958	1	US-08-456-837-6	Sequence 6, Appl	1359	41.4	4.2	768	4	US-09-252-991A-13985	Sequence 13985, A
1287	41.8	4.2	28958	1	US-08-457-342-6	Sequence 6, Appl	1360	41.4	4.2	782	4	US-09-489-039A-3197	Sequence 3197, Ap
1288	41.8	4.2	28958	1	US-08-457-646A-6	Sequence 6, Appl	1361	41.4	4.2	822	4	US-09-252-991A-7005	Sequence 7005, Ap
1289	41.8	4.2	28958	1	US-08-458-076A-6	Sequence 6, Appl	1362	41.4	4.2	822	4	US-09-252-991A-11668	Sequence 11668, A
1290	41.8	4.2	28958	1	US-08-764-233A-4	Sequence 4, Appl	1363	41.4	4.2	858	4	US-09-252-991A-14072	Sequence 14072, A
1291	41.8	4.2	28958	1	US-08-457-335A-6	Sequence 6, Appl	1364	41.4	4.2	918	4	US-09-252-991A-9633	Sequence 9633, Ap
1292	41.8	4.2	28958	1	US-08-729-214-6	Sequence 6, Appl	1365	41.4	4.2	927	4	US-09-252-991A-1526	Sequence 1526, Ap
1293	41.8	4.2	28958	3	US-09-028-934-6	Sequence 6, Appl	1366	41.4	4.2	1029	4	US-09-252-991A-1533	Sequence 153, App
1294	41.8	4.2	43280	2	US-08-804-227C-1	Sequence 1, Appl	1367	41.4	4.2	1077	4	US-09-252-991A-13983	Sequence 13983, Ap
1295	41.8	4.2	49377	1	US-08-764-233A-1	Sequence 1, Appl	1368	41.4	4.2	1089	4	US-09-252-991A-1313	Sequence 1313, Ap
1296	41.6	4.2	486	4	US-09-252-991A-13452	Sequence 13452, A	1369	41.4	4.2	1098	4	US-09-252-991A-14024	Sequence 14024, A
1297	41.6	4.2	618	4	US-09-252-991A-9054	Sequence 9054, A	1370	41.4	4.2	1108	4	US-09-252-991A-1733	Sequence 173, App
1298	41.6	4.2	804	4	US-09-724-797-75	Sequence 75, Appl	1371	41.4	4.2	1128	4	US-09-252-991A-14237	Sequence 14237, A
1299	41.6	4.2	891	4	US-09-252-991A-3092	Sequence 3092, Ap	1372	41.4	4.2	1134	4	US-09-252-991A-1648	Sequence 1648, Ap
1300	41.6	4.2	945	4	US-09-252-991A-2878	Sequence 2878, Ap	1373	41.4	4.2	1251	4	US-09-252-991A-163	Sequence 163, App
1301	41.6	4.2	978	4	US-09-252-991A-80	Sequence 30, Appl	1374	41.4	4.2	1257	4	US-09-252-991A-4253	Sequence 4253, Ap
1302	41.6	4.2	1035	1	US-08-012-735-30	Sequence 30, Appl	1375	41.4	4.2	1275	4	US-09-489-039A-2457	Sequence 2457, Ap
1303	41.6	4.2	1035	1	US-09-252-991A-13551	Sequence 8724, Ap	1376	41.4	4.2	1281	4	US-09-252-991A-3454	Sequence 3454, Ap
1304	41.6	4.2	1200	4	US-09-252-991A-13551	Sequence 13551, A	1377	41.4	4.2	1488	4	US-09-252-991A-7333	Sequence 7333, Ap
1305	41.6	4.2	1209	4	US-09-724-797-35	Sequence 35, Appl	1378	41.4	4.2	1506	3	US-09-158-767-7	Sequence 7, Appl
1306	41.6	4.2	1209	4	US-09-252-991A-16257	Sequence 16257, A	1379	41.4	4.2	1506	3	US-09-158-767-9	Sequence 9, Appl
1307	41.6	4.2	1227	4	US-09-252-991A-13890	Sequence 13890, A	1380	41.4	4.2	1506	4	US-09-713-794-7	Sequence 7, Appl
1308	41.6	4.2	1230	4	US-09-252-991A-13787	Sequence 13787, A	1381	41.4	4.2	1506	4	US-09-713-794-8	Sequence 8, Appl
1309	41.6	4.2	1239	4	US-09-252-991A-14352	Sequence 14352, A	1382	41.4	4.2	1506	4	US-09-713-794-9	Sequence 9, Appl
1310	41.6	4.2	1251	4	US-09-252-991A-6826	Sequence 6826, Ap	1383	41.4	4.2	1512	4	US-09-252-991A-183	Sequence 183, App
1311	41.6	4.2	1284	4	US-08-440-856A-9	Sequence 9, Appl	1384	41.4	4.2	1512	4	US-09-594-193-1	Sequence 1, Appl
1312	41.6	4.2	1288	1	US-09-252-991A-6918	Sequence 6918, Ap	1385	41.4	4.2	1520	4	PCT-US92-05332-1	Sequence 1, Appl
1313	41.6	4.2	1305	4	US-09-252-991A-8343	Sequence 8343, Ap	1386	41.4	4.2	1545	4	US-09-252-991A-13771	Sequence 13771, A
1314	41.6	4.2	1308	4	US-08-832-399-1	Sequence 1, Appl	1387	41.4	4.2	1554	4	US-09-620-312D-802	Sequence 802, App
1315	41.6	4.2	1342	3	US-09-372-498-1	Sequence 1, Appl	1388	41.4	4.2	1554	4	US-09-252-991A-1695	Sequence 1695, Ap
1316	41.6	4.2	1342	3	US-09-252-991A-4180	Sequence 4180, Ap	1389	41.4	4.2	1566	4	US-09-252-991A-7412	Sequence 7412, Ap
1317	41.6	4.2	1409	4	US-09-252-991A-8377	Sequence 8377, Ap	1390	41.4	4.2	1593	4	US-09-252-991A-14150	Sequence 14150, A
1318	41.6	4.2	1479	4	US-09-252-991A-166	Sequence 166, App	1391	41.4	4.2	1611	4	US-09-252-991A-183	Sequence 183, App
1319	41.6	4.2	1560	4	US-08-858-876A-1	Sequence 1, Appl	1392	41.4	4.2	1611	4	US-09-594-193-1	Sequence 1, Appl
1320	41.6	4.2	1575	3	US-09-472-880-1	Sequence 1, Appl	1393	41.4	4.2	1739	4	PCT-US92-05332-1	Sequence 1, Appl
1321	41.6	4.2	1575	3	US-09-252-991A-10519	Sequence 10519, A	1394	41.4	4.2	1910	5	US-09-252-991A-9831	Sequence 9831, Ap
1322	41.6	4.2	1776	4	US-09-252-991A-16369	Sequence 16369, A	1395	41.4	4.2	2136	4	US-09-252-991A-13657	Sequence 13657, A
1323	41.6	4.2	1860	4	US-09-593-711A-3	Sequence 3, Appl	1396	41.4	4.2	2175	4	US-09-252-991A-14150	Sequence 14150, A
1324	41.6	4.2	1910	3	US-07-601-094-1	Sequence 1, Appl	1397	41.4	4.2	2244	5	US-08-476-519-10	Sequence 10, Appl
1325	41.6	4.2	1914	1	US-08-012-735-1	Sequence 1, Appl	1398	41.4	4.2	2244	5	US-08-272-882D-1	Sequence 1, Appl
1326	41.6	4.2	1914	1	US-09-252-991A-9222	Sequence 9222, Ap	1399	41.4	4.2	2261	3	US-09-158-767-1	Sequence 1, Appl
1327	41.6	4.2	2079	4	US-09-252-991A-8731	Sequence 8731, Ap	1400	41.4	4.2	2261	3	US-09-252-991A-13575	Sequence 1, Appl
1328	41.6	4.2	2304	4	US-09-252-991A-886	Sequence 886, App	1401	41.4	4.2	2292	4	US-08-476-519-1	Sequence 1, Appl
1329	41.6	4.2	2472	4	US-09-252-991A-2990	Sequence 2990, Ap	1402	41.4	4.2	2334	1	US-08-476-519-1	Sequence 1, Appl
1330	41.6	4.2	2523	4	US-09-252-991A-175	Sequence 175, App	1403	41.4	4.2	2334	5	PCT-US95-09323-10	Sequence 10, Appl
1331	41.6	4.2	2610	4	US-09-010-928B-3	Sequence 3, Appl	1404	41.4	4.2	2334	5	US-08-272-882D-1	Sequence 1, Appl
1332	41.6	4.2	2824	2	US-09-196-390-5	Sequence 5, Appl	1405	41.4	4.2	2335	4	US-09-492-361-1	Sequence 1, Appl
1333	41.6	4.2	2825	3	US-09-952-677-5	Sequence 5, Appl	1406	41.4	4.2	2721	6	US-09-252-991A-9923	Sequence 9923, Ap
1334	41.6	4.2	2825	3	US-08-714-677-10	Sequence 10, Appl	1407	41.4	4.2	3024	4	US-09-252-991A-9533	Sequence 9533, Ap
1335	41.6	4.2	2936	2	US-08-393-540-10	Sequence 10, Appl	1408	41.4	4.2	3654	3	US-08-750-357-1	Sequence 1, Appl
1336	41.6	4.2	2936	2	US-08-714-537-10	Sequence 10, Appl	1409	41.4	4.2	4059	3	US-08-750-357-1	Sequence 57, Appl
1337	41.6	4.2	2936	2	US-09-252-991A-797	Sequence 797, App	1410	41.4	4.2	4695	2	US-08-231-133A-57	Sequence 57, Appl
1338	41.6	4.2	2955	4	US-09-252-991A-864	Sequence 864, App	1411	41.4	4.2	4695	2	US-08-486-273A-57	Sequence 57, Appl
1339	41.6	4.2	2970	4	US-09-252-991A-10834	Sequence 10834, A	1412	41.4	4.2	4695	3	US-08-940-086A-57	Sequence 57, Appl
1340	41.6	4.2	3066	4	US-09-252-991A-10899	Sequence 10899, A	1413	41.4	4.2	4695	3	US-08-940-035A-57	Sequence 57, Appl
1341	41.6	4.2	3624	4	US-09-105-537-36	Sequence 36, Appl	1414	41.4	4.2	4695	3	US-08-935-105A-57	Sequence 57, Appl
1342	41.6	4.2	4041	3	US-09-566-047-3	Sequence 3, Appl	1415	41.4	4.2	4695	4	US-09-648-797-57	Sequence 57, Appl
1343	41.6	4.2	4315	3	US-09-566-047-3	Sequence 3, Appl	1416	41.4	4.2	4695	4	US-09-386-123-57	Sequence 57, Appl
1344	41.6	4.2	4315	3	US-09-566-047-3	Sequence 3, Appl	1417	41.4	4.2	4824	2	US-08-485-139-5	Sequence 5, Appl
1345	41.6	4.2	4466	4	US-09-410-551B-20	Sequence 20, Appl	1418	41.4	4.2	4824	2	US-08-750-357-5	Sequence 5, Appl
1346	41.6	4.2	4466	4	US-09-940-316B-20	Sequence 20, Appl	1419	41.4	4.2	6085	3	US-09-029-603-4	Sequence 4, Appl
1347	41.6	4.2	4478	4	US-09-410-551B-16	Sequence 16, Appl	1420	41.4	4.2	75395	4	US-09-984-890-3	Sequence 3, Appl

c1421	41.4	4.2	75395	4	US-10-274-194-3	Sequence 3, Appli	1494	41.2	4.2	2539	3	US-09-514-340-3	Sequence 3, Appli
1422	41.2	4.2	425	1	US-08-519-777-28	Sequence 28, Appl	1495	41.2	4.2	2588	2	US-08-796-414B-6	Sequence 6, Appli
1423	41.2	4.2	425	1	US-08-742-035-28	Sequence 28, Appl	c1496	41.2	4.2	2610	4	US-09-252-991A-5719	Sequence 5719, Ap
1424	41.2	4.2	425	1	US-08-777-019-28	Sequence 28, Appl	1497	41.2	4.2	2712	4	US-09-252-991A-12204	Sequence 12204, A
1425	41.2	4.2	425	2	US-08-777-143-28	Sequence 28, Appl	1498	41.2	4.2	2772	4	US-09-799-451-887	Sequence 887, Appl
1426	41.2	4.2	425	3	US-08-775-414-28	Sequence 28, Appl	1499	41.2	4.2	2809	3	US-09-000-016-1	Sequence 1, Appli
1427	41.2	4.2	425	3	US-08-931-858B-28	Sequence 28, Appl	1500	41.2	4.2	2809	3	US-09-514-340-1	Sequence 1, Appli
1428	41.2	4.2	425	3	US-08-981-733-28	Sequence 28, Appl							
1429	41.2	4.2	425	4	US-09-128-026-28	Sequence 28, Appl							
1430	41.2	4.2	425	4	US-09-220-616-28	Sequence 28, Appl							
1431	41.2	4.2	425	4	US-09-220-527-28	Sequence 28, Appl							
1432	41.2	4.2	425	4	US-09-220-407-28	Sequence 28, Appl							
1433	41.2	4.2	425	4	US-09-219-952-28	Sequence 28, Appl							
1434	41.2	4.2	432	3	US-08-775-414-87	Sequence 87, Appl							
1435	41.2	4.2	432	4	US-09-219-952-87	Sequence 87, Appl							
c1436	41.2	4.2	450	4	US-09-252-991A-12285	Sequence 12285, A							
1437	41.2	4.2	456	3	US-08-775-414-89	Sequence 89, Appl							
1438	41.2	4.2	456	4	US-09-219-952-89	Sequence 89, Appl							
c1439	41.2	4.2	576	4	US-09-252-991A-7380	Sequence 7380, Ap							
1440	41.2	4.2	591	1	US-08-519-777-11	Sequence 11, Appl							
1441	41.2	4.2	591	1	US-08-742-035-11	Sequence 11, Appl							
1442	41.2	4.2	591	1	US-08-777-019-11	Sequence 11, Appl							
1443	41.2	4.2	591	2	US-08-777-143-11	Sequence 11, Appl							
1444	41.2	4.2	591	3	US-08-775-414-11	Sequence 11, Appl							
1445	41.2	4.2	591	3	US-08-931-858B-11	Sequence 11, Appl							
1446	41.2	4.2	591	3	US-08-981-739-11	Sequence 11, Appl							
1447	41.2	4.2	591	4	US-09-128-026-11	Sequence 11, Appl							
1448	41.2	4.2	591	4	US-09-220-616-11	Sequence 11, Appl							
1449	41.2	4.2	591	4	US-09-220-527-11	Sequence 11, Appl							
1450	41.2	4.2	591	4	US-09-220-407-11	Sequence 11, Appl							
1451	41.2	4.2	591	4	US-09-219-952-11	Sequence 11, Appl							
c1452	41.2	4.2	621	4	US-09-252-991A-7514	Sequence 7514, Ap							
1453	41.2	4.2	630	4	US-09-252-991A-12004	Sequence 12004, A							
c1454	41.2	4.2	693	4	US-09-252-991A-7308	Sequence 7308, Ap							
1455	41.2	4.2	705	4	US-09-252-991A-15939	Sequence 15939, A							
1456	41.2	4.2	722	4	US-09-270-767-2450	Sequence 2450, Ap							
1457	41.2	4.2	722	4	US-09-270-767-17732	Sequence 17732, A							
1458	41.2	4.2	756	4	US-09-252-991A-7245	Sequence 7245, Ap							
1459	41.2	4.2	777	4	US-09-252-991A-9681	Sequence 9681, Ap							
1460	41.2	4.2	816	4	US-09-252-991A-12133	Sequence 12133, A							
1461	41.2	4.2	894	4	US-09-252-991A-12271	Sequence 12271, A							
c1462	41.2	4.2	915	4	US-09-252-991A-7455	Sequence 7455, Ap							
1463	41.2	4.2	927	4	US-09-252-991A-9722	Sequence 9722, Ap							
c1464	41.2	4.2	942	1	US-07-985-690A-2	Sequence 2, Appli							
c1465	41.2	4.2	984	4	US-09-252-991A-14377	Sequence 14377, App							
1466	41.2	4.2	984	4	US-09-252-991A-14759	Sequence 14759, A							
1467	41.2	4.2	1092	4	US-09-252-991A-14406	Sequence 14406, A							
1468	41.2	4.2	1194	4	US-09-252-991A-7586	Sequence 7586, Ap							
c1469	41.2	4.2	1312	1	US-08-205-506A-1	Sequence 1, Appli							
1470	41.2	4.2	1312	5	PCT-US94-02389-1	Sequence 1, Appli							
1471	41.2	4.2	1401	2	US-08-812-412-1	Sequence 1, Appli							
1472	41.2	4.2	1401	3	US-09-180-271-4	Sequence 4, Appli							
1473	41.2	4.2	1601	4	US-09-252-991A-14296	Sequence 14296, A							
c1474	41.2	4.2	1626	4	US-09-252-991A-11125	Sequence 11125, A							
1475	41.2	4.2	1647	4	US-09-252-991A-12389	Sequence 12389, A							
c1476	41.2	4.2	1662	4	US-09-679-686B-11	Sequence 11, Appl							
1477	41.2	4.2	1776	4	US-09-252-991A-3891	Sequence 3891, Ap							
1478	41.2	4.2	1800	4	US-09-252-991A-4025	Sequence 4025, Ap							
c1479	41.2	4.2	1824	4	US-09-252-991A-9566	Sequence 9566, Ap							
c1480	41.2	4.2	1824	4	US-09-252-991A-3919	Sequence 3919, Ap							
1481	41.2	4.2	1875	4	US-09-434-288-5	Sequence 5, Appli							
c1482	41.2	4.2	1881	3	US-09-252-991A-12032	Sequence 12032, A							
1483	41.2	4.2	1956	4	US-08-919-421A-1	Sequence 1, Appli							
1484	41.2	4.2	1962	3	US-09-342-819-1	Sequence 1, Appli							
1485	41.2	4.2	1962	4	US-09-526-833-1	Sequence 1, Appli							
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SUMMARIES

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36	989	100.0	989	15	US-10-211-884-21	Sequence 21, Appl
39	989	100.0	989	15	US-10-013-909A-305	Sequence 305, Appl
62	989	100.0	989	15	US-10-211-858-21	Sequence 21, Appl
68	989	100.0	989	16	US-10-307-817-121	Sequence 121, Appl
69	989	100.0	989	16	US-10-307-817-125	Sequence 125, Appl
71	985.8	99.7	1037	9	US-09-844-468-1	Sequence 1, Appl
72	938.2	94.9	967	15	US-10-106-698-521	Sequence 521, Appl
73	789	79.8	789	9	US-09-844-468-3	Sequence 3, Appl
74	583.6	59.0	787	16	US-10-307-817-123	Sequence 123, Appl
75	548.6	55.5	620	16	US-10-240-425-182	Sequence 182, Appl
76	422	42.7	474	10	US-09-918-995-22407	Sequence 22407, A
77	413	41.8	458	10	US-09-918-995-23102	Sequence 23102, A

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	82	182.4	18.4	85692	16	US-10-461-194-1	Sequence 1, Appl
	83	179.2	18.1	86941	16	US-10-461-194-2	Sequence 2, Appl
	84	171	17.3	693	18	US-10-425-115-49671	Sequence 49671, A
	85	161.8	16.4	953	9	US-09-452-239-45	Sequence 45, Appl
	86	159.2	16.1	1049	9	US-09-452-239-43	Sequence 43, Appl
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	96	152.4	15.4	991	18	US-10-425-115-53827	Sequence 53827, A
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	104	149.6	15.1	1377	18	US-10-425-115-138007	Sequence 138007
	105	149.2	15.1	1003	15	US-10-361-460-33	Sequence 33, Appl
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	107	148	15.0	1097	16	US-10-425-114-16291	Sequence 16291, A
	108	148	15.0	1097	16	US-10-425-114-16291	Sequence 3691, Ap
	109	148	15.0	1118	9	US-09-452-239-37	Sequence 37, Appl
	110	148	15.0	1146	9	US-09-452-239-3	Sequence 3, Appl
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	115	145.2	14.7	1114	16	US-10-425-114-3140	Sequence 3140, Ap
	116	145.2	14.7	1287	18	US-10-425-115-113175	Sequence 113175
	117	145	14.7	905	17	US-10-437-963-41715	Sequence 41715, A
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	126	139.6	14.1	1506	18	US-10-425-115-113176	Sequence 113176
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	128	135.4	13.7	1281	18	US-10-425-115-138015	Sequence 138015
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	130	134.6	13.6	1107	18	US-10-425-115-138003	Sequence 138003
	131	129.6	13.1	1146	18	US-10-425-115-53825	Sequence 53825, A
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	136	126	12.7	944	15	US-10-361-460-32	Sequence 32, Appl
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	139	125	12.6	1051	15	US-10-289-757-146	Sequence 146, Appl
	140	123.4	12.5	1059	15	US-10-289-757-36	Sequence 36, Appl
	141	122.6	12.4	1063	15	US-10-289-757-37	Sequence 37, Appl
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c	146	103.6	10.5	343	16	US-10-152-319A-298	Sequence 298, App
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153	88	8.9	931	9	US-09-452-239-17	Sequence 17, Appl	226	59.2	6.0	4667	18	US-10-723-860-5759	Sequence 5759, Ap
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159	85.6	8.7	617	17	US-10-021-323-15391	Sequence 15391, A	232	58.8	5.9	688	16	US-10-425-114-18343	Sequence 18343, A
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164	84	8.5	1072	9	US-09-770-445-132	Sequence 132, App	237	58.6	5.9	5999	17	US-10-156-761-5999	Sequence 5999, Ap
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196	64.6	6.5	553	16	US-10-264-049-1169	Sequence 1169, Ap	269	56.6	5.7	25085	15	US-10-132-134-35	Sequence 35, Appl
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214	60.6	6.1	2808	15	US-10-156-761-2021	Sequence 2021, Ap	287	56	5.7	2109	9	US-09-738-973-153	Sequence 153, App
215	60.4	6.1	1544	17	US-10-437-963-72461	Sequence 72461, A	288	56	5.7	2109	9	US-09-854-133-153	Sequence 153, App
216	60.4	6.1	2256646	17	US-10-470-585-1	Sequence 1, Appli	289	56	5.7	2109	9	US-10-144-649A-153	Sequence 1, Appli
217	60	6.1	729	9	US-09-938-842A-2400	Sequence 2400, Ap	290	56	5.7	4257	9	US-09-825-288A-1	Sequence 48, Appl
218	60	6.1	729	11	US-09-938-842A-2400	Sequence 2400, Ap	291	56	5.7	4888	15	US-10-288-798-48	Sequence 48, Appl
219	60	6.1	966	18	US-10-739-930-382	Sequence 382, App	292	56	5.7	4888	15	US-10-362-892-48	Sequence 48, Appl
220	60	6.1	982	9	US-09-452-239-31	Sequence 31, Appl	293	56	5.7	13862	16	US-09-764-891-5477	Sequence 5477, Ap
221	60	6.1	1143	16	US-10-282-122A-25877	Sequence 25877, A	294	56	5.7	13862	10	US-09-764-891-5477	Sequence 5477, Ap
222	59.8	6.0	1041	17	US-10-437-963-8597	Sequence 8597, Ap	295	56	5.7	13862	10	US-09-764-891-5477	Sequence 10204, A
223	59.6	6.0	399	15	US-10-174-693-194	Sequence 194, App	296	56	5.7	13862	10	US-09-764-891-5477	Sequence 10204, A

443	52.4	5.3	1891	15	US-10-007-926A-234	Sequence 234, App	516	51.8	5.2	4469	18	US-10-788-792-21	Sequence 21, Appl
444	52.4	5.3	1891	18	US-10-684-422-210	Sequence 210, App	517	51.8	5.2	4469	18	US-10-473-974-203	Sequence 203, App
445	52.4	5.3	1891	17	US-10-437-963-28971	Sequence 28971, A	518	51.8	5.2	4469	18	US-10-817-525-1	Sequence 1, Appl
446	52.4	5.3	3114	15	US-10-172-118-24	Sequence 24, Appl	519	51.6	5.2	786	15	US-10-156-761-4529	Sequence 4529, App
447	52.4	5.3	5117	16	US-10-342-887-24	Sequence 24, Appl	520	51.6	5.2	893	15	US-10-180-375-107	Sequence 107, App
448	52.4	5.3	5204	16	US-10-037-417-7	Sequence 7, Appl	521	51.6	5.2	893	15	US-10-183-687-123	Sequence 123, App
449	52.4	5.3	5403	16	US-10-112-944-583	Sequence 583, App	522	51.6	5.2	1177	17	US-10-103-963-12093	Sequence 12093, A
450	52.4	5.3	5640	15	US-10-037-270-41	Sequence 41, Appl	523	51.6	5.2	1242	16	US-10-437-963-125883	Sequence 25883, A
451	52.4	5.3	5640	15	US-10-117-722-41	Sequence 41, Appl	524	51.6	5.2	2055	15	US-10-369-493-35729	Sequence 35729, A
452	52.4	5.3	8296	14	US-10-037-182-35	Sequence 35, Appl	525	51.6	5.2	2211	17	US-10-437-963-63253	Sequence 63253, A
453	52.4	5.3	10991	15	US-10-312-088-9	Sequence 9, Appl	526	51.6	5.2	2283	16	US-10-109-048-1143	Sequence 1143, App
454	52.4	5.3	11118	15	US-10-312-088-8	Sequence 8, Appl	527	51.6	5.2	2865	17	US-10-156-761-4107	Sequence 4107, App
455	52.4	5.3	12338	14	US-10-205-032-15	Sequence 15, Appl	528	51.6	5.2	2973	15	US-10-156-761-1330	Sequence 1330, App
456	52.4	5.3	13350	14	US-10-037-182-1	Sequence 1, Appl	529	51.6	5.2	9369	15	US-10-200-562-190	Sequence 190, App
457	52.4	5.3	13367	16	US-10-112-944-103	Sequence 103, App	530	51.6	5.2	9369	15	US-10-237-551-190	Sequence 247, App
458	52.4	5.3	13640	16	US-10-112-944-103	Sequence 103, App	531	51.6	5.2	9369	15	US-10-237-551-247	Sequence 165006, A
459	52.4	5.3	14520	15	US-10-156-761-2885	Sequence 1, Appl	532	51.6	5.2	673	18	US-10-425-115-155006	Sequence 79440, A
460	52.4	5.3	60196	15	US-10-205-032-1	Sequence 1, Appl	533	51.4	5.2	1130	17	US-10-437-963-79440	Sequence 5404, App
461	52.4	5.3	125746	15	US-10-156-761-15102	Sequence 15102, A	534	51.4	5.2	1230	15	US-10-156-761-5404	Sequence 6586, App
462	52.2	5.3	897	17	US-10-437-963-43305	Sequence 43305, A	535	51.4	5.2	1359	15	US-10-156-761-6586	Sequence 6587, App
463	52.2	5.3	1126	17	US-10-767-701-13291	Sequence 13291, A	536	51.4	5.2	1359	15	US-10-156-761-6587	Sequence 60807, A
464	52.2	5.3	1193	16	US-10-425-114-24011	Sequence 24011, A	537	51.4	5.2	1359	15	US-10-156-761-6587	Sequence 3330, App
465	52.2	5.3	1308	18	US-10-425-115-49576	Sequence 49576, A	538	51.4	5.2	1530	17	US-10-437-963-60807	Sequence 99040, A
466	52.2	5.3	1671	17	US-10-437-963-65581	Sequence 65581, A	539	51.4	5.2	1629	15	US-10-156-761-3330	Sequence 81510, A
467	52.2	5.3	1687	18	US-10-425-115-71979	Sequence 71979, A	540	51.4	5.2	2021	17	US-10-437-963-99040	Sequence 81510, A
468	52.2	5.3	1746	15	US-10-156-761-4388	Sequence 4388, App	541	51.4	5.2	2031	17	US-10-437-963-81510	Sequence 81510, A
469	52.2	5.3	2505	15	US-10-369-493-31754	Sequence 31754, A	542	51.4	5.2	2526	18	US-10-723-860-818	Sequence 818, App
470	52.2	5.3	2757	16	US-10-282-122A-26027	Sequence 26027, A	543	51.4	5.2	2526	18	US-10-723-860-818	Sequence 5422, App
471	52.2	5.3	6297	15	US-10-133-134-37	Sequence 37, Appl	544	51.4	5.2	4725	15	US-10-205-032-17	Sequence 17, Appl
472	52	5.3	1062	17	US-10-767-701-9233	Sequence 9233, App	545	51.4	5.2	6891	17	US-10-437-963-54940	Sequence 54940, A
473	52	5.3	1065	15	US-10-156-761-6270	Sequence 6270, App	546	51.4	5.2	7847	16	US-10-302-172-591	Sequence 591, App
474	52	5.3	1159	17	US-10-437-963-54428	Sequence 54428, A	547	51.4	5.2	11817	15	US-10-156-761-2884	Sequence 2884, App
475	52	5.3	1218	15	US-10-214-446-37	Sequence 37, Appl	548	51.4	5.2	30000	12	US-09-980-217-2	Sequence 2, Appl
476	52	5.3	1230	15	US-10-156-761-6139	Sequence 6139, App	549	51.4	5.2	447	11	US-09-732-627A-4334	Sequence 4334, App
477	52	5.3	1439	18	US-10-425-115-161558	Sequence 161558, A	550	51.2	5.2	507	17	US-10-437-963-12967	Sequence 12967, A
478	52	5.3	1459	17	US-10-437-963-26984	Sequence 26984, A	551	51.2	5.2	507	17	US-10-437-963-12967	Sequence 12967, A
479	52	5.3	1491	10	US-09-899-575-99	Sequence 99, Appl	552	51.2	5.2	699	9	US-09-938-842A-1739	Sequence 1739, App
480	52	5.3	1556	16	US-10-425-114-19808	Sequence 19808, A	553	51.2	5.2	792	9	US-09-770-445-841	Sequence 841, App
481	52	5.3	1586	16	US-10-156-761-1751	Sequence 1751, App	554	51.2	5.2	699	11	US-09-938-842A-1739	Sequence 1739, App
482	52	5.3	1707	15	US-10-156-761-4723	Sequence 4723, App	555	51.2	5.2	699	9	US-09-938-842A-1739	Sequence 1739, App
483	52	5.3	2763	15	US-10-156-761-2534	Sequence 2534, App	556	51.2	5.2	898	17	US-10-437-963-12968	Sequence 12968, A
484	52	5.3	3597	15	US-10-156-761-1819	Sequence 1819, App	557	51.2	5.2	1002	15	US-10-156-761-2043	Sequence 2043, App
485	51.8	5.2	672	15	US-10-156-761-6700	Sequence 6700, App	558	51.2	5.2	1107	16	US-10-282-122A-14710	Sequence 14710, A
486	51.8	5.2	918	15	US-10-156-761-6700	Sequence 15076, A	559	51.2	5.2	1134	15	US-10-156-761-3946	Sequence 3946, App
487	51.8	5.2	1227	16	US-10-087-192-1322	Sequence 1322, App	560	51.2	5.2	1188	15	US-10-156-761-421	Sequence 421, App
488	51.8	5.2	1253	13	US-10-156-761-1108	Sequence 1108, App	561	51.2	5.2	1267	18	US-10-425-115-15750	Sequence 15750, A
489	51.8	5.2	1344	15	US-10-369-493-43202	Sequence 43202, A	562	51.2	5.2	1290	18	US-10-739-930-2596	Sequence 2596, App
490	51.8	5.2	1347	15	US-10-156-761-5226	Sequence 5226, App	563	51.2	5.2	1493	18	US-10-739-930-2577	Sequence 2577, App
491	51.8	5.2	1593	15	US-10-425-114-32254	Sequence 32254, A	564	51.2	5.2	1536	15	US-10-156-761-7115	Sequence 7115, App
492	51.8	5.2	1640	16	US-10-425-114-30266	Sequence 30266, A	565	51.2	5.2	1557	17	US-10-437-963-89570	Sequence 89570, A
493	51.8	5.2	1645	15	US-10-369-493-39901	Sequence 39901, A	566	51.2	5.2	1637	17	US-10-437-963-73981	Sequence 73981, A
494	51.8	5.2	1659	15	US-10-369-493-39150	Sequence 39150, A	567	51.2	5.2	1683	15	US-10-205-032-3	Sequence 3, Appl
495	51.8	5.2	1677	15	US-10-369-493-39150	Sequence 39150, A	568	51.2	5.2	1841	17	US-10-437-963-89571	Sequence 89571, A
496	51.8	5.2	1677	15	US-10-369-493-39150	Sequence 39150, A	569	51.2	5.2	1959	18	US-10-739-930-3025	Sequence 3025, App
497	51.8	5.2	1704	18	US-10-739-930-2739	Sequence 2739, App	570	51.2	5.2	2034	9	US-09-815-242-8002	Sequence 8002, App
498	51.8	5.2	1779	15	US-10-156-761-1559	Sequence 1559, App	571	51.2	5.2	2067	15	US-10-156-761-6391	Sequence 6391, App
499	51.8	5.2	1796	17	US-10-437-963-43317	Sequence 43317, A	572	51.2	5.2	2067	15	US-10-156-761-6391	Sequence 6391, App
500	51.8	5.2	1803	18	US-10-425-115-133999	Sequence 133999, A	573	51.2	5.2	10000	15	US-10-156-761-15103	Sequence 15103, App
501	51.8	5.2	1880	17	US-10-437-963-23751	Sequence 23751, A	574	51.2	5.2	687	15	US-10-156-761-2253	Sequence 2253, App
502	51.8	5.2	1894	17	US-10-437-963-89370	Sequence 89370, A	575	51.2	5.2	694	18	US-10-425-115-101015	Sequence 101015, A
503	51.8	5.2	2075	15	US-10-138-434A-2	Sequence 2, Appl	576	51.2	5.2	894	18	US-10-739-930-2948	Sequence 2948, App
504	51.8	5.2	2075	15	US-10-425-586-1	Sequence 1, Appl	577	51.2	5.2	1008	17	US-10-437-963-16086	Sequence 16086, A
505	51.8	5.2	2075	16	US-10-466-136-1	Sequence 1, Appl	578	51.2	5.2	1160	16	US-10-425-114-2979	Sequence 2979, App
506	51.8	5.2	2145	16	US-10-282-122A-31855	Sequence 31855, A	579	51.2	5.2	1203	18	US-10-425-115-1045	Sequence 1045, App
507	51.8	5.2	2322	18	US-10-739-930-2737	Sequence 2737, App	580	51.2	5.2	1218	15	US-10-156-761-6041	Sequence 6041, App
508	51.8	5.2	2847	15	US-10-156-761-2404	Sequence 2404, App	581	51.2	5.2	1497	16	US-10-282-122A-25509	Sequence 25509, A
509	51.8	5.2	4462	9	US-09-974-298-28	Sequence 28, Appl	582	51.2	5.2	1503	16	US-10-260-238-1244	Sequence 1244, App
510	51.8	5.2	4469	9	US-09-796-008-1	Sequence 1, Appl	583	51.2	5.2	1632	15	US-10-132-350-39	Sequence 39, Appl
511	51.8	5.2	4469	15	US-10-133-937-42	Sequence 42, Appl	584	51.2	5.2	1755	15	US-10-369-493-32171	Sequence 32171, A
512	51.8	5.2	4469	15	US-10-172-118-857	Sequence 857, App	585	51.2	5.2	1803	15	US-10-132-350-37	Sequence 37, Appl
513	51.8	5.2	4469	16	US-10-159-563-42	Sequence 42, App	586	51.2	5.2	1878	17	US-10-437-963-42117	Sequence 42117, A
514	51.8	5.2	4469	16	US-10-342-887-857	Sequence 857, App	587	51.2	5.2	2220	15	US-10-156-761-5063	Sequence 5063, App
515	51.8	5.2	4469	18	US-10-786-720-15	Sequence 15, Appl	588	51.2	5.2	2266	18	US-10-425-115-130993	Sequence 130993, A
										2370	15	US-10-156-761-4813	Sequence 4813, App

589	51	5.2	2561	9	US-09-976-740-48	Sequence 48, Appl	662	50.2	5.1	4826	17	US-10-717-381-1	Sequence 1, Appl
590	51	5.2	2561	13	US-10-023-529-48	Sequence 48, Appl	c 663	50	5.1	390	9	US-09-960-352-14023	Sequence 14023, A
591	51	5.2	2561	13	US-10-023-523-48	Sequence 48, Appl	c 664	50	5.1	1020	17	US-10-437-963-98512	Sequence 98512, A
592	51	5.2	2561	16	US-10-616-187-48	Sequence 48, Appl	665	50	5.1	1057	16	US-10-425-114-24158	Sequence 24158, A
593	51	5.2	2561	16	US-10-671-242-48	Sequence 48, Appl	666	50	5.1	1213	18	US-10-425-115-125558	Sequence 12558, A
594	51	5.2	2601	17	US-10-437-963-72883	Sequence 72883, A	667	50	5.1	1272	17	US-10-437-963-37456	Sequence 37456, A
595	51	5.2	2710	16	US-10-250-613-33	Sequence 33, Appl	668	50	5.1	1317	15	US-10-369-493-31645	Sequence 31645, A
596	51	5.2	2765	17	US-10-437-963-2941	Sequence 2941, Ap	669	50	5.1	1337	15	US-10-369-493-42992	Sequence 42992, A
597	51	5.2	3606	15	US-10-156-761-3063	Sequence 3063, Ap	670	50	5.1	1365	16	US-10-282-122A-13750	Sequence 13750, A
598	50.8	5.1	819	15	US-10-156-761-4765	Sequence 4765, Ap	c 671	50	5.1	1582	18	US-10-739-930-2333	Sequence 2333, Ap
599	50.8	5.1	1125	16	US-10-282-122A-31378	Sequence 31378, A	672	50	5.1	1806	15	US-10-329-079-38	Sequence 38, Appl
600	50.8	5.1	1155	15	US-10-193-002-12	Sequence 12, Appl	673	50	5.1	1806	15	US-10-329-027-29	Sequence 29, Appl
601	50.8	5.1	1155	15	US-10-084-843-12	Sequence 12, Appl	674	50	5.1	1860	15	US-10-156-761-6889	Sequence 6889, Ap
602	50.8	5.1	1178	16	US-10-260-238-706	Sequence 706, App	675	50	5.1	2148	15	US-10-369-493-42943	Sequence 42943, A
603	50.8	5.1	1183	15	US-10-156-761-421	Sequence 421, App	676	50	5.1	3012	17	US-10-437-963-78726	Sequence 78726, A
604	50.8	5.1	1230	17	US-10-437-963-96421	Sequence 96421, A	677	50	5.1	3135	15	US-10-156-761-2721	Sequence 2721, A
605	50.8	5.1	1317	9	US-09-815-242-4148	Sequence 4148, Ap	678	50	5.1	3374	17	US-10-437-963-10004	Sequence 10004, A
606	50.8	5.1	1317	16	US-10-282-122A-7337	Sequence 7337, Ap	679	50	5.1	5061	17	US-10-437-963-9832	Sequence 9832, Ap
607	50.8	5.1	1479	9	US-09-887-576-820	Sequence 820, App	c 680	50	5.1	10692	15	US-10-156-761-414	Sequence 414, App
608	50.8	5.1	1551	15	US-10-156-761-1622	Sequence 1622, Ap	681	50	5.1	13842	9	US-09-861-289-30	Sequence 30, Appl
609	50.8	5.1	1682	18	US-10-479-638-10	Sequence 10, Appl	682	50	5.1	13842	9	US-09-860-846-30	Sequence 30, Appl
610	50.8	5.1	2230	17	US-10-437-963-65821	Sequence 65821, A	683	50	5.1	13842	10	US-09-988-3848-30	Sequence 30, Appl
611	50.8	5.1	5760	14	US-10-152-886-14	Sequence 14, Appl	684	50	5.1	13842	10	US-09-836-821-30	Sequence 30, Appl
612	50.8	5.1	10000	15	US-10-156-761-15103	Sequence 15103, A	685	50	5.1	13842	15	US-10-271-889-30	Sequence 30, Appl
613	50.6	5.1	508	9	US-09-452-239-15	Sequence 15, Appl	686	50	5.1	15738	15	US-10-329-079-12	Sequence 12, Appl
614	50.6	5.1	940	18	US-10-425-115-176490	Sequence 176490, Sequence 16490,	687	50	5.1	32329	16	US-10-374-903A-1	Sequence 1, Appl
615	50.6	5.1	1032	17	US-10-437-963-36005	Sequence 36005, A	688	50	5.1	36778	9	US-09-861-289-5	Sequence 5, Appl
616	50.6	5.1	1041	15	US-10-156-761-7418	Sequence 7418, Ap	689	50	5.1	36778	9	US-09-860-846-5	Sequence 5, Appl
617	50.6	5.1	1371	15	US-10-282-122A-25436	Sequence 25436, A	690	50	5.1	36778	15	US-10-271-889-48	Sequence 48, Appl
618	50.6	5.1	1400	18	US-10-425-115-20597	Sequence 20597, A	691	50	5.1	36778	15	US-10-329-079-6	Sequence 6, Appl
619	50.6	5.1	1449	17	US-10-437-963-64629	Sequence 64629, A	692	50	5.1	37360	15	US-10-988-3848-5	Sequence 5, Appl
620	50.6	5.1	1695	15	US-10-156-761-3949	Sequence 3949, Ap	693	50	5.1	37360	15	US-09-988-3848-5	Sequence 5, Appl
621	50.6	5.1	1848	17	US-10-437-963-22612	Sequence 22612, A	694	50	5.1	38506	15	US-09-793-708-19	Sequence 19, Appl
622	50.6	5.1	2300	18	US-10-425-115-134362	Sequence 134362, Sequence 170055,	695	50	5.1	38506	15	US-10-201-365-1	Sequence 1, Appl
623	50.6	5.1	2477	18	US-10-425-115-170055	Sequence 170055, Sequence 148395,	696	50	5.1	38506	15	US-10-160-539-19	Sequence 19, Appl
624	50.6	5.1	2741	18	US-10-425-115-148395	Sequence 148395, Sequence 184346,	c 697	50	5.1	229354	9	US-09-785-400-64	Sequence 64, Appl
625	50.6	5.1	3418	18	US-10-425-115-184346	Sequence 184346, Sequence 184346,	698	49.8	5.0	856	9	US-09-823-245A-99	Sequence 99, Appl
626	50.6	5.1	3418	18	US-10-425-115-184346	Sequence 184346, Sequence 184346,	699	49.8	5.0	880	16	US-10-425-114-32836	Sequence 32836, A
627	50.6	5.1	4233	18	US-10-723-860-4143	Sequence 4143, Ap	c 700	49.8	5.0	915	15	US-10-156-761-2013	Sequence 2013, Ap
628	50.6	5.1	4244	18	US-10-723-860-8016	Sequence 8016, Ap	701	49.8	5.0	940	16	US-10-425-114-35300	Sequence 35300, A
629	50.4	5.1	549	15	US-10-260-238-239	Sequence 239, App	702	49.8	5.0	948	18	US-10-425-115-43218	Sequence 43218, A
630	50.4	5.1	645	15	US-10-156-761-6059	Sequence 6059, App	703	49.8	5.0	1227	15	US-10-156-761-6074	Sequence 6074, Ap
631	50.4	5.1	662	17	US-10-437-963-74146	Sequence 74146, A	704	49.8	5.0	1245	11	US-09-758-759-22	Sequence 22, Appl
632	50.4	5.1	669	15	US-10-107-431-166	Sequence 166, App	705	49.8	5.0	1272	15	US-10-107-431-32	Sequence 32, Appl
633	50.4	5.1	777	18	US-10-425-115-127687	Sequence 127687, Sequence 83763, A	706	49.8	5.0	1293	14	US-10-145-415-17	Sequence 17, Appl
634	50.4	5.1	838	18	US-10-425-115-127687	Sequence 127687, Sequence 83763, A	707	49.8	5.0	1374	16	US-10-282-122A-14455	Sequence 14455, A
635	50.4	5.1	891	17	US-10-437-963-41595	Sequence 41595, A	708	49.8	5.0	1410	17	US-10-437-963-97868	Sequence 97868, A
636	50.4	5.1	1062	17	US-10-437-963-34793	Sequence 34793, A	709	49.8	5.0	1440	15	US-10-156-761-5216	Sequence 5216, Ap
637	50.4	5.1	1159	16	US-10-374-780A-879	Sequence 879, App	710	49.8	5.0	1572	15	US-10-156-761-4159	Sequence 4159, Ap
638	50.4	5.1	1454	18	US-10-425-115-68094	Sequence 68094, A	711	49.8	5.0	1581	16	US-10-464-368-113	Sequence 113, App
639	50.4	5.1	1587	15	US-10-156-761-5134	Sequence 5134, Ap	712	49.8	5.0	1694	17	US-10-437-963-42666	Sequence 42666, A
640	50.4	5.1	1848	15	US-10-156-761-3850	Sequence 3850, Ap	713	49.8	5.0	1791	15	US-10-156-761-2352	Sequence 2352, Ap
641	50.4	5.1	1910	17	US-10-437-963-23941	Sequence 23941, A	714	49.8	5.0	1814	14	US-10-060-036-182	Sequence 182, App
642	50.4	5.1	1951	17	US-10-437-963-31078	Sequence 31078, A	c 715	49.8	5.0	1929	9	US-09-761-534A-9	Sequence 9, Appl
643	50.4	5.1	2082	15	US-10-156-761-6082	Sequence 6082, Ap	716	49.8	5.0	2031	15	US-10-156-761-2451	Sequence 2451, Ap
644	50.4	5.1	3048	15	US-10-156-761-3146	Sequence 3146, Ap	717	49.8	5.0	2115	15	US-10-156-761-5640	Sequence 5640, Ap
645	50.4	5.1	3456	17	US-10-437-963-50711	Sequence 50711, A	718	49.8	5.0	2136	17	US-10-437-963-49142	Sequence 49142, A
646	50.4	5.1	5003	17	US-10-437-963-18350	Sequence 18350, A	719	49.8	5.0	2520	17	US-09-873-367C-159	Sequence 159, App
647	50.4	5.1	6375	16	US-10-389-647-144	Sequence 144, App	c 720	49.8	5.0	2535	17	US-10-437-963-11953	Sequence 11953, A
648	50.4	5.1	14427	15	US-10-156-761-1540	Sequence 1540, Ap	721	49.8	5.0	2664	15	US-10-156-761-1241	Sequence 1241, Ap
649	50.4	5.1	45055	15	US-10-107-431-277	Sequence 277, App	722	49.8	5.0	3066	15	US-10-156-761-1742	Sequence 1742, Ap
650	50.2	5.1	595	16	US-10-260-238-3262	Sequence 3262, Ap	723	49.8	5.0	3113	9	US-09-894-998-52	Sequence 52, Appl
651	50.2	5.1	740	17	US-10-437-963-67956	Sequence 67956, A	724	49.8	5.0	3113	14	US-10-121-988-52	Sequence 52, Appl
652	50.2	5.1	841	16	US-10-282-122A-14618	Sequence 14618, A	725	49.8	5.0	3113	15	US-10-200-562-52	Sequence 52, Appl
653	50.2	5.1	1002	15	US-10-156-761-696	Sequence 696, App	726	49.8	5.0	3113	15	US-10-237-551-52	Sequence 52, Appl
654	50.2	5.1	1093	18	US-10-425-115-106454	Sequence 106454, Sequence 1435, Ap	727	49.8	5.0	3345	9	US-09-894-998-49	Sequence 49, Appl
655	50.2	5.1	1426	17	US-10-437-963-1435	Sequence 1435, Ap	728	49.8	5.0	3345	14	US-10-121-988-49	Sequence 49, Appl
656	50.2	5.1	1586	17	US-10-437-963-59660	Sequence 59660, A	729	49.8	5.0	3345	15	US-10-200-562-49	Sequence 49, Appl
657	50.2	5.1	1896	15	US-10-156-761-5658	Sequence 5658, Ap	730	49.8	5.0	3345	15	US-10-200-562-189	Sequence 189, App
658	50.2	5.1	2832	17	US-10-437-963-61943	Sequence 61943, A	731	49.8	5.0	3345	15	US-10-237-551-49	Sequence 49, Appl
659	50.2	5.1	3032	17	US-10-437-963-16502	Sequence 16502, A	732	49.8	5.0	3345	15	US-10-237-551-189	Sequence 189, App
660	50.2	5.1	3039	15	US-10-369-493-42391	Sequence 42391, A	733	49.8	5.0	4323	16	US-10-282-122A-26577	Sequence 26577, A
661	50.2	5.1	4826	9	US-09-772-304A-1	Sequence 1, Appl	c 734	49.8	5.0	37116	15	US-10-107-431-279	Sequence 279, App

735	49.8	5.0	65140	17	US-10-203-295-1	Sequence 1, Appli	808	49.4	5.0	2091	15	US-10-237-551-78	Sequence 78, Appl
736	49.6	5.0	125401	17	US-10-203-295-35	Sequence 35, Appl	809	49.4	5.0	2091	15	US-10-237-551-226	Sequence 226, App
737	49.6	5.0	242	9	US-09-923-876-781	Sequence 781, App	810	49.4	5.0	2118	14	US-10-121-988-87	Sequence 87, Appl
738	49.6	5.0	242	10	US-09-923-876-781	Sequence 781, App	811	49.4	5.0	2118	15	US-10-200-552-87	Sequence 87, Appl
739	49.6	5.0	746	16	US-10-425-114-12136	Sequence 12136, A	812	49.4	5.0	2211	15	US-10-237-551-87	Sequence 86, Appl
740	49.6	5.0	806	17	US-10-767-701-1614	Sequence 1614, Ap	813	49.4	5.0	2211	14	US-10-121-988-86	Sequence 86, Appl
741	49.6	5.0	876	18	US-10-425-115-55664	Sequence 55664, A	814	49.4	5.0	2211	15	US-10-200-552-86	Sequence 86, Appl
742	49.6	5.0	976	16	US-10-425-114-13780	Sequence 13780, A	815	49.4	5.0	2211	15	US-10-237-551-86	Sequence 86, Appl
743	49.6	5.0	981	15	US-10-156-761-6381	Sequence 6381, Ap	816	49.4	5.0	2270	17	US-10-437-963-53336	Sequence 53336, A
744	49.6	5.0	981	17	US-10-437-963-58326	Sequence 58326, A	817	49.4	5.0	2502	16	US-10-282-122A-17902	Sequence 17902, A
745	49.6	5.0	1089	15	US-10-156-761-2655	Sequence 2655, Ap	818	49.4	5.0	2517	15	US-10-493-43322	Sequence 4322, A
746	49.6	5.0	1151	16	US-10-425-114-23559	Sequence 23559, A	819	49.4	5.0	3038	15	US-10-251-661-11	Sequence 11, Appl
747	49.6	5.0	1176	16	US-10-425-114-21556	Sequence 21556, A	820	49.4	5.0	3038	17	US-10-680-087-45	Sequence 45, Appl
748	49.6	5.0	1204	17	US-10-437-963-102262	Sequence 102262, A	821	49.4	5.0	3331	10	US-09-373-658-31	Sequence 31, Appl
749	49.6	5.0	1205	17	US-10-437-963-84924	Sequence 84924, A	822	49.4	5.0	3331	11	US-09-389-687-31	Sequence 31, Appl
750	49.6	5.0	1329	15	US-10-156-761-5851	Sequence 5851, Ap	823	49.4	5.0	3352	18	US-10-425-115-84048	Sequence 84048, A
751	49.6	5.0	1362	16	US-10-282-122A-33594	Sequence 33594, A	824	49.4	5.0	3489	11	US-09-894-273-1	Sequence 1, Appli
752	49.6	5.0	1404	15	US-10-369-493-31750	Sequence 31750, A	825	49.4	5.0	3489	15	US-10-294-804-1	Sequence 1, Appli
753	49.6	5.0	1651	17	US-10-437-963-23386	Sequence 23386, A	826	49.4	5.0	3489	18	US-10-194-046-1	Sequence 1, Appli
754	49.6	5.0	1743	15	US-10-172-118-1387	Sequence 1387, Ap	827	49.4	5.0	4255	16	US-10-282-122A-14875	Sequence 14875, A
755	49.6	5.0	1743	16	US-10-342-887-1387	Sequence 1387, Ap	828	49.4	5.0	4353	16	US-10-226-638A-15	Sequence 15, Appl
756	49.6	5.0	1761	15	US-10-156-761-1503	Sequence 1503, Ap	829	49.4	5.0	14061	15	US-10-093-463-73	Sequence 73, Appl
757	49.6	5.0	1765	15	US-10-237-551-225	Sequence 225, App	830	49.4	5.0	30000	12	US-09-980-217-3	Sequence 3, Appli
758	49.6	5.0	1929	17	US-10-437-963-70663	Sequence 70663, A	831	49.4	5.0	23229	16	US-10-374-903A-1	Sequence 1, Appli
759	49.6	5.0	1978	17	US-10-437-963-88743	Sequence 88743, A	832	49.4	5.0	59816	16	US-10-084-846A-1	Sequence 1, Appli
760	49.6	5.0	2040	9	US-09-815-242-4027	Sequence 4027, Ap	833	49.4	5.0	59816	11	US-10-084-846A-2	Sequence 2, Appli
761	49.6	5.0	2040	16	US-10-282-122A-7316	Sequence 7316, Ap	834	49.4	5.0	109519	11	US-09-758-759-1	Sequence 1, Appli
762	49.6	5.0	2059	17	US-10-437-963-59377	Sequence 59377, A	835	49.2	5.0	955	16	US-10-425-114-17203	Sequence 17203, A
763	49.6	5.0	2065	17	US-10-437-963-31244	Sequence 31244, A	836	49.2	5.0	972	15	US-10-369-493-32340	Sequence 32340, A
764	49.6	5.0	2218	16	US-10-108-260A-2174	Sequence 2174, Ap	837	49.2	5.0	975	18	US-10-332-859-324	Sequence 324, App
765	49.6	5.0	2271	15	US-10-101-510-133	Sequence 133, App	838	49.2	5.0	1004	16	US-10-425-115-17915	Sequence 17915, A
766	49.6	5.0	2471	17	US-10-437-963-62969	Sequence 62969, A	839	49.2	5.0	1051	18	US-10-437-963-94232	Sequence 94232, A
767	49.6	5.0	2487	15	US-10-205-823-135	Sequence 135, App	840	49.2	5.0	1256	17	US-10-437-963-82846	Sequence 82846, A
768	49.6	5.0	2487	15	US-10-172-118-1045	Sequence 1045, Ap	841	49.2	5.0	1295	17	US-10-437-963-82846	Sequence 82846, A
769	49.6	5.0	2487	16	US-10-342-887-1045	Sequence 1045, Ap	842	49.2	5.0	1317	17	US-10-156-761-3647	Sequence 3647, Ap
770	49.6	5.0	2700	15	US-10-156-761-7310	Sequence 7310, Ap	843	49.2	5.0	1357	17	US-10-437-963-18242	Sequence 18242, A
771	49.6	5.0	2742	9	US-09-815-242-4163	Sequence 4163, Ap	844	49.2	5.0	1493	16	US-10-425-114-3264	Sequence 3264, Ap
772	49.6	5.0	3459	15	US-10-282-122A-7408	Sequence 7408, Ap	845	49.2	5.0	1587	9	US-10-156-761-4508	Sequence 4508, Ap
773	49.6	5.0	3459	15	US-10-369-493-31552	Sequence 31552, A	846	49.2	5.0	1602	9	US-09-833-790-417	Sequence 417, App
774	49.6	5.0	3729	16	US-10-671-403-86	Sequence 86, Appl	847	49.2	5.0	1602	15	US-10-293-582-15	Sequence 15, Appl
775	49.6	5.0	3729	16	US-10-671-419-86	Sequence 86, Appl	848	49.2	5.0	1602	17	US-10-761-169-5	Sequence 5, Appli
776	49.6	5.0	3729	16	US-10-670-844-86	Sequence 86, Appl	849	49.2	5.0	1613	16	US-10-425-114-3572	Sequence 3572, Ap
777	49.6	5.0	3729	16	US-10-671-134-86	Sequence 86, Appl	850	49.2	5.0	1679	17	US-10-437-963-32154	Sequence 32154, A
778	49.6	5.0	3729	16	US-10-673-098-86	Sequence 86, Appl	851	49.2	5.0	1908	15	US-10-156-761-260	Sequence 260, App
779	49.6	5.0	3729	16	US-10-672-638-86	Sequence 86, Appl	852	49.2	5.0	2331	17	US-10-437-963-14511	Sequence 14511, A
780	49.6	5.0	3729	16	US-10-673-127-86	Sequence 86, Appl	853	49.2	5.0	2455	9	US-09-917-800A-1386	Sequence 1386, Ap
781	49.6	5.0	3729	17	US-10-670-817-86	Sequence 86, Appl	854	49.2	5.0	2455	15	US-10-316-253-27	Sequence 27, Appl
782	49.6	5.0	3729	17	US-10-673-119-86	Sequence 86, Appl	855	49.2	5.0	2455	16	US-10-388-934-21	Sequence 21, Appl
783	49.6	5.0	3729	18	US-10-671-207-86	Sequence 86, Appl	856	49.2	5.0	2455	16	US-10-152-319A-1964	Sequence 13, Appl
784	49.6	5.0	3942	15	US-10-156-761-5692	Sequence 5692, Ap	857	49.2	5.0	2607	17	US-10-247-671-13	Sequence 13, Appl
785	49.6	5.0	5181	11	US-09-968-007A-802	Sequence 802, App	858	49.2	5.0	2607	18	US-10-723-860-8011	Sequence 8011, Ap
786	49.4	5.0	426	17	US-10-437-963-99472	Sequence 99472, A	859	49.2	5.0	3540	15	US-10-369-493-32003	Sequence 32003, A
787	49.4	5.0	843	15	US-10-156-761-1994	Sequence 1994, Ap	860	49.2	5.0	4161	15	US-10-156-761-5450	Sequence 5450, Ap
788	49.4	5.0	876	15	US-10-156-761-4743	Sequence 4743, Ap	861	49.2	5.0	137560	18	US-10-481-112-1	Sequence 1, Appli
789	49.4	5.0	951	15	US-10-259-165-313	Sequence 313, App	862	49	5.0	399	15	US-10-174-693-193	Sequence 193, App
790	49.4	5.0	1005	17	US-10-437-963-39562	Sequence 39562, A	863	49	5.0	717	16	US-10-282-122A-25697	Sequence 25697, A
791	49.4	5.0	1029	16	US-10-084-846A-87	Sequence 87, Appl	864	49	5.0	1011	15	US-10-156-761-7058	Sequence 7058, Ap
792	49.4	5.0	1173	16	US-10-282-122A-25963	Sequence 25963, A	865	49	5.0	1261	17	US-10-437-963-70724	Sequence 70724, A
793	49.4	5.0	1191	16	US-10-282-122A-15207	Sequence 15207, A	866	49	5.0	1276	17	US-10-437-963-27235	Sequence 27235, A
794	49.4	5.0	1281	15	US-10-156-761-2281	Sequence 2281, Ap	867	49	5.0	1292	17	US-10-437-963-23001	Sequence 23001, A
795	49.4	5.0	1385	16	US-10-435-114-26389	Sequence 26389, A	868	49	5.0	1355	15	US-10-458-108-6	Sequence 6, Appli
796	49.4	5.0	1401	17	US-10-437-963-95208	Sequence 95208, A	869	49	5.0	1400	17	US-10-437-963-2506	Sequence 2506, Ap
797	49.4	5.0	1557	16	US-10-425-114-18927	Sequence 18927, A	870	49	5.0	1462	14	US-10-175-523-163	Sequence 163, App
798	49.4	5.0	1587	16	US-10-282-122A-28573	Sequence 28573, A	871	49	5.0	1473	9	US-10-411-910A-261	Sequence 261, App
799	49.4	5.0	1590	16	US-10-282-122A-26270	Sequence 26270, A	872	49	5.0	1614	9	US-09-976-740-45	Sequence 45, Appl
800	49.4	5.0	1612	17	US-10-437-963-102480	Sequence 102480, A	873	49	5.0	1614	13	US-10-023-529-45	Sequence 45, Appl
801	49.4	5.0	1619	16	US-10-435-114-24202	Sequence 24202, A	874	49	5.0	1614	13	US-10-023-523-45	Sequence 45, Appl
802	49.4	5.0	1619	16	US-10-435-114-24326	Sequence 24326, A	875	49	5.0	1614	16	US-10-616-187-45	Sequence 45, Appl
803	49.4	5.0	1633	18	US-10-435-115-157740	Sequence 157740, A	876	49	5.0	1614	16	US-10-671-242-45	Sequence 45, Appl
804	49.4	5.0	1697	16	US-10-425-114-29187	Sequence 29187, A	877	49	5.0	1797	17	US-10-437-963-28602	Sequence 28602, A
805	49.4	5.0	1707	18	US-10-425-115-11341	Sequence 11341, A	878	49	5.0	1852	9	US-09-969-852-4	Sequence 4, Appli
806	49.4	5.0	2091	14	US-10-121-988-78	Sequence 78, Appl	879	49	5.0	1891	17	US-10-310-154-280	Sequence 280, App
807	49.4	5.0	2091	15	US-10-200-562-78	Sequence 78, Appl	880	49	5.0	1946	17	US-10-437-963-22064	Sequence 22064, A

881	49	5.0	1974	17	US-10-437-963-87831	Sequence 87831, A	954	48.6	4.9	796	17	US-10-767-701-7856	Sequence 7856, Ap
882	49	5.0	2067	17	US-10-437-963-18405	Sequence 18405, A	955	48.6	4.9	847	18	US-10-425-115-41717	Sequence 41717, A
883	49	5.0	2143	16	US-10-425-114-23617	Sequence 23617, A	956	48.6	4.9	934	16	US-10-425-114-17266	Sequence 17266, A
C 884	49	5.0	2204	17	US-10-437-963-11022	Sequence 11022, A	957	48.6	4.9	974	16	US-10-425-114-18881	Sequence 18881, A
885	49	5.0	2239	16	US-10-425-114-5232	Sequence 5232, Ap	958	48.6	4.9	1107	18	US-10-425-115-161174	Sequence 161174, A
886	49	5.0	2271	17	US-10-437-963-74809	Sequence 74809, A	959	48.6	4.9	1143	15	US-10-156-761-6453	Sequence 6453, Ap
C 887	49	5.0	2439	15	US-10-156-761-2569	Sequence 2569, Ap	960	48.6	4.9	1170	18	US-10-425-115-162747	Sequence 162747, A
888	49	5.0	2536	18	US-10-425-115-91117	Sequence 91117, A	961	48.6	4.9	1203	15	US-10-369-493-34414	Sequence 34414, A
C 889	49	5.0	2939	17	US-10-437-963-58050	Sequence 58050, A	962	48.6	4.9	1302	18	US-10-425-115-164928	Sequence 164928, A
C 890	49	5.0	12425	9	US-09-976-740-50	Sequence 50, Appl	963	48.6	4.9	1366	18	US-10-425-115-28293	Sequence 28293, A
C 891	49	5.0	12425	13	US-10-023-529-50	Sequence 50, Appl	964	48.6	4.9	1453	17	US-10-437-963-78719	Sequence 78719, A
C 892	49	5.0	12425	13	US-10-023-529-50	Sequence 50, Appl	965	48.6	4.9	1461	15	US-10-156-761-2205	Sequence 2205, Ap
C 893	49	5.0	12425	16	US-10-616-187-50	Sequence 50, Appl	966	48.6	4.9	1479	13	US-10-016-283-35	Sequence 35, Appl
C 894	49	5.0	12425	16	US-10-671-242-50	Sequence 50, Appl	967	48.6	4.9	1533	18	US-09-814-353-20197	Sequence 20197, A
C 895	49	5.0	77536	10	US-09-940-316B-1	Sequence 1, Appl	968	48.6	4.9	1617	18	US-10-425-115-164014	Sequence 164014, A
896	48.8	4.9	363	15	US-10-156-761-5224	Sequence 5224, Ap	969	48.6	4.9	1685	16	US-10-425-114-27558	Sequence 27558, A
C 897	48.8	4.9	389	18	US-10-425-115-178702	Sequence 178702, A	970	48.6	4.9	1783	17	US-10-437-963-340	Sequence 340, App
C 898	48.8	4.9	458	17	US-10-437-963-3998	Sequence 3998, Ap	971	48.6	4.9	1839	11	US-09-758-759-150	Sequence 150, App
C 899	48.8	4.9	513	15	US-10-156-761-5057	Sequence 5057, Ap	972	48.6	4.9	1862	17	US-10-437-963-89753	Sequence 89753, A
900	48.8	4.9	516	17	US-10-437-963-75898	Sequence 75898, A	973	48.6	4.9	2040	9	US-09-874-923-5	Sequence 5, Appl
901	48.8	4.9	602	18	US-10-425-115-172234	Sequence 172234, A	974	48.6	4.9	2040	9	US-09-991-496-5	Sequence 72, Appl
902	48.8	4.9	618	15	US-10-156-761-4061	Sequence 4061, Ap	975	48.6	4.9	2040	15	US-10-098-732A-72	Sequence 35019, A
903	48.8	4.9	728	16	US-10-425-114-14002	Sequence 14002, A	976	48.6	4.9	2238	17	US-10-437-963-35019	Sequence 68, Appl
904	48.8	4.9	827	16	US-10-425-114-18832	Sequence 18832, A	977	48.6	4.9	2279	15	US-10-021-660-68	Sequence 212, App
905	48.8	4.9	828	15	US-10-156-761-1422	Sequence 1422, Ap	978	48.6	4.9	2279	16	US-10-211-462-212	Sequence 9, Appl
906	48.8	4.9	933	15	US-10-156-761-1758	Sequence 1758, Ap	979	48.6	4.9	2577	17	US-10-332-413-9	Sequence 4, Appl
907	48.8	4.9	1068	15	US-10-156-761-1861	Sequence 1861, Ap	980	48.6	4.9	2712	17	US-09-748-033-4	Sequence 4, Appl
908	48.8	4.9	1084	16	US-10-425-114-3	Sequence 3, Appl	981	48.6	4.9	3298	16	US-10-362-247-4	Sequence 4, Appl
909	48.8	4.9	1094	17	US-10-767-701-13435	Sequence 13435, A	982	48.6	4.9	3872	17	US-10-437-963-57556	Sequence 57556, A
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C 911	48.8	4.9	1164	17	US-10-767-701-12837	Sequence 12837, A	984	48.6	4.9	5065	14	US-10-067-457-4	Sequence 4, Appl
912	48.8	4.9	1194	15	US-10-214-446-33	Sequence 33, Appl	985	48.6	4.9	5499	16	US-10-276-774-973	Sequence 973, App
913	48.8	4.9	1224	16	US-10-425-114-21138	Sequence 21138, A	986	48.4	4.9	562	15	US-10-174-693-53	Sequence 53, Appl
914	48.8	4.9	1224	15	US-10-425-114-21138	Sequence 21138, A	987	48.4	4.9	642	15	US-10-156-761-6149	Sequence 6149, Ap
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916	48.8	4.9	1290	17	US-10-767-701-9008	Sequence 9008, Ap	989	48.4	4.9	800	18	US-10-425-115-25676	Sequence 25676, A
917	48.8	4.9	1335	15	US-10-156-761-7202	Sequence 7202, Ap	990	48.4	4.9	819	18	US-10-425-115-151084	Sequence 151084, A
918	48.8	4.9	1392	15	US-10-156-761-4350	Sequence 4350, Ap	991	48.4	4.9	1059	15	US-10-259-165-215	Sequence 215, App
919	48.8	4.9	1455	16	US-10-425-114-31249	Sequence 31249, A	992	48.4	4.9	1164	16	US-10-425-114-21717	Sequence 21717, A
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930	48.8	4.9	9166	16	US-10-359-120-168	Sequence 168, App	1003	48.4	4.9	2565	17	US-10-437-963-96575	Sequence 96575, A
931	48.8	4.9	9167	16	US-10-359-120-171	Sequence 171, App	1004	48.4	4.9	2892	15	US-10-156-761-3066	Sequence 3066, Ap
932	48.8	4.9	9169	16	US-10-359-120-169	Sequence 169, App	1005	48.4	4.9	3377	17	US-10-437-963-92668	Sequence 92668, A
933	48.8	4.9	9170	16	US-10-359-120-166	Sequence 166, App	1006	48.4	4.9	3751	16	US-10-311-795-5	Sequence 5, Appl
934	48.8	4.9	9189	16	US-10-359-120-155	Sequence 159, App	1007	48.4	4.9	4833	16	US-10-282-122A-25605	Sequence 25605, A
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941	48.8	4.9	9788	16	US-10-359-120-174	Sequence 174, App	1014	48.2	4.9	618	16	US-10-425-114-6672	Sequence 6672, Ap
942	48.8	4.9	10035	15	US-10-359-120-170	Sequence 170, App	1015	48.2	4.9	729	18	US-10-425-115-154823	Sequence 154823, A
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C 944	48.8	4.9	12411	16	US-10-359-120-165	Sequence 165, App	1017	48.2	4.9	786	16	US-10-260-238-458	Sequence 458, App
945	48.8	4.9	13638	15	US-10-156-761-412	Sequence 412, App	1018	48.2	4.9	789	16	US-10-425-114-27917	Sequence 27917, A
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948	48.6	4.9	528	9	US-09-452-239-33	Sequence 33, Appl	1021	48.2	4.9	823	14	US-10-153-668-54	Sequence 56, Appl
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C 951	48.6	4.9	687	16	US-10-282-122A-26299	Sequence 26299, A	1024	48.2	4.9	861	15	US-10-156-761-3921	Sequence 3921, Ap
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953	48.6	4.9	761	18	US-10-425-115-127921	Sequence 127921, A	1026	48.2	4.9	920	15	US-10-117-722-132	Sequence 132, App

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1038	48.2	4.9	1059	16	US-10-389-647-304	Sequence 304, App	1111	48	4.9	1232	16	US-10-425-114-17219	Sequence 17219, A
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1057	48.2	4.9	1994	10	US-09-851-673-1	Sequence 1, Appli	1130	48	4.9	3435	11	US-09-758-759-166	Sequence 166, App
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1059	48.2	4.9	1997	18	US-10-425-115-111418	Sequence 111418, A	c1132	48	4.9	3489	16	US-10-282-122A-30110	Sequence 30110, A
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1061	48.2	4.9	2034	18	US-10-761-370-2	Sequence 2, Appli	1134	48	4.9	37116	15	US-10-374-780A-1253	Sequence 1253, Ap
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1075	48.2	4.9	20222	10	US-10-203-295-2	Sequence 2, Appli	c1148	47.8	4.8	1191	18	US-10-425-115-79775	Sequence 14756, A
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1084	48	4.9	579	11	US-09-758-759-174	Sequence 174, App	1157	47.8	4.8	1612	17	US-10-437-963-15030	Sequence 102, App
1085	48	4.9	652	17	US-10-767-701-5497	Sequence 5497, Ap	1158	47.8	4.8	1671	11	US-09-758-759-102	Sequence 58741, A
1086	48	4.9	712	18	US-10-363-345A-27449	Sequence 27449, A	1159	47.8	4.8	1711	18	US-10-425-115-58741	Sequence 7, Appli
c1087	48	4.9	712	18	US-10-363-345A-27450	Sequence 27450, A	1160	47.8	4.8	1771	9	US-09-874-923-7	Sequence 7, Appli
c1088	48	4.9	756	15	US-10-107-431-132	Sequence 132, App	1161	47.8	4.8	1771	9	US-09-991-496-7	Sequence 8656, A
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1093	48	4.9	954	15	US-10-156-761-4757	Sequence 4757, Ap	1166	47.8	4.8	3824	15	US-10-116-275-197	Sequence 307, App
1094	48	4.9	1128	10	US-09-875-076-15	Sequence 15, Appl	1167	47.8	4.8	3824	16	US-10-159-563-307	Sequence 2600, Ap
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1098	48	4.9	1128	15	US-10-272-983-15	Sequence 15, Appl	c1171	47.8	4.8	71989	9	US-09-727-889-2	Sequence 2, Appli
1099	48	4.9	1128	15	US-10-393-807-15	Sequence 15, Appl	c1172	47.8	4.8	71989	18	US-10-849-462-2	Sequence 2, Appli

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1174	47.6	4.8	633	15	US-10-369-493-4191	Sequence 4191, A	1259	47.4	4.8	693	15	US-10-156-761-1183	Sequence 1183, Ap
1175	47.6	4.8	780	15	US-10-156-761-6288	Sequence 6288, Ap	1260	47.4	4.8	862	17	US-10-767-701-10425	Sequence 10425, A
1176	47.6	4.8	878	16	US-10-425-114-15378	Sequence 15378, A	1261	47.4	4.8	931	17	US-10-437-963-91705	Sequence 91705, A
1177	47.6	4.8	891	15	US-10-156-761-7285	Sequence 7285, Ap	1262	47.4	4.8	958	17	US-10-437-963-86145	Sequence 86145, A
c1178	47.6	4.8	921	16	US-10-282-122A-7524	Sequence 7524, Ap	1263	47.4	4.8	996	15	US-10-156-761-7396	Sequence 7396, Ap
c1179	47.6	4.8	967	18	US-10-425-115-66497	Sequence 66497, A	1264	47.4	4.8	1050	17	US-10-767-701-12642	Sequence 12642, A
1180	47.6	4.8	968	16	US-10-425-114-19397	Sequence 19397, A	1265	47.4	4.8	1050	17	US-10-425-115-12635	Sequence 12635, A
c1181	47.6	4.8	1002	16	US-10-259-194A-618	Sequence 618, App	1266	47.4	4.8	1195	18	US-10-425-115-17233	Sequence 17233, A
c1182	47.6	4.8	1026	16	US-10-242-535A-53529	Sequence 53529, A	1267	47.4	4.8	1203	15	US-10-156-761-14664	Sequence 14664, Ap
c1183	47.6	4.8	1026	16	US-10-085-783A-53529	Sequence 53529, A	1268	47.4	4.8	1256	18	US-10-425-115-73921	Sequence 73921, A
1184	47.6	4.8	1049	14	US-10-123-155-358	Sequence 358, App	1269	47.4	4.8	1345	16	US-10-425-114-24589	Sequence 24589, A
1197	47.6	4.8	1060	18	US-10-425-115-124347	Sequence 124347, A	1270	47.4	4.8	1420	16	US-10-425-114-21968	Sequence 21968, A
1198	47.6	4.8	1110	15	US-10-156-761-4246	Sequence 4246, Ap	1271	47.4	4.8	1438	18	US-10-425-115-84149	Sequence 84149, A
1199	47.6	4.8	1176	15	US-10-369-493-40494	Sequence 40494, A	1272	47.4	4.8	1443	15	US-10-156-761-3397	Sequence 3397, Ap
1200	47.6	4.8	1203	16	US-10-282-122A-25722	Sequence 25722, A	1273	47.4	4.8	1468	18	US-10-425-115-115629	Sequence 115629, A
c1201	47.6	4.8	1257	17	US-10-437-963-64185	Sequence 64185, A	1274	47.4	4.8	1649	17	US-10-425-115-89113	Sequence 89113, A
c1202	47.6	4.8	1282	16	US-10-425-114-23644	Sequence 23644, A	1275	47.4	4.8	1672	17	US-10-437-963-81182	Sequence 81182, A
1203	47.6	4.8	1329	15	US-10-156-761-1297	Sequence 1297, Ap	1276	47.4	4.8	1695	17	US-10-437-963-76703	Sequence 76703, A
1204	47.6	4.8	1344	16	US-10-425-114-16346	Sequence 16346, A	1277	47.4	4.8	1723	17	US-10-437-963-11515	Sequence 11515, A
c1205	47.6	4.8	1376	17	US-10-437-963-10544	Sequence 10544, A	1278	47.4	4.8	1734	16	US-10-282-122A-25721	Sequence 25721, A
1206	47.6	4.8	1403	18	US-10-425-115-68130	Sequence 68130, A	1279	47.4	4.8	1741	16	US-10-425-114-17536	Sequence 17536, A
1207	47.6	4.8	1410	15	US-10-369-493-42819	Sequence 42819, A	1280	47.4	4.8	1848	15	US-10-156-761-3041	Sequence 3041, Ap
1208	47.6	4.8	1469	16	US-10-425-114-11292	Sequence 11292, A	1281	47.4	4.8	1900	17	US-10-437-963-28228	Sequence 28228, A
1209	47.6	4.8	1572	15	US-10-369-493-31928	Sequence 31928, A	1282	47.4	4.8	1992	16	US-10-425-114-28230	Sequence 28230, A
1210	47.6	4.8	1644	18	US-10-425-115-14950	Sequence 14950, A	1283	47.4	4.8	2041	18	US-10-425-115-41669	Sequence 41669, A
c1211	47.6	4.8	1661	17	US-10-437-963-12797	Sequence 12797, A	1284	47.4	4.8	2076	15	US-10-156-761-5585	Sequence 5585, Ap
1212	47.6	4.8	1689	16	US-10-425-114-17162	Sequence 17162, A	1285	47.4	4.8	2124	17	US-10-437-963-57642	Sequence 57642, A
1213	47.6	4.8	1713	17	US-10-324-967-33	Sequence 33, Appl	1286	47.4	4.8	2181	17	US-10-437-963-102020	Sequence 102020, A
1214	47.6	4.8	1956	15	US-10-156-761-5591	Sequence 5591, Ap	1287	47.4	4.8	2316	15	US-10-156-761-4416	Sequence 4416, Ap
1215	47.6	4.8	1970	16	US-10-425-114-22993	Sequence 22993, A	1288	47.4	4.8	2354	16	US-10-425-114-28070	Sequence 28070, A
1216	47.6	4.8	1971	15	US-10-190-435-49	Sequence 49, Appl	1289	47.4	4.8	2354	18	US-10-425-115-33746	Sequence 33746, A
1217	47.6	4.8	1971	15	US-10-241-009-38	Sequence 38, Appl	1290	47.4	4.8	2354	18	US-10-715-872-155	Sequence 155, App
1218	47.6	4.8	1971	15	US-10-190-434B-38	Sequence 38, Appl	1291	47.4	4.8	2463	16	US-10-282-122A-13810	Sequence 13810, A
1219	47.6	4.8	1971	15	US-10-190-305A-48	Sequence 48, Appl	1292	47.4	4.8	2565	16	US-10-425-114-3437	Sequence 3437, Ap
1220	47.6	4.8	1971	15	US-10-190-305A-54	Sequence 54, Appl	1293	47.4	4.8	2699	17	US-10-425-114-3437	Sequence 1877, Ap
c1221	47.6	4.8	2111	17	US-10-437-963-31473	Sequence 31473, A	1294	47.4	4.8	2883	16	US-10-282-122A-11335	Sequence 11335, A
1222	47.6	4.8	2175	15	US-10-369-493-40571	Sequence 40571, A	1295	47.4	4.8	3629	15	US-10-289-757-9	Sequence 9, Appl
1223	47.6	4.8	2305	15	US-10-387-336-80	Sequence 80, Appl	1296	47.4	4.8	3633	15	US-10-289-757-130	Sequence 130, App
1224	47.6	4.8	2306	15	US-10-387-336-82	Sequence 82, Appl	1297	47.4	4.8	8244	15	US-10-402-842-3	Sequence 3, Appl
1225	47.6	4.8	2337	16	US-10-282-122A-25485	Sequence 25485, A	1298	47.4	4.8	8244	15	US-10-402-842-1	Sequence 1, Appl
1226	47.6	4.8	2424	16	US-10-282-122A-15037	Sequence 15037, A	1299	47.4	4.8	8798	15	US-09-808-880-1	Sequence 1, Appl
1227	47.6	4.8	2457	15	US-10-190-435-44	Sequence 44, Appl	1300	47.4	4.8	50937	10	US-09-808-880-1	Sequence 1, Appl
1228	47.6	4.8	2457	15	US-10-190-305A-38	Sequence 38, Appl	1301	47.4	4.8	50937	10	US-09-808-880-1	Sequence 1, Appl
1229	47.6	4.8	2463	10	US-08-899-575-31	Sequence 31, Appl	1302	47.2	4.8	137560	18	US-10-481-112-1	Sequence 1, Appl
1230	47.6	4.8	2466	15	US-10-241-009-31	Sequence 31, Appl	1303	47.2	4.8	564	17	US-10-437-963-78292	Sequence 78292, A
1231	47.6	4.8	2466	15	US-10-190-434B-31	Sequence 31, Appl	1304	47.2	4.8	619	18	US-10-425-115-183789	Sequence 183789, A
1232	47.6	4.8	2466	15	US-10-190-305A-33	Sequence 33, Appl	1305	47.2	4.8	852	16	US-10-282-122A-11557	Sequence 11557, A
c1233	47.6	4.8	2466	15	US-09-894-998-35	Sequence 35, Appl	1306	47.2	4.8	867	18	US-10-425-115-105816	Sequence 105816, A
c1234	47.6	4.8	2481	14	US-10-121-988-35	Sequence 35, Appl	1307	47.2	4.8	918	15	US-10-156-761-5990	Sequence 5990, Ap
c1235	47.6	4.8	2481	15	US-10-200-562-35	Sequence 35, Appl	1308	47.2	4.8	962	17	US-10-767-701-9413	Sequence 9413, Ap
c1236	47.6	4.8	2481	15	US-10-237-551-35	Sequence 35, Appl	1309	47.2	4.8	1011	18	US-10-425-115-135441	Sequence 135441, A
1237	47.6	4.8	2652	15	US-10-369-493-42921	Sequence 42921, A	1310	47.2	4.8	1014	15	US-10-156-761-5551	Sequence 5551, Ap
c1238	47.6	4.8	3066	14	US-10-121-988-152	Sequence 152, App	1311	47.2	4.8	1014	15	US-10-156-761-4338	Sequence 4338, Ap
c1239	47.6	4.8	3066	15	US-10-200-562-152	Sequence 152, App	1312	47.2	4.8	1134	16	US-10-282-122A-14824	Sequence 14824, A
c1240	47.6	4.8	3066	15	US-10-237-551-152	Sequence 152, App	1313	47.2	4.8	1152	15	US-10-156-761-1776	Sequence 1776, Ap
1241	47.6	4.8	3093	15	US-10-369-493-40513	Sequence 40513, A	1314	47.2	4.8	1200	15	US-10-156-761-4546	Sequence 4546, Ap
1242	47.6	4.8	3783	15	US-10-316-253-96	Sequence 96, Appl	1315	47.2	4.8	1224	17	US-10-437-963-16908	Sequence 16908, A
1243	47.6	4.8	5780	16	US-10-336-472-19	Sequence 19, Appl	1316	47.2	4.8	1237	18	US-10-425-114-14166	Sequence 14166, A
1244	47.6	4.8	5802	14	US-10-152-886-84	Sequence 84, Appl	1317	47.2	4.8	1242	16	US-10-425-115-137466	Sequence 137466, A
1245	47.6	4.8	5886	18	US-10-798-037-3	Sequence 3, Appl	1318	47.2	4.8	1266	15	US-10-156-761-6436	Sequence 6436, Ap
1246	47.6	4.8	6008	16	US-10-336-472-21	Sequence 21, Appl	1319	47.2	4.8	1314	16	US-10-425-115-119307	Sequence 119307, A
1247	47.6	4.8	6008	17	US-10-717-597-197	Sequence 197, App	1320	47.2	4.8	1374	16	US-10-282-122A-11447	Sequence 11447, A
1248	47.6	4.8	10692	15	US-10-156-761-414	Sequence 414, App	1321	47.2	4.8	1382	18	US-10-425-115-120130	Sequence 120130, A
1249	47.6	4.8	12801	18	US-10-798-037-5	Sequence 5, Appl	1322	47.2	4.8	1386	15	US-10-369-493-42300	Sequence 42300, A
c1250	47.6	4.8	2541	17	US-10-203-295-2	Sequence 2, Appl	1323	47.2	4.8	1395	16	US-10-282-122A-14398	Sequence 14398, A
1251	47.4	4.8	349	18	US-10-425-115-40892	Sequence 40892, A	1324	47.2	4.8	1410	16	US-10-282-122A-25555	Sequence 25555, A
c1252	47.4	4.8	414	15	US-10-259-165-779	Sequence 779, App	1325	47.2	4.8	1428	16	US-10-425-114-17352	Sequence 17352, A
1253	47.4	4.8	463	17	US-10-767-701-559	Sequence 559, App	1326	47.2	4.8	1431	15	US-10-156-761-7327	Sequence 7327, Ap
1254	47.4	4.8	497	18	US-10-425-115-51767	Sequence 51767, A	1327	47.2	4.8	1461	17	US-10-437-963-41312	Sequence 41312, A
1255	47.4	4.8	504	16	US-10-260-238-5853	Sequence 5853, Ap	1328	47.2	4.8	1508	18	US-10-425-115-5536	Sequence 5536, Ap
1256	47.4	4.8	601	17	US-10-767-701-4418	Sequence 4418, Ap	1329	47.2	4.8	1532	16	US-10-425-114-33896	Sequence 33896, A
1257	47.4	4.8	670	15	US-10-132-350-29	Sequence 29, Appl	1330	47.2	4.8	1532	17	US-10-437-963-66895	Sequence 66895, A

1331	47.2	4.8	1616	16	US-10-264-049-889	Sequence 889, App	1404	47	4.8	1713	15	US-10-156-761-2661	Sequence 2661, Ap
1332	47.2	4.8	1633	17	US-10-437-963-47476	Sequence 47476, A	c1405	47	4.8	1714	18	US-10-739-930-1853	Sequence 1853, Ap
1333	47.2	4.8	1680	10	US-09-899-575-76	Sequence 76, Appl	c1406	47	4.8	1791	17	US-10-437-963-41437	Sequence 41437, A
1334	47.2	4.8	1737	15	US-10-029-386-25063	Sequence 25063, A	1407	47	4.8	1881	17	US-10-437-963-61846	Sequence 61846, A
c1335	47.2	4.8	1738	15	US-10-029-386-25470	Sequence 25470, A	1408	47	4.8	1968	16	US-10-282-122A-11496	Sequence 11496, A
1336	47.2	4.8	1758	16	US-10-425-114-16348	Sequence 16348, A	1409	47	4.8	2013	15	US-10-156-761-1281	Sequence 1281, Ap
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c1339	47.2	4.8	1977	10	US-09-899-575-70	Sequence 70, Appl	1412	47	4.8	2890	16	US-10-425-114-32060	Sequence 32060, A
1340	47.2	4.8	1977	15	US-10-241-009-41	Sequence 41, Appl	c1413	47	4.8	3281	18	US-10-425-115-128924	Sequence 128924, A
1341	47.2	4.8	1977	15	US-10-190-305A-51	Sequence 51, Appl	c1414	47	4.8	80161	16	US-10-329-148A-1	Sequence 1, Appli
1342	47.2	4.8	1977	15	US-10-241-009-47	Sequence 47, Appl	c1415	47	4.8	85692	16	US-10-461-194-1	Sequence 1, Appli
1343	47.2	4.8	1989	15	US-10-190-305A-47	Sequence 47, Appl	1416	46.8	4.7	236	15	US-10-174-693-195	Sequence 195, App
1344	47.2	4.8	1989	15	US-10-190-305A-47	Sequence 47, Appl	1417	46.8	4.7	469	17	US-10-767-701-29716	Sequence 29716, A
1345	47.2	4.8	1989	15	US-10-190-305A-47	Sequence 47, Appl	1418	46.8	4.7	514	9	US-09-833-381-1970	Sequence 1970, Ap
c1346	47.2	4.8	2052	15	US-10-156-761-4847	Sequence 4847, Ap	1419	46.8	4.7	527	18	US-10-425-115-97681	Sequence 97681, A
1347	47.2	4.8	2145	15	US-10-241-009-35	Sequence 35, Appl	c1420	46.8	4.7	528	17	US-10-437-963-18519	Sequence 18519, A
1348	47.2	4.8	2145	15	US-10-190-305A-35	Sequence 35, Appl	1421	46.8	4.7	584	17	US-10-437-963-76371	Sequence 76371, A
1349	47.2	4.8	2145	15	US-10-190-305A-43	Sequence 43, Appl	c1422	46.8	4.7	588	17	US-10-767-701-2473	Sequence 2473, Ap
1350	47.2	4.8	2156	17	US-10-437-963-614	Sequence 614, App	1423	46.8	4.7	588	17	US-10-767-701-29714	Sequence 29714, A
1351	47.2	4.8	2312	15	US-10-387-336-84	Sequence 84, Appl	1424	46.8	4.7	642	17	US-10-437-963-7127	Sequence 7127, Ap
1352	47.2	4.8	2472	15	US-10-241-009-32	Sequence 32, Appl	c1425	46.8	4.7	663	16	US-10-389-647-191	Sequence 191, App
1353	47.2	4.8	2472	15	US-10-190-305A-32	Sequence 32, Appl	1426	46.8	4.7	758	9	US-09-938-842A-812	Sequence 812, App
1354	47.2	4.8	2472	15	US-10-190-305A-34	Sequence 34, Appl	1427	46.8	4.7	801	11	US-09-894-273-3	Sequence 3, Appli
1355	47.2	4.8	2472	15	US-10-437-963-82289	Sequence 82289, A	1428	46.8	4.7	984	16	US-10-425-114-14294	Sequence 14294, A
1356	47.2	4.8	2653	18	US-10-425-115-59271	Sequence 59271, A	1429	46.8	4.7	984	16	US-10-282-122A-25620	Sequence 25620, A
1357	47.2	4.8	2691	16	US-09-934-070-9	Sequence 9, Appli	1430	46.8	4.7	1139	16	US-10-425-114-33569	Sequence 33569, A
1358	47.2	4.8	2691	16	US-10-222-772-9	Sequence 9, Appli	1431	46.8	4.7	1269	18	US-10-425-115-100962	Sequence 100962, A
1359	47.2	4.8	2706	16	US-10-416-793-1	Sequence 1, Appli	1432	46.8	4.7	1345	16	US-10-425-115-93858	Sequence 93858, A
c1360	47.2	4.8	2751	16	US-10-282-122A-26039	Sequence 26039, A	c1433	46.8	4.7	1345	16	US-10-425-115-93858	Sequence 93858, A
1361	47.2	4.8	2898	9	US-09-737-149-3	Sequence 3, Appli	1434	46.8	4.7	1375	16	US-10-425-114-2375	Sequence 2375, A
1362	47.2	4.8	2898	9	US-09-737-149-5	Sequence 5, Appli	1435	46.8	4.7	1413	18	US-10-425-115-135998	Sequence 135998, A
1363	47.2	4.8	2916	16	US-10-701-283-5	Sequence 5, Appli	c1436	46.8	4.7	1464	16	US-10-282-122A-28163	Sequence 28163, A
1364	47.2	4.8	3015	10	US-09-899-575-62	Sequence 62, Appl	1437	46.8	4.7	1695	17	US-10-437-963-51411	Sequence 51411, A
1365	47.2	4.8	3015	15	US-10-190-305A-44	Sequence 44, Appl	c1438	46.8	4.7	1735	17	US-10-437-963-32738	Sequence 32738, A
1366	47.2	4.8	3096	10	US-09-934-070-5	Sequence 5, Appli	c1439	46.8	4.7	1735	17	US-10-437-963-85706	Sequence 85706, A
1367	47.2	4.8	3096	16	US-10-222-772-51	Sequence 51, Appl	1440	46.8	4.7	1773	17	US-10-437-963-90868	Sequence 90868, A
1368	47.2	4.8	3097	16	US-10-222-772-61	Sequence 61, Appl	1441	46.8	4.7	1819	17	US-10-437-963-90823	Sequence 90823, A
1369	47.2	4.8	3132	9	US-09-737-149-7	Sequence 7, Appli	1442	46.8	4.7	2034	15	US-10-369-493-31439	Sequence 31439, A
1370	47.2	4.8	3132	16	US-10-701-283-7	Sequence 7, Appli	1443	46.8	4.7	2151	16	US-10-425-114-24961	Sequence 24961, A
1371	47.2	4.8	3639	15	US-10-241-009-33	Sequence 33, Appl	1444	46.8	4.7	2226	15	US-10-156-761-5313	Sequence 5313, Ap
1372	47.2	4.8	3639	15	US-10-190-434B-33	Sequence 33, Appl	1445	46.8	4.7	2274	15	US-10-369-493-47118	Sequence 47118, A
1373	47.2	4.8	3639	15	US-10-190-434B-33	Sequence 33, Appl	1446	46.8	4.7	2739	16	US-10-282-122A-25536	Sequence 25536, A
1374	47.2	4.8	3639	15	US-10-190-305A-33	Sequence 33, Appl	1447	46.8	4.7	3240	17	US-10-437-963-3533	Sequence 3533, Ap
1375	47.2	4.8	3955	16	US-10-108-260A-804	Sequence 804, App	1448	46.8	4.7	3972	15	US-10-156-761-5427	Sequence 5427, Ap
1376	47.2	4.8	4319	15	US-10-387-336-6	Sequence 6, Appli	1449	46.8	4.7	4176	13	US-10-098-841-34	Sequence 34, Appl
1377	47.2	4.8	4319	9	US-09-861-289-32	Sequence 32, Appl	1450	46.8	4.7	5862	15	US-10-132-134-15	Sequence 15, Appl
1378	47.2	4.8	4319	9	US-09-860-846-32	Sequence 32, Appl	1451	46.8	4.7	5862	15	US-10-282-122A-25487	Sequence 25487, A
1379	47.2	4.8	4319	10	US-09-988-384B-32	Sequence 32, Appl	1452	46.8	4.7	10232	16	US-09-968-007A-215	Sequence 215, App
1380	47.2	4.8	4319	10	US-09-836-821-32	Sequence 32, Appl	1453	46.8	4.7	25000	11	US-10-437-963-204	Sequence 204, App
1381	47.2	4.8	4319	10	US-09-836-821-32	Sequence 32, Appl	1454	46.6	4.7	462	17	US-10-425-115-7683	Sequence 7683, Ap
1382	47.2	4.8	30000	12	US-09-980-217-1	Sequence 1, Appli	1458	46.6	4.7	487	18	US-10-437-963-90008	Sequence 90008, A
1383	47.2	4.8	450	18	US-10-425-115-95875	Sequence 95875, A	c1459	46.6	4.7	507	17	US-10-437-963-90008	Sequence 24524, A
1384	47.2	4.8	536	16	US-10-338-110-119	Sequence 119, App	c1460	46.6	4.7	575	17	US-10-767-701-24524	Sequence 25903, A
c1385	47.2	4.8	546	18	US-10-425-115-77636	Sequence 77636, A	1461	46.6	4.7	723	16	US-10-282-122A-25903	Sequence 43424, A
1386	47.2	4.8	552	17	US-10-437-963-58537	Sequence 58537, A	1462	46.6	4.7	762	15	US-10-369-493-43242	Sequence 82140, A
1387	47.2	4.8	647	16	US-10-425-114-16774	Sequence 16774, A	c1463	46.6	4.7	763	17	US-10-437-963-82140	Sequence 2207, Ap
c1388	47.2	4.8	660	17	US-10-767-701-9246	Sequence 9246, Ap	1464	46.6	4.7	765	15	US-10-156-761-2207	Sequence 2330, Ap
1389	47.2	4.8	675	16	US-10-282-122A-14648	Sequence 14648, A	1465	46.6	4.7	801	15	US-10-156-761-2530	Sequence 119601, A
c1390	47.2	4.8	703	13	US-10-027-633-174146	Sequence 174146, A	c1466	46.6	4.7	848	18	US-10-425-115-119601	Sequence 2069, Ap
c1391	47.2	4.8	703	15	US-10-027-633-174146	Sequence 174146, A	1467	46.6	4.7	981	15	US-10-156-761-2069	Sequence 3202, Ap
1392	47.2	4.8	758	9	US-09-902-331-5	Sequence 5, Appli	c1468	46.6	4.7	1032	16	US-10-354-437-17	Sequence 17, Appl
1393	47.2	4.8	799	18	US-10-425-115-40891	Sequence 40891, A	1469	46.6	4.7	1287	15	US-10-282-122A-25956	Sequence 25956, A
1394	47.2	4.8	851	18	US-10-425-115-38550	Sequence 38550, A	1470	46.6	4.7	1287	15	US-10-156-761-3398	Sequence 3398, Ap
1395	47.2	4.8	930	9	US-09-960-631A-4	Sequence 4, Appli	1471	46.6	4.7	1287	15	US-10-156-761-3398	Sequence 9, Appli
1396	47.2	4.8	942	15	US-10-156-761-1702	Sequence 1702, Ap	1472	46.6	4.7	1299	14	US-10-145-415-9	Sequence 11203, A
1397	47.2	4.8	1001	18	US-10-425-115-54065	Sequence 54065, A	1473	46.6	4.7	1347	17	US-10-767-701-11203	Sequence 36, Appl
1398	47.2	4.8	1120	16	US-10-294-445-22	Sequence 22, Appl	1474	46.6	4.7	1476	15	US-10-187-267A-36	Sequence 42144, A
1399	47.2	4.8	1245	15	US-10-156-761-2391	Sequence 2391, Ap	c1475	46.6	4.7	1476	17	US-10-437-963-88833	Sequence 88833, A
1400	47.2	4.8	1293	15	US-10-107-431-46	Sequence 46, Appl	c1476	46.6	4.7	1488	17	US-10-437-963-3944	Sequence 3944, Ap
1401	47.2	4.8	1354	16	US-10-264-049-523	Sequence 523, App	1477	46.6	4.7	1503	18	US-10-739-930-2932	Sequence 2932, Ap
1402	47.2	4.8	1506	16	US-10-282-122A-15096	Sequence 15096, A	c1478	46.6	4.7	1524	18	US-10-739-930-2932	Sequence 5960, Ap
1403	47.2	4.8	17361	18	US-10-425-115-168526	Sequence 168526, A	c1479	46.6	4.7	1602	15	US-10-156-761-5960	Sequence 5960, Ap

1480	46.6	4.7	1561	16	US-10-425-114-929	Sequence 929, App
1481	46.6	4.7	1561	18	US-10-425-115-175072	Sequence 175072, A
1482	46.6	4.7	1740	16	US-10-425-114-21361	Sequence 21361, A
c1483	46.6	4.7	1742	17	US-10-437-963-38960	Sequence 38960, A
1484	46.6	4.7	1837	18	US-10-425-115-23782	Sequence 23782, A
c1485	46.6	4.7	1855	17	US-10-437-963-78779	Sequence 78779, A
1486	46.6	4.7	1866	15	US-10-156-761-4468	Sequence 4468, Ap
1487	46.6	4.7	1967	17	US-10-437-963-30977	Sequence 30977, A
1488	46.6	4.7	1992	15	US-10-156-761-7241	Sequence 7241, Ap
c1489	46.6	4.7	2500	15	US-10-190-312A-66	Sequence 66, Appl
1490	46.6	4.7	2909	16	US-10-425-114-30367	Sequence 30367, A
c1491	46.6	4.7	3285	15	US-10-228-063-46	Sequence 46, Appl
1492	46.6	4.7	3509	18	US-10-425-115-136015	Sequence 136015, A
1493	46.6	4.7	3723	17	US-10-437-963-3749	Sequence 3749, Ap
1494	46.6	4.7	3876	17	US-10-437-963-61988	Sequence 61988, A
1495	46.6	4.7	3963	16	US-10-282-122A-14119	Sequence 14319, A
1496	46.6	4.7	5721	15	US-10-156-761-2880	Sequence 2880, Ap
1497	46.6	4.7	5811	14	US-10-152-886-2	Sequence 2, Appli
1498	46.6	4.7	9495	18	US-10-669-161-71	Sequence 71, Appl
1499	46.6	4.7	14800	9	US-09-954-456-1601	Sequence 1601, Ap
1500	46.6	4.7	14800	15	US-10-269-909-61	Sequence 61, Appl

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Run on: January 12, 2005, 14:48:22 ; Search time 4197 Seconds
(without alignments)
11143.558 Million cell updates/sec

Title: US-10-017-407A-305

Perfect score: 989

Sequence: 1 gcgggcccgcagtcgcgaga.....caaaaaaaaaaaaaaaaaaaaaa 989

Scoring table:

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Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

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Post-processing: Minimum Match 0%

Maximum Match 100%

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Database :

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4: gb_om.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pl.*

9: gb_pr.*

10: gb_ro.*

11: gb_ats.*

12: gb_sy.*

13: gb_un.*

14: gb_vl.*

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SUMMARIES

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1	989	100.0	989	6	AX201342 Sequence
2	989	100.0	989	6	AX697237 Sequence
3	989	100.0	989	9	AX358476 Homo sapi
4	985.8	99.7	1037	6	AX338454 Sequence
5	985.8	99.7	1041	9	BC047774 Homo sapi
6	981.8	99.3	985	6	BD222712 Homo sapi
7	938.2	94.9	988	9	AK074421 Human sig
8	907.8	91.8	913	9	BC023663 Homo sapi
9	789	79.8	789	6	CQ721501 Homo sapi
10	789	79.8	789	6	AX338456 Sequence
11	625	63.2	946	10	BC049670 Mus muscu
12	312	31.5	326	6	AX407985 Sequence
13	309.2	31.3	237829	2	AL120475 Rattus no
14	256.8	26.0	38679	9	AL390034 Human DNA
15	256.8	26.0	169612	2	AC027393 Homo sapi
16	224.6	22.7	157428	10	AL606832 Mouse DNA
17	224.6	22.7	209643	10	AC080018 Mus muscu
18	200	20.2	14100	1	U24657 Myxococcus
19	194.8	19.7	11171	6	CQ801141 Sequence

20	193.8	19.6	675	6	CQ801150	Sequence
21	188.8	19.1	10840	1	AE004550	Pseudomon
22	185.8	18.8	2381	1	STMDMBC	M93958 Streptomyce
23	185.8	18.8	2381	6	E06690	E06690 DNA encodin
24	185.4	18.7	304282	1	AE016910	Chromobac
25	185	18.7	663	12	AY657514	AY657514 Synthetic
26	182.4	18.4	69644	1	AY179507	AY179507 Streptomy
27	161.8	16.4	953	6	AR236716	Sequence
28	161.8	16.4	953	8	BT009394	Triticum
29	159.6	16.1	976	8	AB110168	Oryza sat
30	159.6	16.1	996	8	AK104326	Oryza sat
31	159.6	16.1	1096	8	AK104801	Oryza sat
32	159.6	16.1	1098	8	AK071482	Oryza sat
33	159.2	16.1	1049	6	AR236715	Sequence
34	158.6	16.0	997	6	AR236700	Sequence
35	158.6	16.0	1338	6	AX654529	Sequence
36	157.2	15.9	1078	6	AR236714	Sequence
37	157.2	15.9	1078	8	BT009389	Triticum
38	155.6	15.7	1018	6	AR236711	Sequence
39	154	15.6	891	6	AR236694	Sequence
40	154	15.6	1167	8	ZMA242981	Zea mays
41	153	15.5	77534	1	AF235504	Streptomy
42	153	15.5	77536	6	BD235937	BD235937 Polyketid
43	153	15.5	77536	6	AR271638	Sequence
44	152.8	15.4	1112	6	AX660732	Sequence
45	152.4	15.4	1218	6	AX146637	Sequence
46	151.4	15.3	82746	1	AF453501	AF453501 Actinosyn
47	150.2	15.2	1158	8	AY644637	Oryza sat
48	150.2	15.2	1895	8	AK106735	Oryza sat
49	150.2	15.2	137354	8	AP000364	Oryza sat
50	148	15.0	798	6	AX660925	Sequence
51	148	15.0	1118	6	AR236712	Sequence
52	148	15.0	1118	8	BT009186	Triticum
53	148	15.0	1136	8	ZMA242980	Zea mays
54	148	15.0	1146	6	AR236695	Sequence
55	146.8	14.8	10882	1	AE002493	Neisseria
56	146.8	14.8	34980	6	AX044032	Sequence
57	146.2	14.8	875	8	AB158406	Triticum
58	146.2	14.8	1018	8	BT009093	Triticum
59	145	14.7	959	8	AK108479	Oryza sat
60	144.6	14.6	329861	1	NMA522491	Neisseria
61	144.4	14.6	1057	6	AR236696	Sequence
62	143.6	14.5	1052	8	AK065744	Oryza sat
63	141.8	14.3	783	6	AX654528	Sequence
64	141.8	14.3	1149	8	AK061757	Oryza sat
65	140.6	14.2	1058	6	AR236699	Sequence
66	140	14.2	783	6	AX654276	Sequence
67	137	13.9	1116	8	AX644638	Oryza sat
68	129.6	13.1	1466	8	AK065515	Sequence
69	128.2	13.0	237221	1	AP003599	Nostoc sp
70	127.4	12.9	651	6	AX196012	Sequence
71	127.4	12.9	109519	6	AX195929	Sequence
72	126	12.7	923	6	AR236697	Sequence
73	125.4	12.7	835	6	AX660084	Sequence
74	123.2	12.5	300465	1	AE016962	Sequence
75	122.8	12.4	1810	6	E09625	AE016962 Coxiiella
76	122.8	12.4	3267	1	STMACYA	D30759 Streptomyce
77	118.6	12.0	201	11	BV202015	BV202015 sqm20798
78	118.6	12.0	89888	2	AY294423	Continuation (4 of
79	118.6	12.0	161371	10	AC132590	AC132590 Mus muscu
80	116.8	11.8	188267	2	AC137230	AC137230 Rattus no
81	116.8	11.8	228354	2	AC137429	AC137429 Rattus no
82	116.8	11.8	266634	2	AC123487	AC123487 Rattus no
83	110	11.1	1013	8	AF168780	AF168780 Eucalyptu
84	110	11.1	1944	1	AF145250	AF145250 Rhodother
85	109.8	11.1	1006	8	AF045122	AF045122 Eucalyptu
86	109.8	11.1	1068	8	EG12228	EG12228 E.gunnii mR
87	109.6	11.1	110000	2	AC105718	Continuation (4 of
88	107.8	10.9	486	8	AY651026	AY651026 Boehmeria
89	107.4	10.9	304282	1	AE016910	AE016910 Chromobac
90	106.2	10.7	976	8	VVCCOAMT	Z54233 V.vinifera
91	103.6	10.5	343	6	AX400599	AX400599 Sequence
92	102	10.3	134199	1	SYCSLRF	D64004 Synechocyst

c	93	101.4	10.3	300425	1	AP005044	Streptomy	166	82.2	8.3	105815	8	AP002536	AP002536	Oryza sat
	94	99.4	10.1	300800	1	SV0939112	Streptomy	167	82.2	8.3	156054	8	AB023482	AB023482	Oryza sat
	95	98.4	9.9	772	8	FWJ1447	Fragaria	168	81	8.2	622	8	AB076979	AB076979	Avena sat
	96	98.4	9.9	1012	6	B224370	Materials	169	79.6	8.0	1258	6	A22706	A22706	Caffeoyl-Co
	97	96.8	9.8	1012	6	B224370	Materials	170	79.2	8.0	1258	6	A22706	A22706	Caffeoyl-Co
	98	96.8	9.8	1012	6	AR216420	Sequence	171	78	7.9	1098	8	AY128822	AY128822	Arabidops
	99	96.8	9.8	1026	6	AR432822	Sequence	172	78	7.9	1185	8	AY087981	AY087981	Arabidops
	100	96.8	9.8	1026	6	AR074097	Sequence	173	78	7.9	1201	8	AY093172	AY093172	Arabidops
	101	96.8	9.8	1026	6	AR143609	Sequence	174	77.4	7.8	837	8	AY094008	AY094008	Arabidops
	102	96.8	9.8	1026	6	AR143609	Sequence	175	77.4	7.8	837	8	AY094008	AY094008	Arabidops
	103	96.8	9.8	1026	6	BD224282	Materials	176	76.2	7.7	760	6	AR074116	AR074116	Sequence
	104	96.8	9.8	1026	6	AR432734	Sequence	177	76.2	7.7	760	6	BD224301	BD224301	Materials
	105	96.8	9.8	1026	6	BD005645	Materials	178	76.2	7.7	760	6	BD224301	BD224301	Materials
	106	96.8	9.8	1172	8	AV279007	Zea mays	179	76.2	7.7	760	6	AR432753	AR432753	Sequence
	107	96.4	9.7	1136	8	AV279011	Zea mays	180	76.2	7.7	760	6	BD005664	BD005664	Materials
	108	96.4	9.7	1145	8	AV279031	Zea mays	181	76.2	7.7	760	6	BD005664	BD005664	Materials
	109	96.4	9.7	1150	8	AV279012	Zea mays	182	75.8	7.7	1046	8	PTU27116	PTU27116	Populus tre
	110	96.4	9.7	1150	8	AV279013	Zea mays	183	74.8	7.6	816	8	AF022775	AF022775	Nicotiana
	111	96.4	9.7	1150	8	AV279030	Zea mays	184	74.4	7.5	929	6	AR236703	AR236703	Sequence
	112	96.4	9.7	1150	8	AV279033	Zea mays	185	74.4	7.5	1104	8	AF053553	AF053553	Mesembrya
	113	96.4	9.7	1150	8	AV279035	Zea mays	186	74.2	7.5	726	8	AF240466	AF240466	Populus t
	114	95.2	9.6	1172	8	AV279006	Zea mays	187	73.8	7.5	920	4	AY340812	AY340812	Canis fam
	115	95.2	9.6	1172	8	AV279006	Zea mays	188	73.8	7.5	1834	8	AK105550	AK105550	Oryza sat
	116	95.2	9.6	1172	8	AV279025	Zea mays	189	73.8	7.5	2768	8	AK105550	AK105550	Oryza sat
	117	95.2	9.6	1180	8	AV279027	Sequence	c 190	73.8	7.5	170021	8	AF003256	AF003256	Oryza sat
	118	95.2	9.6	1182	8	AV279009	Zea mays	c 191	73.8	7.5	176261	8	AF003274	AF003274	Oryza sat
	119	95.2	9.6	1438	8	AV279021	Zea mays	c 192	73.4	7.4	145828	8	AF005392	AF005392	Oryza sat
	120	95.2	9.6	1442	8	AV279019	Zea mays	c 193	73.4	7.4	154188	8	AP005633	AP005633	Oryza sat
	121	95.2	9.6	1444	8	AV279017	Zea mays	c 194	73.2	7.4	870	6	AR225246	AR225246	Sequence
	122	95.2	9.6	1445	8	AV279018	Zea mays	195	72.8	7.4	706	8	PBA110841	PBA110841	Populus b
	123	95.2	9.6	1445	8	AV279022	Zea mays	196	72.6	7.3	1213	9	BC011935	BC011935	Homo sapi
	124	95.2	9.6	1451	8	AV279004	Zea mays	c 197	71.8	7.3	280558	1	AE017301	AE017301	Thermus t
	125	95.2	9.6	1451	8	AV279020	Zea mays	c 198	71.6	7.2	744	8	AF327458	AF327458	Populus a
	126	95.2	9.6	1464	8	AV279016	Zea mays	c 199	71.2	7.2	601	11	BV167609	BV167609	sgnm6022
	127	95.2	9.6	1464	8	AV279016	Zea mays	c 200	71.2	7.2	2084	11	BV177509	BV177509	sgnm95100
	128	94.6	9.6	1152	8	AV279023	Zea mays	c 201	71.2	7.2	2084	11	BV177509	BV177509	sgnm95100
	129	94.6	9.6	1152	8	AV279032	Zea mays	c 202	71	7.2	816	9	CR456997	CR456997	Homo sapi
	130	93.4	9.4	675	6	AR390021	Sequence	c 203	71	7.2	1025	8	PBTJ4894	PBTJ4894	Populus b
	131	93	9.4	1136	8	AV279034	Zea mays	c 204	71	7.2	1107	6	CO812330	CO812330	Sequence
	132	93	9.4	1181	8	AV279005	Zea mays	c 205	71	7.2	1107	6	HUMCOMTA	HUMCOMTA	Homo sapien
	133	93	9.4	1181	8	AV279005	Zea mays	c 206	71	7.2	1291	6	CO716680	CO716680	Sequence
	134	93	9.4	1181	8	AV279024	Zea mays	c 207	70.6	7.1	918	8	ZEU13151	ZEU13151	Zinnia eleg
	135	93	9.4	1181	8	AV279026	Zea mays	c 208	70.6	7.1	2084	11	BV177077	BV177077	Rattus no
	136	93	9.4	1206	8	AV279008	Zea mays	c 209	70.4	7.1	189038	2	AC120323	AC120323	Sequence
	137	93	9.4	1209	8	AV279028	Zea mays	c 210	70	7.1	811	6	AR225247	AR225247	Sequence
	138	93	9.4	1222	8	AV279029	Zea mays	c 211	69.8	7.1	5222	1	DRU52145	DRU52145	Deinococcus
	139	93	9.4	1232	8	AF036095	Pinus tae	c 212	69.6	7.0	60090	1	U30252	U30252	Synechococc
	140	93	9.4	1434	8	AV279014	Zea mays	c 213	69.4	7.0	873	9	CR456422	CR456422	Homo sapi
	141	93	9.4	1434	8	AV279014	Zea mays	c 214	69.4	7.0	1206	6	AX774876	AX774876	Sequence
	142	88	8.9	931	6	AR236702	Sequence	c 215	69.4	7.0	1206	6	HUMCOMTC	HUMCOMTC	Homo sapien
	143	87.8	8.9	534	6	AR236717	Sequence	c 216	69.2	7.0	297850	1	AP006577	AP006577	Gloeobact
	144	87.4	8.8	1210	8	AK063541	Oryza sat	c 217	68	6.9	976	11	PM12D6G	PM12D6G	Penicill
	145	87.2	8.8	2955	1	AF075724	Legionell	c 218	67.8	6.9	1217	9	BC000419	BC000419	Homo sapi
	146	86.2	8.7	347660	1	AP002994	Mesorhizo	c 219	67.8	6.9	1217	9	BC005867	BC005867	Homo sapi
	147	85.6	8.7	962	6	AR236705	Sequence	c 220	67.6	6.9	239130	2	AC079420	AC079420	Mus muscu
	148	85.6	8.7	1023	6	AR236706	Sequence	c 221	67.6	6.8	930	8	AB000408	AB000408	Populus k
	149	85.4	8.6	6020	8	AY098515	Ananas co	c 222	67.4	6.8	890	8	AY145521	AY145521	Mesembrya
	150	85.4	8.6	125020	9	AF429315	Homo sapi	c 223	67.4	6.8	12454	1	AE002019	AE002019	Deinococc
	151	84.4	8.5	939	8	PBTJ4896	Populus b	c 224	67.2	6.8	132151	8	AC144491	AC144491	Oryza sat
	152	84.4	8.5	963	8	AY620245	Amni mabu	c 225	67.2	6.8	160738	8	AC073556	AC073556	Oryza sat
	153	84.4	8.5	1049	8	PBTJ4895	Populus b	c 226	67	6.8	110000	2	LMFLCHR32_06	LMFLCHR32_06	Coffea ca
	154	84	8.5	780	6	CO804646	Sequence	c 227	67	6.8	110000	2	LMFLCHR32_06	LMFLCHR32_06	Continuation (7 of
	155	84	8.5	780	6	CO805684	Sequence	c 228	67	6.8	110000	2	LMFLCHR32_06	LMFLCHR32_06	Continuation (7 of
	156	84	8.5	780	8	AY143979	Arabidops	c 229	67	6.8	152525	2	AC022045	AC022045	Homo sapi
	157	84	8.5	815	8	AY081457	Arabidops	c 230	66.8	6.8	1023	8	AB061268	AB061268	Solanum t
	158	84	8.5	999	8	AY062630	Arabidops	c 231	66.8	6.8	1074	6	AB074145	AB074145	Sequence
	159	84	8.5	1026	8	AY057554	Arabidops	c 232	66.8	6.8	1074	6	BD224330	BD224330	Materials
	160	83.6	8.5	1033	8	AY088577	Arabidops	c 233	66.8	6.8	1074	6	AR216380	AR216380	Sequence
	161	82.8	8.4	1258	6	AY122016	Sequence 1	c 234	66.8	6.8	1074	6	AR432782	AR432782	Sequence
	162	82.8	8.4	1258	6	I92681	Sequence 1	c 235	66.8	6.8	1074	6	BD005693	BD005693	Materials
	163	82.8	8.4	1258	6	M69184	Petroselinu	c 236	66.8	6.8	1075	6	AR074146	AR074146	Sequence
	164	82.6	8.4	125020	9	AF429315	Homo sapi	c 237	66.8	6.8	1075	6	BD224331	BD224331	Materials
	165	82.2	8.3	1272	8	AY644636	Oryza sat	c 238	66.8	6.8	1075	6	BD224331	BD224331	Materials

239	66.8	6.8	1075	6	AR216381	Sequence	312	60.8	6.1	1578	6	A38265	A38265 Sequence 1
240	66.8	6.8	1075	6	AR432783	Sequence	313	60.8	6.1	1578	6	AR001081	AR001081 Sequence
241	66.8	6.8	1075	6	BD005694	Materials	c 314	60.8	6.1	2357	14	AY363172	AY363172 Pseudorab
242	66.8	6.8	33950	1	SC0939108	Streptomy	315	60.8	6.1	2510	14	SH1UL2XA	M95285 Suid herpes
243	66.6	6.7	13533	1	AF257324	Streptomy	c 316	60.8	6.1	9382	14	SH1ULGNS	L00676 Pseudorabie
244	66.4	6.7	744	6	C0760958	Sequence	c 317	60.8	6.1	300316	8	AE016894	AE016894 Eremothec
245	66.4	6.7	744	6	AX259371	Sequence	c 318	60.6	6.1	917	8	AY087244	AY087244 Arabidops
246	66.4	6.7	966	8	MS020736	U20736 Medicago sa	319	60.6	6.1	7413	1	PAAPRAPG	X64558 Pseudomonas
247	66.4	6.7	1906	6	C0760964	Sequence	320	60.6	6.1	11588	1	AE004554	AE004554 Pseudomon
248	66.4	6.7	8600	2	AC136951	Leighmani	c 321	60.6	6.1	201050	1	AL646064	AL646064 Ralstonia
249	66.4	6.7	346301	1	BX640432	Bordetell	322	60.6	6.1	298550	1	AP005029	AP005029 Streptomy
250	66.4	6.7	348642	1	BX640446	Bordetell	323	60.6	6.1	301068	1	AE017231	AE017231 Mycobacte
251	66.2	6.7	912	6	AR236707	Sequence	c 324	60.4	6.1	1094	11	FM7G11B	AL685196 Penicilli
252	66	6.7	300425	1	AP005041	Streptomy	325	60.4	6.1	10445	1	AE014716	AE014716 Bifidobac
253	66	6.7	300800	1	SC0939112	Streptomy	c 326	60.4	6.1	25883	1	AB008466	AB008466 Streptomy
254	65.8	6.7	6375	1	AY632768	AY632768 Mycobacte	c 327	60.4	6.1	136753	2	AC149968	AC149968 Strongylo
255	65.4	6.6	101	11	BV185588	sqm14856	328	60.4	6.1	349980	6	AX533951	AX533951 Sequence
256	64.8	6.6	908	8	AY500159	AY500159 Corchorus	329	60.4	6.1	34980	6	AX533951	AX533951 Sequence
257	64.8	6.6	967	6	AR225249	Sequence	330	60.2	6.1	1007	11	FM3H11G	AL685749 Penicilli
258	64.8	6.6	283100	1	SC0939110	Streptomy	331	60.2	6.1	1062	6	BD180422	BD180422 Highly th
259	64.6	6.5	2832	8	AY452532	AY452532 Chlamydom	c 332	60.2	6.1	3797	14	PVULSGENE	X87247 Pseudorabie
260	64.6	6.5	110000	2	LMFLCHR36_07	Continuation (8 of	333	60.2	6.1	6653	1	AY162971	AY162971 Micromono
261	64.6	6.5	311000	1	SC0939122	Streptomy	334	60.2	6.1	211161	2	AC098271	AC098271 Rattus no
262	64.4	6.5	143	6	AX899499	Sequence	335	60	6.1	729	6	AX507705	AX507705 Sequence
263	64.4	6.5	143	6	BD035032	Sequence	336	60	6.1	730	8	AY056313	AY056313 Arabidops
264	64.2	6.5	600	6	AR236713	Sequence	337	60	6.1	956	8	AF360317	AF360317 Arabidops
265	64.2	6.5	346362	1	BX640439	BX640439 Bordetell	c 338	60	6.1	982	6	AR236709	AR236709 Sequence
266	64.2	6.5	346362	1	BX640439	BX640439 Bordetell	c 339	60	6.1	1065	11	PM2B12B	AL684695 Penicilli
267	64	6.5	954	8	AK073585	Oryza sat	340	60	6.1	1227	8	NT282982	Z82982 Nicotina ta
268	64	6.5	1543	8	AK058441	AK058441 Oryza sat	c 341	60	6.1	1279	11	PM2H12G	AL684840 Penicilli
269	64	6.5	85130	2	AC074054	AC074054 Oryza sat	342	60	6.1	123019	9	AC111006	AC111006 Homo sapi
270	64	6.5	135876	8	AC113337	AC113337 Genomic s	c 343	60	6.1	277000	1	SC0939109	AL939109 Streptomy
271	64	6.5	145510	8	AC074355	AC074355 Oryza sat	344	59.8	6.0	1242	6	BD180349	BD180349 Streptomy
272	64	6.5	181419	2	AC148515	AC148515 Sus scrof	345	59.6	6.0	399	6	BD224470	BD224470 Materiale
273	64	6.5	299886	1	AE017240	AE017240 Mycobacte	346	59.6	6.0	399	6	AR216520	AR216520 Sequence
274	64	6.5	305096	8	AE017062	AE017062 Oryza sat	c 347	59.6	6.0	956	11	PM2B12B	AL684743 Penicilli
275	63.8	6.4	12541	1	AE001956	AE001956 Deinococc	348	59.6	6.0	1980	14	AC2NKR24	M18041 Avian trans
276	63.6	6.4	510	6	AR236698	Sequence	349	59.6	6.0	2253	5	GDQFOS	M37000 Chicken c-f
277	63.6	6.4	1279	11	PM2H12G	PM2H12G	c 350	59.6	6.0	2253	5	GDQFOS	Y00659 Chicken fos
278	63.6	6.4	2039	9	AK130031	AK130031 Homo sapi	351	59.6	6.0	7185	6	AX803764	AX803764 Sequence
279	63.4	6.4	296300	1	AP005035	AP005035 Streptomy	c 352	59.6	6.0	48177	7	AY369265	AY369265 Burkholde
280	63.2	6.4	1016	8	NTCCOAMT	Z58282 N.tabacum m	c 353	59.6	6.0	61944	6	AX803750	AX803750 Sequence
281	63.2	6.4	1065	11	PM2B12B	AL684695 Penicilli	c 354	59.6	6.0	110000	1	AE016822_23	Continuation (24 o
282	63.2	6.4	136753	2	AC149968	AC149968 Strongylo	c 355	59.6	6.0	110000	1	AE016822_24	Continuation (25 o
283	63.2	6.4	299425	1	AP005037	AP005037 Streptomy	c 356	59.6	6.0	283100	1	SC0939110	AL939110 Streptomy
284	63.2	6.4	301068	1	AE017231	AE017231 Mycobacte	c 357	59.6	6.0	295150	1	SC0939125	AL939125 Streptomy
285	63.2	6.4	349672	1	BX640419	BX640419 Bordetell	358	59.6	6.0	308015	1	AE015783	AE015783 Pseudomon
286	63	6.4	135005	9	H8860F19	AL035460 Human DNA	c 359	59.4	6.0	116305	8	AP003992	AP003992 Oryza sat
287	62.8	6.3	2595	10	RATTREX	M60647 Rat tropoel	360	59.4	6.0	122615	8	AP005456	AP005456 Oryza sat
288	62.8	6.3	75216	6	AX704275	AX704275 Sequence	c 361	59.4	6.0	170051	8	AP005772	AP005772 Oryza sat
289	62.8	6.3	110000	1	AE000516_13	Continuation (14 o	c 362	59.4	6.0	189910	2	AC148233	AC148233 Oryctolag
290	62.8	6.3	299450	1	BX248338	BX248338 Mycobacte	363	59.4	6.0	197050	1	AL646081	AL646081 Ralstonia
291	62.8	6.3	349306	1	BX842575	BX842575 Mycobacte	c 364	59.4	6.0	296500	1	SC0939128	AL939128 Streptomy
292	62.6	6.3	1014	8	NTU62734	U62734 Nicotiana t	365	59.2	6.0	1791	6	BD179866	BD179866 Highly th
293	62.6	6.3	216050	1	AL646076	AL646076 Ralstonia	366	59.2	6.0	273285	1	AE017304	AE017304 Thermus t
294	62.6	6.3	348257	1	BX640425	BX640425 Bordetell	367	59.2	6.0	298450	1	SC0939107	AL939107 Streptomy
295	62.4	6.3	110000	1	AE000516_02	Continuation (3 of	368	59	6.0	2531	8	AY341851	AY341851 Oryza sat
296	62.4	6.3	219952	2	AC084804	AC084804 Mus muscu	369	59	6.0	3152	8	AY341843	AY341843 Oryza sat
297	62.4	6.3	341957	1	BX842572	BX842572 Mycobacte	370	59	6.0	10800	6	AX512249	AX512249 Sequence
298	62.4	6.3	343050	1	BX248334	BX248334 Mycobacte	371	59	6.0	10809	6	AX512245	AX512245 Sequence
299	62.2	6.3	300029	1	AE017178	AE017178 Porphyrom	372	59	6.0	110000	2	LMFLCHR36_03	Continuation (4 of
300	62.2	6.3	301332	1	AE017237	AE017237 Mycobacte	c 373	59	6.0	139298	8	OSJN00012	AL606441 Oryza sat
301	62	6.3	181718	2	AC148913	AC148913 Sus scrof	374	59	6.0	277000	1	SC0939109	AL939109 Streptomy
302	62	6.3	295150	1	SC0939126	AL939126 Streptomy	375	58.8	5.9	1393	11	PM11H12G	AL684264 Penicilli
303	61.8	6.2	186752	9	AC111200	AC111200 Homo sapi	c 376	58.8	5.9	2320	8	AK069799	AK069799 Oryza sat
304	61.8	6.2	281450	1	AP005032	AP005032 Streptomy	c 377	58.8	5.9	2793	8	AK067140	AK067140 Oryza sat
305	61.6	6.2	845	6	AR225248	AR225248 Sequence	378	58.8	5.9	3849	6	AX058889	AX058889 Sequence
306	61.6	6.2	276289	1	AE017306	AE017306 Thermus t	379	58.8	5.9	5858	3	AF350276	AF350276 Nephila m
307	61.4	6.2	146111	10	AC132340	AC132340 Mus muscu	380	58.8	5.9	12744	1	AP204401	AP204401 Streptomy
308	61.2	6.2	302325	1	AE017236	AE017236 Mycobacte	381	58.8	5.9	187517	5	AY519500	AY519500 Gallus ga
309	61	6.2	976	11	PM1206G	AL684370 Penicilli	c 382	58.8	5.9	247910	1	AE017307	AE017307 Thermus t
310	61	6.2	151085	8	AP003239	AP003239 Oryza sat	c 383	58.8	5.9	299800	1	AP005040	AP005040 Streptomy
311	61	6.2	292100	1	SC0939121	AL939121 Streptomy	c 384	58.8	5.9	311000	1	SC0939122	AL939122 Streptomy

C 385	58.6	5.9	48024	7	AV368235	AV368235 Burkholde	C 458	57.2	5.8	272101	1	AE017302	AE017302 Thermus t
C 386	58.6	5.9	274676	1	AE017305	AE017305 Thermus t	459	57	5.8	10136	1	AF546156	AF546156 Micromono
C 387	58.6	5.9	283308	1	AE017242	AE017242 Mycobacte	460	57	5.8	11219	1	SERERYAA	M63676 Saccharopol
C 388	58.6	5.9	293050	1	SC0939116	AL939116 Streptomy	461	57	5.8	11219	6	AR049367	AR049367 Sequence
C 389	58.6	5.9	299925	1	AF005045	AP005045 Streptomy	462	57	5.8	11219	6	AR095528	AR095528 Sequence
C 390	58.6	5.9	300327	1	AE017228	AE017228 Mycobacte	C 463	57	5.8	38494	6	AR345349	AR345349 Sequence
C 391	58.4	5.9	1288	5	AR007563	AR007563 Sequence	C 464	57	5.8	38503	1	MSGB1912CS	L01536 M. leprae g
C 392	58.4	5.9	3958	5	CHKROS	M18043 Chicken c-f	C 465	57	5.8	38675	1	MLU15180	U15180 Mycobacteri
C 393	58.4	5.9	7413	14	FVUL508	X87246 Suid herpes	C 466	57	5.8	281450	1	AP005032	AP005032 Streptomy
C 394	58.4	5.9	127304	2	AC119051	AC119051 Gallus ga	C 467	57	5.8	384850	1	MLEPRTN4	BL179631 Highly th
C 395	58.4	5.9	309050	1	SC0939117	AL939117 Streptomy	C 468	57	5.8	384850	6	BDU62735	U62735 Nicotiana t
C 396	58.2	5.9	1970	5	GGY17794	Y17794 Gallus gall	469	56.8	5.7	1003	8	NTU62735	AR151710 Sequence
C 397	58.2	5.9	4237	8	D84400	D84400 Oryza sativ	470	56.8	5.7	1182	6	AR151710	AR151710 Sequence
C 398	58.2	5.9	89576	1	AF562270	AF632270 Actinopla	471	56.8	5.7	1182	6	AR352531	AR352531 Sequence
C 399	58.2	5.9	91839	2	AC098688	AC098688 Bos tauru	472	56.8	5.7	1306	8	AY323238	AY323238 Zea mays
C 400	58.2	5.9	197805	2	AC105307	AC105307 Bos tauru	473	56.8	5.7	1306	8	AY323240	AY323240 Zea mays
C 401	58.2	5.9	295150	1	SC0939125	AL939125 Streptomy	474	56.8	5.7	1306	8	AY323262	AY323262 Zea mays
C 402	58.2	5.9	299925	1	AP005039	AP005039 Streptomy	475	56.8	5.7	1306	8	AY323270	AY323270 Zea mays
C 403	58	5.9	897	6	AX654732	AX654732 Sequence	476	56.8	5.7	1308	8	AY323269	AY323269 Zea mays
C 404	58	5.9	2329	1	SGHRDT	X79979 S. griseus h	477	56.8	5.7	1308	8	AY323239	AY323239 Zea mays
C 405	58	5.9	2329	1	AF425994	AF425994 Streptomy	478	56.8	5.7	1309	8	AY323256	AY323256 Zea mays
C 406	58	5.9	10444	14	PVI422133	AF422133 Suid herp	479	56.8	5.7	1309	8	AY323266	AY323266 Zea mays
C 407	58	5.9	88421	6	AX417445	AX417445 Sequence	480	56.8	5.7	1311	8	AY323267	AY323267 Zea mays
C 408	58	5.9	186752	9	AC111200	AC111200 Homo sapi	481	56.8	5.7	1314	8	AY323253	AY323253 Zea mays
C 409	58	5.9	290850	1	SC0939127	AL939127 Streptomy	482	56.8	5.7	1314	8	AY323268	AY323268 Zea mays
C 410	58	5.9	308050	1	SC0939124	AL939124 Streptomy	483	56.8	5.7	1320	8	AY323271	AY323271 Zea mays
C 411	57.8	5.8	9678	1	AB110645	AB110645 Streptomy	484	56.8	5.7	1544	8	AY323246	AY323246 Zea mays
C 412	57.8	5.8	245210	2	AC137771	AC137771 Homo sapi	485	56.8	5.7	1546	8	AY323244	AY323244 Zea mays
C 413	57.8	5.8	299550	1	AP005031	AP005031 Streptomy	486	56.8	5.7	2000	6	AX655393	AX655393 Sequence
C 414	57.8	5.8	347894	1	EX640431	EX640431 Bordetell	487	56.8	5.7	3900	1	AF262754	AF262754 Amycolato
C 415	57.6	5.8	3297	6	BD180129	BD180129 Highly th	488	56.8	5.7	5269	1	AF262754	AF262754 Amycolato
C 416	57.6	5.8	106873	14	AB096160	AB096160 Cercopith	C 489	56.8	5.7	5269	1	AF262754	AF262754 Amycolato
C 417	57.6	5.8	166789	14	AF533768	AF533768 Cercopith	C 490	56.8	5.7	6584	1	SCPAHCAS	AB001610 Deinococc
C 418	57.6	5.8	166789	2	AC145332	AC145332 Felis cat	491	56.8	5.7	11604	6	AR151704	AR151704 Sequence
C 419	57.6	5.8	299050	1	SC0939119	AL939119 Streptomy	492	56.8	5.7	15079	6	AR352525	AR352525 Sequence
C 420	57.6	5.8	321250	1	SC0939111	AL939111 Streptomy	493	56.8	5.7	15079	6	AR151702	AR151702 Sequence
C 421	57.4	5.8	1029	6	BD174410	BD174410 DNA resto	494	56.8	5.7	15120	1	SCU87785	U87786 Streptomyce
C 422	57.4	5.8	1298	8	AY323254	AY323254 Zea mays	495	56.8	5.7	15120	6	AR352523	AR352523 Sequence
C 423	57.4	5.8	1298	8	AY323255	AY323255 Zea mays	C 496	56.8	5.7	22976	6	AX000035	AX000035 Sequence
C 424	57.4	5.8	1298	8	AY323258	AY323258 Zea mays	C 497	56.8	5.7	22976	6	AX000035	AX000035 Sequence
C 425	57.4	5.8	1298	8	AY323259	AY323259 Zea mays	C 498	56.8	5.7	22976	6	AX000035	AX000035 Sequence
C 426	57.4	5.8	1298	8	AY323260	AY323260 Zea mays	C 499	56.8	5.7	22976	6	AX000035	AX000035 Sequence
C 427	57.4	5.8	1298	8	AY323261	AY323261 Zea mays	C 500	56.8	5.7	22976	6	AX000035	AX000035 Sequence
C 428	57.4	5.8	1298	8	AY323262	AY323262 Zea mays	C 501	56.8	5.7	22976	6	AX000035	AX000035 Sequence
C 429	57.4	5.8	1298	8	AY323263	AY323263 Zea mays	C 502	56.8	5.7	22976	6	AX000035	AX000035 Sequence
C 430	57.4	5.8	1298	8	AY323265	AY323265 Zea mays	C 503	56.8	5.7	22976	6	AX000035	AX000035 Sequence
C 431	57.4	5.8	1298	8	AY323267	AY323267 Zea mays	C 504	56.8	5.7	22976	6	AX000035	AX000035 Sequence
C 432	57.4	5.8	1298	8	AY323268	AY323268 Zea mays	C 505	56.8	5.7	22976	6	AX000035	AX000035 Sequence
C 433	57.4	5.8	1298	8	AY323269	AY323269 Zea mays	C 506	56.8	5.7	22976	6	AX000035	AX000035 Sequence
C 434	57.4	5.8	1298	8	AY323270	AY323270 Zea mays	C 507	56.8	5.7	22976	6	AX000035	AX000035 Sequence
C 435	57.4	5.8	1298	8	AY323271	AY323271 Zea mays	C 508	56.8	5.7	22976	6	AX000035	AX000035 Sequence
C 436	57.4	5.8	1298	8	AY323272	AY323272 Zea mays	C 509	56.8	5.7	22976	6	AX000035	AX000035 Sequence
C 437	57.4	5.8	1298	8	AY323273	AY323273 Zea mays	C 510	56.8	5.7	22976	6	AX000035	AX000035 Sequence
C 438	57.4	5.8	1298	8	AY323274	AY323274 Zea mays	C 511	56.8	5.7	22976	6	AX000035	AX000035 Sequence
C 439	57.4	5.8	1298	8	AY323275	AY323275 Zea mays	C 512	56.8	5.7	22976	6	AX000035	AX000035 Sequence
C 440	57.4	5.8	1298	8	AY323276	AY323276 Zea mays	C 513	56.8	5.7	22976	6	AX000035	AX000035 Sequence
C 441	57.4	5.8	1298	8	AY323277	AY323277 Zea mays	C 514	56.8	5.7	22976	6	AX000035	AX000035 Sequence
C 442	57.4	5.8	1298	8	AY323278	AY323278 Zea mays	C 515	56.8	5.7	22976	6	AX000035	AX000035 Sequence
C 443	57.4	5.8	1298	8	AY323279	AY323279 Zea mays	C 516	56.8	5.7	22976	6	AX000035	AX000035 Sequence
C 444	57.4	5.8	1298	8	AY323280	AY323280 Zea mays	C 517	56.8	5.7	22976	6	AX000035	AX000035 Sequence
C 445	57.4	5.8	1298	8	AY323281	AY323281 Zea mays	C 518	56.8	5.7	22976	6	AX000035	AX000035 Sequence
C 446	57.4	5.8	1298	8	AY323282	AY323282 Zea mays	C 519	56.8	5.7	22976	6	AX000035	AX000035 Sequence
C 447	57.4	5.8	1298	8	AY323283	AY323283 Zea mays	C 520	56.8	5.7	22976	6	AX000035	AX000035 Sequence
C 448	57.4	5.8	1298	8	AY323284	AY323284 Zea mays	C 521	56.8	5.7	22976	6	AX000035	AX000035 Sequence
C 449	57.4	5.8	1298	8	AY323285	AY323285 Zea mays	C 522	56.8	5.7	22976	6	AX000035	AX000035 Sequence
C 450	57.4	5.8	1298	8	AY323286	AY323286 Zea mays	C 523	56.8	5.7	22976	6	AX000035	AX000035 Sequence
C 451	57.4	5.8	1298	8	AY323287	AY323287 Zea mays	C 524	56.8	5.7	22976	6	AX000035	AX000035 Sequence
C 452	57.4	5.8	1298	8	AY323288	AY323288 Zea mays	C 525	56.8	5.7	22976	6	AX000035	AX000035 Sequence
C 453	57.4	5.8	1298	8	AY323289	AY323289 Zea mays	C 526	56.8	5.7	22976	6	AX000035	AX000035 Sequence
C 454	57.4	5.8	1298	8	AY323290	AY323290 Zea mays	C 527	56.8	5.7	22976	6	AX000035	AX000035 Sequence
C 455	57.4	5.8	1298	8	AY323291	AY323291 Zea mays	C 528	56.8	5.7	22976	6	AX000035	AX000035 Sequence
C 456	57.4	5.8	1298	8	AY323292	AY323292 Zea mays	C 529	56.8	5.7	22976	6	AX000035	AX000035 Sequence
C 457	57.4	5.8	1298	8	AY323293	AY323293 Zea mays	C 530	56.8	5.7	22976	6	AX000035	AX000035 Sequence

531	56.4	5.7	9450	1	AF190463	AF190463 Comamonas	C 604	55.8	5.6	1393	11	PM11H12G	AL684264 Penicilli
532	56.4	5.7	15738	6	AX803762	Sequence	605	55.8	5.6	1427	8	AK109606	AK109606 Oryza sat
533	56.4	5.7	154746	14	HSV2HG52	Z86099 Herpes simp	606	55.8	5.6	1926	6	AR217866	AR217866 Sequence
c 534	56.4	5.7	154746	14	HSV2HG52	Z86099 Herpes simp	607	55.8	5.6	1926	6	AR254714	AR254714 Sequence
535	56.4	5.7	187829	2	AC025388	AC025388 Homo sapi	608	55.8	5.6	1926	6	AX107940	AX107940 Sequence
536	56.4	5.7	289308	1	AE017242	AE017242 Mycobacte	609	55.8	5.6	2580	6	AR108994	AR108994 Sequence
c 537	56.4	5.7	348866	1	EX540426	EX540426 Bordetell	610	55.8	5.6	2651	10	MMU08210	U08210 Mus musculu
538	56.2	5.7	1143	6	AX574142	AX574142 Sequence	c 611	55.8	5.6	2810	1	STMTCR3	D38215 Streptomyce
539	56.2	5.7	2793	6	AR009990	AR009990 Sequence	612	55.8	5.6	3281	3	LMA243459	AJ243459 Leishmani
540	56.2	5.7	2793	6	I95876	I95876 Sequence 1	613	55.8	5.6	3643	10	BC051649	BC051649 Mus muscu
541	56.2	5.7	3060	3	AF027735	AF027735 Nephila c	c 614	55.8	5.6	5452	6	AR083151	AR083151 Sequence
542	56.2	5.7	13513	1	AY423269	AY423269 Streptomy	615	55.8	5.6	5452	12	U02454	U02454 Cloning vec
543	56.2	5.7	14186	6	AX204987	AX204987 Sequence	c 616	55.8	5.6	8705	6	BD225380	BD225380 Targeting
544	56.2	5.7	48221	6	AX574200	AX574200 Sequence	c 617	55.8	5.6	8705	6	AR349578	AR349578 Sequence
c 545	56.2	5.7	58996	1	AB034704	AB034704 Rubriviva	c 618	55.8	5.6	9482	6	CQ829527	CQ829527 Sequence
546	56.2	5.7	226251	10	AL833803	AL833803 Mouse DNA	619	55.8	5.6	9551	6	AR076233	AR076233 Sequence
547	56.2	5.7	300425	1	AP005038	AP005038 Streptomy	620	55.8	5.6	9551	6	I39845	I39845 Sequence 93
c 548	56.2	5.7	339650	1	SC0939108	AL939108 Streptomy	621	55.8	5.6	9551	9	HUMTRHYAL	L09190 Human trich
549	56.2	5.7	343243	1	EX640414	EX640414 Bordetell	622	55.8	5.6	9600	6	A32665	A92665 Sequence 1
c 550	56.2	5.7	349260	1	EX572595	EX572595 Rhodopseu	623	55.8	5.6	9600	6	AR158345	AR158345 Sequence
551	56	5.7	1104	5	AF364329	AF364329 Coturnix	624	55.8	5.6	9600	6	AR241207	AR241207 Sequence
552	56	5.7	1302	8	AK070743	AK070743 Oryza sat	c 625	55.8	5.6	10285	6	AX551315	AX551315 Sequence
553	56	5.7	2043	9	BC032443	BC032443 Homo sapi	c 626	55.8	5.6	10285	6	AX552015	AX552015 Sequence
554	56	5.7	2109	6	BD237101	BD237101 Compounds	c 627	55.8	5.6	10330	6	CQ789661	CQ789661 Sequence
555	56	5.7	2109	6	AR225501	AR225501 Sequence	c 628	55.8	5.6	10477	6	CQ789659	CQ789659 Sequence
556	56	5.7	2142	6	AX321622	AX321622 Sequence	c 629	55.8	5.6	10516	6	CQ789657	CQ789657 Sequence
557	56	5.7	2142	6	AX878471	AX878471 Sequence	c 630	55.8	5.6	10561	6	CQ789655	CQ789655 Sequence
558	56	5.7	2142	6	BD157246	BD157246 Primer fo	631	55.8	5.6	10596	6	I25041	I25041 Sequence 15
559	56	5.7	2142	6	AK021532	AK021532 Homo sapi	632	55.8	5.6	10596	6	I30503	I30503 Sequence 15
560	56	5.7	2198	6	AX876825	AX876825 Sequence	c 633	55.8	5.6	10615	6	CQ789682	CQ789682 Sequence
561	56	5.7	2198	6	BD156336	BD156336 Primer fo	634	55.8	5.6	10737	12	XXU02428	U02428 Cloning vec
562	56	5.7	2198	9	AK001474	AK001474 Homo sapi	c 635	55.8	5.6	10774	6	CQ789660	CQ789660 Sequence
563	56	5.7	2347	9	BC009372	BC009372 Homo sapi	636	55.8	5.6	10850	12	U02455	U02455 Cloning vec
564	56	5.7	2360	9	BC043619	BC043619 Homo sapi	c 637	55.8	5.6	10921	6	CQ789658	CQ789658 Sequence
565	56	5.7	2392	6	AX003981	AX003981 Sequence	c 638	55.8	5.6	10961	6	CQ789656	CQ789656 Sequence
566	56	5.7	2392	6	BD086467	BD086467 DNA demet	c 639	55.8	5.6	11006	6	CQ789654	CQ789654 Sequence
567	56	5.7	2392	9	AF072247	AF072247 Homo sapi	c 640	55.8	5.6	11059	6	CQ789683	CQ789683 Sequence
c 568	56	5.7	2685	9	HUMHBA3	J00184 Homo sapien	641	55.8	5.6	13750	1	AY260903	AY260903 Rhodospir
569	56	5.7	4257	6	AR144708	AR144708 Sequence	c 642	55.8	5.6	16080	6	AR404205	AR404205 Sequence
570	56	5.7	4257	6	AR145616	AR145616 Sequence	c 643	55.8	5.6	17753	6	CQ790449	CQ790449 Sequence
571	56	5.7	4943	6	BD188749	BD188749 Novel tyr	c 644	55.8	5.6	22960	12	AY192024	AY192024 BAC cloni
572	56	5.7	4943	6	AB067470	AB067470 Homo sapi	c 645	55.8	5.6	115245	8	AF005682	AF005682 Oryza sat
573	56	5.7	4988	6	AX766352	AX766352 Sequence	c 646	55.8	5.6	128525	8	AP003118	AP003118 Oryza sat
574	56	5.7	6633	14	HBH5VIG3	X06461 Herpes simp	647	55.8	5.6	132733	8	CNS08CA4	AL772426 Oryza sat
c 575	56	5.7	12001	6	AE0048721	AE0048721 Sequence	648	55.8	5.6	135793	8	CNS08CA5	AL772427 Oryza sat
576	56	5.7	12561	1	AR004557	AR004557 Pseudomon	c 649	55.8	5.6	141983	8	AP003047	AP003047 Oryza sat
577	56	5.7	15559	1	AF074603	AF074603 Streptomy	c 650	55.8	5.6	151578	9	AL589986	AL589986 Human DNA
578	56	5.7	26245	14	HS1US	L00036 Human herpe	651	55.8	5.6	171823	14	HRV507799	AJ507799 Human her
c 579	56	5.7	26245	14	HS1US	L00036 Human herpe	652	55.8	5.6	172281	14	EBV	V01555 Epstein-Bar
c 580	56	5.7	32668	1	MPU575934	AJ575934 Micromono	653	55.8	5.6	184113	14	HS4B958RAJ	M80517 Epstein-Bar
581	56	5.7	33676	1	SCARDIGN	X84374 Saccharothr	654	55.8	5.6	232605	1	AE017222	AE017222 Thermus t
582	56	5.7	38146	1	AY524043	AY524043 Micromono	c 655	55.8	5.6	251872	2	AC125998	AC125998 Rattus no
c 583	56	5.7	43058	6	AX332810	AX332810 Sequence	656	55.8	5.6	270418	1	AE017303	AE017303 Thermus t
c 584	56	5.7	43058	6	AX333047	AX333047 Sequence	657	55.8	5.6	280558	1	AE017301	AE017301 Thermus t
c 585	56	5.7	43058	6	AX411306	AX411306 Sequence	c 658	55.8	5.6	313800	1	SC0939114	AL939114 Streptomy
c 586	56	5.7	43058	9	HSGG1	Z84721 Human DNA s	659	55.8	5.6	726	6	AX865337	AX865337 Sequence
c 587	56	5.7	107955	8	AP005551	AP005551 Oryza sat	660	55.6	5.6	726	6	BD145399	BD145399 Primer fo
c 588	56	5.7	110000	2	LMFLCHR36_13	Continuation (14 o	661	55.6	5.6	150200	8	AP004459	AP004459 Oryza sat
589	56	5.7	121849	8	AC092779	AC092779 Oryza sat	662	55.6	5.6	155069	8	AP004396	AP004396 Oryza sat
590	56	5.7	150155	8	AC097277	AC097277 Oryza sat	663	55.6	5.6	301443	1	AE017239	AE017239 Mycobacte
591	56	5.7	152261	14	HB1CG	X14112 Human herpe	664	55.6	5.6	306906	8	AE016900	AE016900 Erythrothec
c 592	56	5.7	152261	14	HB1CG	X14112 Human herpe	665	55.4	5.6	657	12	AY657485	AY657485 Synthetic
593	56	5.7	170020	8	AC138001	AC138001 Oryza sat	666	55.4	5.6	1251	6	BD180575	BD180575 Highly th
594	56	5.7	172238	8	AC145381	AC145381 Oryza sat	667	55.4	5.6	1726	8	AK064395	AK064395 Oryza sat
c 595	56	5.7	190076	9	AC008403	AC008403 Homo sapi	668	55.4	5.6	3033	6	AX573728	AX573728 Sequence
c 596	56	5.7	258002	9	AE006462	AE006462 Homo sapi	c 669	55.4	5.6	11873	1	AE004710	AE004710 Pseudomon
597	56	5.7	276800	1	SC0939115	AL939115 Streptomy	c 670	55.4	5.6	95209	2	AP004323	AP004323 Oryza sat
598	56	5.7	299925	1	AP005043	AP005043 Streptomy	671	55.4	5.6	128136	1	AF440524	AF440524 Pseudomon
c 599	56	5.7	300100	1	SC0939123	AL939123 Streptomy	672	55.4	5.6	133534	10	AL929233	AL929233 Mouse DNA
c 600	56	5.7	302898	1	AE017238	AE017238 Mycobacte	673	55.4	5.6	158230	1	AF440523	AF440523 Pseudomon
601	55.8	5.6	890	8	NT038612	U38612 Nicotiana t	c 674	55.4	5.6	172186	2	AC137124	AC137124 Mus muscu
602	55.8	5.6	1150	14	HS4ULIR3	J02079 epstein-bar	c 675	55.4	5.6	197050	1	AL646081	AL646081 Ralstonia
603	55.8	5.6	1152	6	AX653506	AX653506 Sequence	676	55.4	5.6	299050	1	SC0939119	AL939119 Streptomy

c 677	55.4	5.6	299800	1	AP005028 Streptomy	750	54.6	5.5	2830	3	AF027972	AF027972 Nephila c
c 678	55.4	5.6	314100	1	SC0933106	751	54.6	5.5	2830	6	AR091362	AR091362 Streptomy
c 679	55.4	5.6	986	8	AF377753 Zea mays	c 752	54.6	5.5	3866	1	D31792	D31792 Streptomyce
680	55.2	5.6	1182	8	AK105138	c 753	54.6	5.5	4761	1	SC0244019	AJ244019 Streptomy
681	55.2	5.6	1324	8	OSLIP19	c 754	54.6	5.5	5520	3	AC084329	AC084329 Leishmani
682	55.2	5.6	1344	8	AK104844	c 755	54.6	5.5	9811	14	AF449714	AF449714 Cercopith
683	55.2	5.6	1375	8	AK065180	756	54.6	5.5	12277	1	AF340166	AF340166 Streptomy
684	55.2	5.6	1679	9	AB001835	757	54.6	5.5	22449	1	SPSNCBCE	Y1548 S.pristinae
685	55.2	5.6	9208	1	STMWRWGT	758	54.6	5.5	22449	1	SPSNCBCE	X98690 S.pristinae
686	55.2	5.6	9509	1	SC0001205	c 759	54.6	5.5	110086	8	AP003373	AP003373 Oryza sat
c 687	55.2	5.6	13508	1	AE005037	760	54.6	5.5	112144	8	AP003758	AP003758 Oryza sat
c 688	55.2	5.6	14219	1	AB070957	c 761	54.6	5.5	127348	8	AC134769	AC134769 Genomic s
c 689	55.2	5.6	6351	2	AC139773	c 762	54.6	5.5	142549	2	AP004271	AP004271 Oryza sat
690	55.2	5.6	6669	1	AME16952	c 763	54.6	5.5	158405	10	MMHC310M6	AF109906 Mus muscu
691	55.2	5.6	85163	1	AY048670	c 764	54.6	5.5	161326	9	AC004067	AC004067 Homo sapi
692	55.2	5.6	95209	2	AP004323	c 765	54.6	5.5	163490	8	CNS08CD4	AL954828 Oryza sat
c 693	55.2	5.6	110000	2	LMFLCHR16_02	c 766	54.6	5.5	170666	8	AP003845	AP003845 Oryza sat
c 694	55.2	5.6	110000	2	LMFLCHR16_03	c 767	54.6	5.5	189050	1	AL646077	AL646077 Ralstonia
c 695	55.2	5.6	137860	10	AC122407	c 768	54.6	5.5	212050	1	AL646060	AL646060 Ralstonia
696	55.2	5.6	145796	8	AC130598	c 769	54.6	5.5	221899	10	AC087117	AC087117 Mus Muscu
c 697	55.2	5.6	146408	8	AC130610	770	54.4	5.5	1443	6	BD180149	BD180149 Highly th
c 698	55.2	5.6	154728	9	AC018730	771	54.4	5.5	1608	5	LFL308119	AJ308119 Lampetra
c 699	55.2	5.6	187782	8	AC135425	772	54.4	5.5	4117	14	AF074327	AF074327 Tupaia he
700	55.2	5.6	299300	1	AP005026	773	54.4	5.5	4120	14	AF074328	AF074328 Tupaia he
701	55.2	5.6	300794	8	AE016884	774	54.4	5.5	6620	1	AB164631	AB164631 Streptomy
c 702	55.2	5.6	348257	1	BX640425	775	54.4	5.5	13461	14	AF084543	AF084543 Tupaia he
c 703	55.2	5.6	349497	1	BX640440	776	54.4	5.5	13889	10	AF292939	AF292939 Mus muscu
704	55	5.6	2205	9	BC009438	c 777	54.4	5.5	54587	2	AC146908_3	Continuation (4 of
705	55	5.6	2490	8	AK100050	778	54.4	5.5	132981	8	AC147802	AC147802 Oryza sat
706	55	5.6	2559	6	AR488839	779	54.4	5.5	163732	8	OSJN00033	AL606632 Oryza sat
707	55	5.6	2562	6	CQ720385	c 780	54.4	5.5	195859	14	AF281817	AF281817 Tupaia he
708	55	5.6	28890	1	AF512431	781	54.4	5.5	213050	1	AL646079	AL646079 Ralstonia
c 709	55	5.6	30943	6	CQ801140	782	54.4	5.5	300810	8	AE016896	AE016896 Erenothec
710	55	5.6	53784	1	MM223012	783	54.4	5.5	302007	1	SC0939132	AL939132 Streptomy
711	55	5.6	53789	6	AG9720	784	54.4	5.5	302898	1	AE017238	AE017238 Mycobacte
712	55	5.6	66280	1	AF195122	785	54.4	5.5	34321	1	BX640429	BX640429 Bordetell
713	55	5.6	103576	8	YUP8H12	c 786	54.4	5.5	348624	1	BX640441	BX640441 Bordetell
714	55	5.6	109528	2	AF040570	787	54.4	5.5	349876	1	BX640442	BX640442 Bordetell
c 715	55	5.6	110000	2	BX255276_15	788	54.2	5.5	825	8	AY533122	AY533122 Oryza sat
c 716	55	5.6	181206	2	AC110907	789	54.2	5.5	825	8	AY533122	AY533122 Oryza sat
c 717	55	5.6	188050	1	SC0939129	790	54.2	5.5	1300	8	AK102889	AK102889 Oryza sat
718	55	5.6	292500	1	SC0939126	791	54.2	5.5	1433	8	AF168779	AF168779 Eucalyptu
719	55	5.6	295150	1	SC0939126	792	54.2	5.5	1602	1	SLU12007	SLU12007 Streptomyce
720	54.8	5.5	594	6	BD224381	793	54.2	5.5	1910	8	AK104793	AK104793 Oryza sat
721	54.8	5.5	594	6	AR216431	794	54.2	5.5	1910	8	AK106154	AK106154 Oryza sat
722	54.8	5.5	594	6	AR432833	795	54.2	5.5	1934	8	AK098925	AK098925 Oryza sat
723	54.8	5.5	607	6	AR074114	796	54.2	5.5	1964	8	AK064950	AK064950 Oryza sat
724	54.8	5.5	607	6	BD224299	797	54.2	5.5	2202	8	AK067226	AK067226 Oryza sat
725	54.8	5.5	607	6	BD273001	798	54.2	5.5	3202	1	AF157829	AF157829 Myxococcu
726	54.8	5.5	607	6	AR216349	799	54.2	5.5	4858	1	AF162663	AF162663 Myxococcu
727	54.8	5.5	607	6	AR432751	c 800	54.2	5.5	8046	1	AF049107	AF049107 Myxococcu
728	54.8	5.5	607	6	BD005662	801	54.2	5.5	15141	14	SH1PROIE	M34651 Pseudorabie
729	54.8	5.5	1795	1	AF118856	802	54.2	5.5	25315	1	AY204472	AY204472 Myxococcu
730	54.8	5.5	2142	1	CC042203	c 803	54.2	5.5	32748	1	AS070951	AS070951 Streptomy
731	54.8	5.5	2365	8	AK102809	c 804	54.2	5.5	3740	6	AX211705	AX211705 Streptomy
c 732	54.8	5.5	2783	1	STMFMET	c 805	54.2	5.5	106562	2	AP004055	AP004055 Oryza sat
c 733	54.8	5.5	3030	8	VCA429230	c 806	54.2	5.5	106562	2	AP004055	AP004055 Oryza sat
734	54.8	5.5	5500	8	ATGLVXP	c 807	54.2	5.5	110098	8	AC093939	AC093939 Oryza sat
735	54.8	5.5	10894	1	AE005785	c 808	54.2	5.5	122218	8	AC093939	AC093939 Oryza sat
c 736	54.8	5.5	12528	1	AE005826	c 809	54.2	5.5	123580	1	AF263912	AF263912 Streptomy
c 737	54.8	5.5	58638	7	AY576796	c 810	54.2	5.5	124010	6	AX211739	AX211739 Sequence
738	54.8	5.5	92620	8	AB026636	c 811	54.2	5.5	136150	8	AP002485	AP002485 Oryza sat
c 739	54.8	5.5	110000	2	BX255276_07	c 812	54.2	5.5	142010	8	AP003928	AP003928 Oryza sat
740	54.8	5.5	156789	14	AF533768	c 813	54.2	5.5	189043	8	AP004366	AP004366 Oryza sat
c 741	54.8	5.5	166182	10	AC084391	c 814	54.2	5.5	196050	1	AL646058	AL646058 Ralstonia
742	54.8	5.5	218310	10	AC034265	c 815	54.2	5.5	202301	1	AE017286	AE017286 Desulfovi
743	54.8	5.5	231001	2	AC130981	c 816	54.2	5.5	245233	2	AC130123	AC130123 Rattus no
744	54.8	5.5	258319	2	AC127770	c 817	54.2	5.5	301443	1	AE017239	AE017239 Mycobacte
745	54.8	5.5	292100	1	SC0939121	c 818	54.2	5.5	339972	8	OSA307662	AJ307662 Oryza sat
746	54.6	5.5	955	8	NTU62736	c 819	54	5.5	885	11	PM7F8G	AL68189 Penicilli
747	54.6	5.5	980	6	AX652989	c 820	54	5.5	1065	6	BD180086	BD180086 Highly th
748	54.6	5.5	1261	8	AK112011	c 821	54	5.5	1217	1	AF038408	AF038408 Streptol
749	54.6	5.5	1308	6	BD217906	c 822	54	5.5	1380	6	E17152	E17152 Micrococcu
								5.5	1485	6	BD180362	BD180362 Highly th
								5.5	2900	1	TTHS16007	AJ516007 Thermus t

C 823	54	5.5	3444	1	SAU75434	U75434 Streptomyces	C 896	53.4	5.4	63082	2	AC022663	AC022663 Homo sapi
C 824	54	5.5	4307	9	BC053992	BC053992 Homo sapi	C 897	53.4	5.4	81767	2	AC021929	AC021929 Homo sapi
C 825	54	5.5	4305	9	AC024444	AC024444 Homo sapi	C 898	53.4	5.4	136254	8	CNS07199	AL713941 Oryza sat
C 826	54	5.5	10274	1	AE005893	AE005893 Caulobact	C 899	53.4	5.4	136551	2	AC048354	AC048354 Homo sapi
C 827	54	5.5	18497	9	AF254411	AF254411 Homo sapi	C 900	53.4	5.4	141066	8	AP005188	AP005188 Oryza sat
C 828	54	5.5	143298	8	AC134240	AC134240 Oryza sat	C 901	53.4	5.4	151699	8	AP003916	AP003916 Oryza sat
C 829	54	5.5	153431	8	AC134235	AC134235 Oryza sat	C 902	53.4	5.4	155337	2	AC116408	AC116408 Mus muscu
C 830	54	5.5	172876	9	AC114489	AC114489 Homo sapi	C 903	53.4	5.4	163778	9	AL391005	AL391005 Human DNA
C 831	54	5.5	174992	2	AC025422	AC025422 Homo sapi	C 904	53.4	5.4	187410	8	AP005579	AP005579 Oryza sat
C 832	54	5.5	179451	2	AC148581	AC148581 Gasterost	C 905	53.4	5.4	226155	2	AC136740	AC136740 Mus muscu
C 833	54	5.5	208936	2	AC010821	AC010821 Homo sapi	C 906	53.4	5.4	233405	2	AC126733	AC126733 Rattus no
C 834	54	5.5	209844	9	AC011495	AC011495 Homo sapi	C 907	53.4	5.4	236502	2	AC098186	AC098186 Rattus no
C 835	54	5.5	210614	1	AB088224	AB088224 Streptomy	C 908	53.4	5.4	272101	1	AE017302	AE017302 Thermus t
C 836	54	5.5	250046	2	AC113592	AC113592 Mus muscu	C 909	53.4	5.4	296500	1	SC0939128	AL393128 Streptomy
C 837	54	5.5	298550	1	AP005047	AP005047 Streptomy	C 910	53.4	5.4	308050	1	SC0939124	AL393124 Streptomy
C 838	54	5.5	299425	1	AP005049	AP005049 Streptomy	C 911	53.4	5.4	348050	1	EX640434	EX640434 Bordetell
C 839	54	5.5	300299	8	AE016881	AE016881 Eremothec	C 912	53.4	5.4	348075	1	EX640449	EX640449 Bordetell
C 840	54	5.5	300239	8	AE016908	AE016908 Eremothec	C 913	53.2	5.4	1183	8	AK109116	AK109116 Oryza sat
C 841	54	5.5	303550	1	SC0939131	AL3939131 Streptomy	C 914	53.2	5.4	1283	8	AK058442	AK058442 Oryza sat
C 842	53.8	5.4	1472	6	CQ801144	CQ801144 Sequence	C 915	53.2	5.4	1341	1	AY337515	AY337515 Myxococcu
C 843	53.8	5.4	2007	14	CHV10C	Z49225 Caprine her	C 916	53.2	5.4	1405	8	AK108620	AK108620 Oryza sat
C 844	53.8	5.4	2082	6	AR452220	AR452220 Sequence	C 917	53.2	5.4	1509	6	BD180173	BD180173 Highly th
C 845	53.8	5.4	2082	6	AX262311	AX262311 Sequence	C 918	53.2	5.4	2672	1	AF159692	AF159692 Myxococcu
C 846	53.8	5.4	11171	6	CQ801141	CQ801141 Sequence	C 919	53.2	5.4	2767	8	SL1224970	AF159692 Spermatoz
C 847	53.8	5.4	15141	14	SH1PROIE	M34651 Pseudorabie	C 920	53.2	5.4	10161	1	AF546153	AF546153 Micromono
C 848	53.8	5.4	24613	1	AY116644	AY116644 Streptomy	C 921	53.2	5.4	13325	1	AE005016	AE005016 Halobacte
C 849	53.8	5.4	64492	1	AE086653	AE086653 Streptomy	C 922	53.2	5.4	110400	8	AP005919	AP005919 Oryza sat
C 850	53.8	5.4	85268	2	AC022648	AC022648 Homo sapi	C 923	53.2	5.4	116887	10	AL929153	AL929153 Mouse DNA
C 851	53.8	5.4	114793	9	AF217796	AF217796 Homo sapi	C 924	53.2	5.4	135638	1	AF484556	AF484556 Streptomy
C 852	53.8	5.4	138390	14	AY261359	AY261359 Bovine he	C 925	53.2	5.4	137468	8	AP003269	AP003269 Oryza sat
C 853	53.8	5.4	139544	8	AP004878	AP004878 Oryza sat	C 926	53.2	5.4	181676	10	AC124194	AC124194 Mus muscu
C 854	53.8	5.4	145014	8	AP004048	AP004048 Oryza sat	C 927	53.2	5.4	197411	10	AC135961	AC135961 Mus muscu
C 855	53.8	5.4	166565	2	AC146324	AC146324 Canis fam	C 928	53.2	5.4	232605	1	AE017222	AE017222 Mycobact
C 856	53.8	5.4	299300	1	AP005026	AP005026 Streptomy	C 929	53.2	5.4	309267	1	AE017235	AE017235 Mycobact
C 857	53.8	5.4	301001	1	SC0939123	AL93123 Streptomy	C 930	53.2	5.4	348525	1	EX640428	EX640428 Bordetell
C 858	53.8	5.4	301457	1	AE016824	AE016824 Chromobac	C 931	53.2	5.4	349354	1	EX640416	EX640416 Bordetell
C 859	53.8	5.4	321250	1	SC0939111	AL939111 Streptomy	C 932	53.2	5.4	349672	1	EX640419	EX640419 Bordetell
C 860	53.8	5.4	340900	1	SME591791	AL591791 Sinorhizo	C 933	53	5.4	632	6	AR227195	AR227195 Sequence
C 861	53.6	5.4	6252	8	AY039003	AY039003 Hordeum v	C 934	53	5.4	765	6	BD180096	BD180096 Highly th
C 862	53.6	5.4	10554	1	AE005956	AE005956 Caulobact	C 935	53	5.4	1929	6	AX811491	AX811491 Sequence
C 863	53.6	5.4	15274	1	AE004994	AE004994 Halobacte	C 936	53	5.4	2304	6	BD179527	BD179527 Highly th
C 864	53.6	5.4	32463	8	CNS08C9W	AL772418 Oryza sat	C 937	53	5.4	2953	10	BC054782	BC054782 Mus muscu
C 865	53.6	5.4	38734	6	BD129566	BD129566 Polynucle	C 938	53	5.4	3518	10	MUSHSP7A2	M35021 Mouse heat
C 866	53.6	5.4	110000	2	BX255276.01	Continuation (2 of	C 939	53	5.4	3701	1	AF172724	AF172724 Caulobact
C 867	53.6	5.4	146585	8	CNS08C9W	AL831809 Oryza sat	C 940	53	5.4	8113	14	HSB2ICP4A	LI4320 Bovine herp
C 868	53.6	5.4	198873	2	AC022811	AC022811 Homo sapi	C 941	53	5.4	10029	1	AE012236	AE012236 Xanthomon
C 869	53.6	5.4	204050	1	AL646073	AL646073 Ralstonia	C 942	53	5.4	10513	1	AE004792	AE004792 Pseudomon
C 870	53.6	5.4	212050	1	AL646060	AL646060 Ralstonia	C 943	53	5.4	11283	1	AE005710	AE005710 Caulobact
C 871	53.6	5.4	236054	2	AC114393	AC114393 Ralstonia	C 944	53	5.4	11923	1	AE005972	AE005972 Caulobact
C 872	53.6	5.4	270418	1	AE017230	AE017230 Mycobacte	C 945	53	5.4	32668	1	MFU575934	AY524043 Micromono
C 873	53.6	5.4	302325	1	AE017236	AE017236 Thermus t	C 946	53	5.4	38146	1	AY524043	AY524043 Micromono
C 874	53.6	5.4	303855	1	AE017230	AE017230 Mycobacte	C 947	53	5.4	100773	9	AF466201	AF466201 Sorghum b
C 875	53.6	5.4	320150	1	AP005033	AP005033 Streptomy	C 948	53	5.4	102591	8	AC002978	AC002978 Homo sapi
C 876	53.6	5.4	348134	1	EX640420	EX640420 Bordetell	C 949	53	5.4	110000	2	LMFLCHR12.13	Continuation (14 o
C 877	53.6	5.4	348642	1	EX640446	EX640446 Bordetell	C 950	53	5.4	135301	14	BHV1CGEN	AJ004801 Bovine he
C 878	53.4	5.4	1706	8	AK058559	AK058559 Oryza sat	C 951	53	5.4	135301	14	BHV1CGEN	AJ004801 Bovine he
C 879	53.4	5.4	1707	8	AK101900	AK101900 Oryza sat	C 952	53	5.4	144093	10	AC109193	AC109193 Mus muscu
C 880	53.4	5.4	1754	8	AF165181	AF165181 Zea mays	C 953	53	5.4	178620	10	AC121865	AC121865 Mus muscu
C 881	53.4	5.4	2248	6	BD249574	BD249574 Modificat	C 954	53	5.4	194387	10	AC105989	AC105989 Mus muscu
C 882	53.4	5.4	2248	6	AR340022	AR340022 Sequence	C 955	53	5.4	301925	1	AP005046	AP005046 Streptomy
C 883	53.4	5.4	2336	3	NEPDSF	M37137 N.clavipes	C 956	53	5.4	303642	1	AE016923	AE016923 Chromobac
C 884	53.4	5.4	2338	6	AR088543	AR088543 Sequence	C 957	53	5.4	347071	1	EX640415	EX640415 Bordetell
C 885	53.4	5.4	2338	6	AR088543	I92789 Sequence 1	C 958	53	5.4	348706	1	EX640445	EX640445 Bordetell
C 886	53.4	5.4	2798	3	AF448524	AF448524 Mytilus g	C 959	52.8	5.3	1094	11	PM7G11B	AL685196 Penicilli
C 887	53.4	5.4	3177	9	AF055989	AF055989 Homo sapi	C 960	52.8	5.3	1236	6	AR007558	AR007558 Sequence
C 888	53.4	5.4	10091	1	AE011852	AE011852 Xanthomon	C 961	52.8	5.3	3157	1	MSGPOLA	LI1920 Mycobacteri
C 889	53.4	5.4	10256	1	AE004894	AE004894 Pseudomon	C 962	52.8	5.3	4423	10	MMUSF217	X77602 M.musculu
C 890	53.4	5.4	11626	1	AE011704	AE011704 Xanthomon	C 963	52.8	5.3	11842	1	AE005053	AE005053 Halobacte
C 891	53.4	5.4	11905	1	APU33059	U33059 Actinosyne	C 964	52.8	5.3	92509	1	AL646086	AL646086 Ralstonia
C 892	53.4	5.4	12111	1	AE010422	AE010422 Methanopy	C 965	52.8	5.3	110000	1	AE000516.18	Continuation (19 o
C 893	53.4	5.4	13750	1	AY260903	AY260903 Rhodospir	C 966	52.8	5.3	114996	8	AY485643	AY485643 Hordeum v
C 894	53.4	5.4	18424	1	AF163841	AF163841 Myxococcu	C 967	52.8	5.3	172647	2	AC130732	AC130732 Oryza sat
C 895	53.4	5.4	39250	1	SV1011500	AJ0111500 Streptomy	C 968	52.8	5.3	239571	2	AC150509	AC150509 Bos tauru

c	969	52.8	5.3	299925	1	AP005039	Streptomy	AP005039	Streptomy	c1042	52.4	5.3	168861	2	AC130786	AC130786	Papio anu
	970	52.8	5.3	300050	1	BX248339	Mycobacte	BX248339	Mycobacte	c1043	52.4	5.3	169162	8	AP004267	AP004267	Papio sat
c	971	52.8	5.3	305584	1	AE016920	Chromobac	AE016920	Chromobac	c1044	52.4	5.3	176647	2	AC130188	AC130188	Papio sat
	972	52.8	5.3	314100	1	SC0939106	Streptomy	AL933106	Streptomy	c1045	52.4	5.3	196558	10	AC073946	AC073946	Mus muscu
	973	52.8	5.3	347137	1	BX640448	Bordetell	BX640448	Bordetell	1046	52.4	5.3	202370	2	AC102341	Mus muscu	
c	974	52.8	5.3	347496	1	BX8442577	Mycobacte	BX8442577	Mycobacte	1047	52.4	5.3	242862	2	AC080020	Mus muscu	
c	975	52.8	5.3	348934	1	BX640417	Bordetell	BX640417	Bordetell	1048	52.4	5.3	247910	1	AE017307	Thermus t	
c	976	52.8	5.3	349028	1	BX640413	Bordetell	BX640413	Bordetell	1049	52.4	5.3	300550	1	AE005030	Streptomy	
c	977	52.8	5.3	349497	1	BX640440	Bordetell	BX640440	Bordetell	c1050	52.4	5.3	320150	1	AE005033	Streptomy	
c	978	52.8	5.3	349726	1	BX640421	Bordetell	BX640421	Bordetell	1051	52.2	5.3	705	6	BD179549	Arabidops	
c	979	52.8	5.3	349798	6	BD180185	Highly th	BX640421	Bordetell	1052	52.2	5.3	833	8	AY088274	Arabidops	
c	980	52.6	5.3	1569	6	AY518690	Gallus ga	AY518690	Gallus ga	1053	52.2	5.3	996	6	BD179727	Highly th	
c	981	52.6	5.3	2466	6	C0759736	Sequence	C0759736	Sequence	c1054	52.2	5.3	1140	11	PM12C4G	Penicilli	
c	982	52.6	5.3	2561	4	AY453841	Oryctolag	AY453841	Oryctolag	1055	52.2	5.3	1611	8	AK071964	Oryza sat	
c	983	52.6	5.3	2561	6	AK409339	Sequence	AK409339	Sequence	1056	52.2	5.3	1719	6	BD180543	Highly th	
c	984	52.6	5.3	2561	6	AK239605	Sequence	AK239605	Sequence	1057	52.2	5.3	1766	8	AF325915	Euglena g	
c	985	52.6	5.3	2619	6	C0759734	Sequence	C0759734	Sequence	1058	52.2	5.3	2085	8	AK119580	Oryza sat	
c	986	52.6	5.3	2619	9	AK128815	Homo sapi	AK128815	Homo sapi	1059	52.2	5.3	2529	1	SRSENRS	Streptomyce	
c	987	52.6	5.3	3342	1	AP200819	Streptomy	AP200819	Streptomy	1060	52.2	5.3	2760	1	SRSENRS	Streptomyce	
c	988	52.6	5.3	3705	6	C0759732	Sequence	C0759732	Sequence	1061	52.2	5.3	6297	6	AX598629	Sequence	
c	989	52.6	5.3	4881	1	ANE318385	Amycolato	AX318385	Amycolato	1062	52.2	5.3	7155	1	RCU64519	Rhodospiril	
c	990	52.6	5.3	7985	14	AB096202	Cercopith	AB096202	Cercopith	1063	52.2	5.3	9353	14	BHV1ULX	Bovine herp	
c	991	52.6	5.3	11064	1	D63799	Thermus the	D63799	Thermus the	1064	52.2	5.3	10460	1	AE011791	Xanthomon	
c	992	52.6	5.3	12162	1	AY034175	Streptomy	AY034175	Streptomy	c1065	52.2	5.3	10696	3	AE012103	Xanthomon	
c	993	52.6	5.3	13803	1	AE011784	Xanthomon	AE011784	Xanthomon	1066	52.2	5.3	13455	3	AF218623S1	Nephelia m	
c	994	52.6	5.3	13901	1	AY258009	Streptomy	AY258009	Streptomy	1067	52.2	5.3	31444	14	BVH1LFT31	Bovine herp	
c	995	52.6	5.3	23132	1	STH575648	Streptomy	AY258009	Streptomy	1067	52.2	5.3	31444	14	BVH1LFT31	Bovine herp	
c	996	52.6	5.3	23132	1	STH575648	Streptomy	AY258009	Streptomy	1068	52.2	5.3	6808	1	SAU421825	Stigmatel	
c	997	52.6	5.3	47090	9	AC092310	Homo sapi	AC092310	Homo sapi	1069	52.2	5.3	76196	1	AY354515	Streptomy	
c	998	52.6	5.3	81767	9	AC092323	Homo sapi	AC092323	Homo sapi	1070	52.2	5.3	82868	6	CQ792587	Streptomy	
c	999	52.6	5.3	81767	9	AC092323	Homo sapi	AC092323	Homo sapi	c1071	52.2	5.3	82868	6	CQ792587	Streptomy	
c	1000	52.6	5.3	110000	1	AE000516	27	Continuation (22 o	Continuation (22 o	1072	52.2	5.3	128098	8	AP004309	Sequence	
c1001	52.6	5.3	110000	1	AE016822	21	Continuation (14 o	Continuation (14 o	c1073	52.2	5.3	133387	2	AP004309	Sequence		
c1002	52.6	5.3	135357	8	AP003896	Oryza sat	AP003896	Oryza sat	c1074	52.2	5.3	143200	8	AP004309	Oryza sat		
c1003	52.6	5.3	138390	14	AY261359	Bovine he	AY261359	Bovine he	c1075	52.2	5.3	159860	8	AP005647	Oryza sat		
c1004	52.6	5.3	163328	8	AP004865	Oryza sat	AP004865	Oryza sat	c1076	52.2	5.3	205144	4	AY495827	Oryza sat		
c1005	52.6	5.3	185495	8	AP005620	Oryza sat	AP005620	Oryza sat	c1077	52.2	5.3	273285	1	AE017304	Oryza sat		
c1006	52.6	5.3	230362	2	AC097942	Rattus no	AC097942	Rattus no	c1078	52.2	5.3	276800	1	SC0939115	Mycobacte		
c1007	52.6	5.3	237915	2	AC134745	Rattus no	AC134745	Rattus no	c1079	52.2	5.3	300327	1	AE017228	Streptomy		
c1008	52.6	5.3	277363	2	AC140280	Mus muscu	AC140280	Mus muscu	c1080	52.2	5.3	300425	1	AE005038	Streptomy		
c1009	52.6	5.3	299425	1	AP005049	Streptomy	AP005049	Streptomy	c1081	52.2	5.3	300425	1	AE016920	Streptomy		
c1010	52.6	5.3	303550	1	SC0939118	Streptomy	AL939118	Streptomy	1082	52.2	5.3	305584	1	SC0939117	Streptomy		
c1011	52.6	5.3	306550	1	BX248342	Mycobacte	BX248342	Mycobacte	1083	52.2	5.3	309500	1	SC0939117	Streptomy		
c1012	52.6	5.3	340501	1	BX842580	Mycobacte	BX842580	Mycobacte	1084	52	5.3	991	11	PM12H12B	Penicilli		
c1013	52.4	5.3	1175	5	CHH1SH5	Oryza sat	X01065 Duck (C. mo	X01065 Duck (C. mo	1085	52	5.3	992	8	AF377751	Zea mays		
c1014	52.4	5.3	1227	6	AX467205	Sequence	AX467205	Sequence	1086	52	5.3	1000	8	AY513932	Zea mays		
c1015	52.4	5.3	1485	8	AK107516	Oryza sat	AK107516	Oryza sat	1087	52	5.3	1155	8	AB028182	Oryza sat		
c1016	52.4	5.3	1891	6	AX337108	Sequence	AX337108	Sequence	1088	52	5.3	1255	8	AK073667	Oryza sat		
c1017	52.4	5.3	1891	6	AX587764	Sequence	AX587764	Sequence	1089	52	5.3	1410	1	AME277083	Oryza sat		
c1018	52.4	5.3	1891	9	HSJUNDR	Human_jund	X56681 Human_jund	X56681 Human_jund	1090	52	5.3	1491	6	AX455983	Sequence		
c1019	52.4	5.3	2796	3	AF043944	Mytilus e	AF043944	Mytilus e	1091	52	5.3	1703	8	AK120673	Oryza sat		
c1020	52.4	5.3	3139	8	D63955	Oryza sativ	D63955	Oryza sativ	1092	52	5.3	1711	1	AF347026	Streptomy		
c1021	52.4	5.3	3378	6	BOVADC	Bovine aden	M25579 Bovine aden	M25579 Bovine aden	1093	52	5.3	2800	1	PSNOS2R	P.stutzeri		
c1022	52.4	5.3	3978	6	AK106654	Sequence	AK106654	Sequence	1094	52	5.3	3113	8	SS95BASAL	Spermatoz		
c1023	52.4	5.3	3980	1	AF546147S1	Streptomy	AF546147	Streptomy	1095	52	5.3	3114	12	AY192356	Synthetic		
c1024	52.4	5.3	5117	6	AB018240	Sequence	AB018240	Sequence	1096	52	5.3	3135	12	AY192357	Synthetic		
c1025	52.4	5.3	5117	9	AB011105	Homo sapi	AB011105	Homo sapi	1097	52	5.3	3150	12	AY192358	Synthetic		
c1026	52.4	5.3	5204	6	AX512251	Sequence	AX512251	Sequence	1098	52	5.3	10352	1	AF546152	Streptomy		
c1027	52.4	5.3	5640	6	AK338550	Sequence	AK338550	Sequence	1099	52	5.3	10854	1	AE001886	Deinococc		
c1028	52.4	5.3	8296	6	AX463772	Sequence	AX463772	Sequence	1100	52	5.3	11506	1	AE004793	Pseudomon		
c1029	52.4	5.3	10911	6	CQ730457	Sequence	CQ730457	Sequence	1101	52	5.3	49269	8	AC135499	Oryza sat		
c1030	52.4	5.3	11238	6	AX697991	Sequence	AX697991	Sequence	1102	52	5.3	110000	1	AE016822	Continuation (23 o		
c1031	52.4	5.3	11329	9	AF443072	Homo sapi	AF443072	Homo sapi	1103	52	5.3	142081	8	AP004572	Oryza sat		
c1032	52.4	5.3	11350	6	AX463738	Sequence	AX463738	Sequence	1104	52	5.3	152974	8	AC135497	Oryza sat		
c1033	52.4	5.3	11367	1	AX704754	Sequence	AX704754	Sequence	1105	52	5.3	186090	2	AC097352	Canis fam		
c1034	52.4	5.3	16197	9	AE002072	Deinococc	AE002072	Deinococc	1106	52	5.3	191916	2	AC095027	Canis fam		
c1035	52.4	5.3	60196	6	AX697977	Sequence	AX697977	Sequence	1107	52	5.3	191996	9	AC092275	Oryza sat		
c1036	52.4	5.3	85434	2	AC066610	Homo sapi	AC066610	Homo sapi	1108	52	5.3	200968	8	AP005516	Oryza sat		
c1037	52.4	5.3	101075	8	CNS08GBU	Oryza sat	AL528757	Oryza sat	1109	52	5.3	211657	10	AL732564	Mouse DNA		
c1038	52.4	5.3	104326	1	AY070940	Streptomy	AB070940	Streptomy	1110	52	5.3	239925	1	AP005045	Streptomy		
c1039	52.4	5.3	138203	1	AY310323	Streptomy	AY310323	Streptomy	1111	52	5.3	300029	8	AE017099	Oryza sat		
c1040	52.4	5.3	149098	8	AP003296	Oryza sat	AP003296	Oryza sat	1112	52	5.3	301846	1	AE016913	Chromobac		
c1041	52.4	5.3	157302	9	AL445209	Human DNA	AL445209	Human DNA	1113	52	5.3	307435	1	AE016914	Chromobac		
c1042	52.4	5.3	157302	9	AL445209	Human DNA	AL445209	Human DNA	1114	52	5.3	307435	1	AE016914	Chromobac		

1115	51.8	5.2	974	8	AF377768	AF377768	Zea mays	c1188	51.6	5.2	113193	1	AF357202	AF357202	Streptomy
1116	51.8	5.2	975	8	AF377745	AF377745	Zea mays	c1189	51.6	5.2	113193	6	AX703543	AX703543	Sequence
1117	51.8	5.2	980	8	AF377759	AF377759	Zea mays	1190	51.6	5.2	114051	8	OSJN00036	OSJN00036	Oryza sat
1118	51.8	5.2	981	8	AF377761	AF377761	Zea mays	c1191	51.6	5.2	169064	2	AC115699	AC115699	Mus muscu
1119	51.8	5.2	980	8	AY513914	AY513914	Zea luxur	1192	51.6	5.2	174139	2	AC116700	AC116700	Mus muscu
1120	51.8	5.2	981	8	AY513920	AY513920	Zea mays	1193	51.6	5.2	192857	8	AP005605	AP005605	Oryza sat
1121	51.8	5.2	981	8	AY513928	AY513928	Zea mays	1194	51.6	5.2	213050	1	AL646067	AL646067	Ralstonia
1122	51.8	5.2	982	8	AF377767	AF377767	Zea mays	1195	51.6	5.2	226889	14	AC146905	AC146905	Human her
1123	51.8	5.2	983	8	AY513929	AY513929	Zea mays	c1196	51.6	5.2	229483	14	AC146851	AC146851	Human her
1124	51.8	5.2	989	8	AY513923	AY513923	Zea mays	c1197	51.6	5.2	231236	14	AY315197	AY315197	Human her
1125	51.8	5.2	995	8	AY513927	AY513927	Zea mays	c1198	51.6	5.2	234881	14	AC146906	AC146906	Human her
1126	51.8	5.2	1255	10	AF076156	AF076156	Mus muscu	c1199	51.6	5.2	290850	1	SC0939127	SC0939127	Streptomy
1127	51.8	5.2	1262	10	BC010402	BC010402	Mus muscu	1200	51.6	5.2	291000	1	SC0939105	SC0939105	Streptomy
1128	51.8	5.2	1673	8	AY600140	AY600140	Broussonie	1201	51.6	5.2	299050	1	SC0939104	SC0939104	Streptomy
1129	51.8	5.2	1705	8	AK069785	AK069785	Oryza sat	c1202	51.6	5.2	299425	1	AP005037	AP005037	Streptomy
1130	51.8	5.2	1926	6	AR217867	AR217867	Sequence	1203	51.6	5.2	299550	1	AP005031	AP005031	Streptomy
c1131	51.8	5.2	1931	6	AR083152	AR083152	Sequence	c1204	51.6	5.2	301399	1	AE017233	AE017233	Mycobacte
1132	51.8	5.2	2036	8	AF050631	AF050631	Zea mays	1205	51.6	5.2	349334	1	EX640417	EX640417	Bordetell
1133	51.8	5.2	2075	6	AR253206	AR253206	Sequence	c1206	51.6	5.2	349997	1	EX640427	EX640427	Bordetell
1134	51.8	5.2	2075	6	AR361924	AR361924	Sequence	c1207	51.6	5.2	349008	1	EX640444	EX640444	Bordetell
1135	51.8	5.2	2075	6	AR433000	AR433000	Sequence	1208	51.6	5.2	349008	1	AP003003	AP003003	Mesorhizo
1136	51.8	5.2	2075	6	AX482567	AX482567	Sequence	1209	51.6	5.2	349116	1	AP003003	AP003003	Mesorhizo
1137	51.8	5.2	2075	6	AX565707	AX565707	Sequence	1210	51.4	5.2	349640	1	EX572600	EX572600	Rhodopseu
1138	51.8	5.2	2075	6	AX565707	AX565707	Sequence	1211	51.4	5.2	985	8	AK058890	AK058890	Oryza sat
1139	51.8	5.2	2075	6	AX597107	AX597107	Sequence	1212	51.4	5.2	1746	1	AP425992	AP425992	Streptomy
1140	51.8	5.2	2075	6	AX701365	AX701365	Sequence	1213	51.4	5.2	1926	6	AX811493	AX811493	Sequence
1141	51.8	5.2	2075	9	AF001900	AF001900	Homo sapi	1214	51.4	5.2	2454	8	AF022816	AF022816	Chlamydom
1142	51.8	5.2	2525	6	CQ782831	CQ782831	Sequence	1215	51.4	5.2	2526	9	HSCERPA	HSCERPA	Y11525 H.eapliens m
1143	51.8	5.2	2525	6	BD127336	BD127336	Primer fo	1215	51.4	5.2	3292	10	MUSHP7A2	MUSHP7A2	M76613 Mouse heat
1144	51.8	5.2	2525	9	AK074866	AK074866	Homo sapi	1216	51.4	5.2	3520	5	AY008272	AY008272	Gallus ga
1145	51.8	5.2	2597	6	AX600203	AX600203	Sequence	1217	51.4	5.2	4725	6	AX697993	AX697993	Sequence
1146	51.8	5.2	2714	9	BC069227	BC069227	Homo sapi	1218	51.4	5.2	7916	1	AY185523	AY185523	Actinoplane
1147	51.8	5.2	2725	9	BC069227	BC069227	Homo sapi	1219	51.4	5.2	10968	1	AY185523	AY185523	Actinoplane
1148	51.8	5.2	4469	6	AX236302	AX236302	Sequence	1220	51.4	5.2	12855	1	AF533985	AF533985	Streptomy
1149	51.8	5.2	4469	6	AX578081	AX578081	Sequence	1221	51.4	5.2	14999	3	AF21862181	AF21862181	Nephila c
c1150	51.8	5.2	4469	9	AF056087	AF056087	Homo sapi	1222	51.4	5.2	30000	6	AX250262	AX250262	Sequence
c1151	51.8	5.2	4612	1	AF317284	AF317284	Burkholde	c1223	51.4	5.2	35138	9	AL353799	AL353799	Human DNA
1152	51.8	5.2	10732	6	E32986	E32986	Gene encodi	1224	51.4	5.2	103450	1	AF40781	AF40781	Streptomy
1153	51.8	5.2	11462	8	AF327876	AF327876	Chlamydom	1225	51.4	5.2	110000	2	AY305378_0	AY305378_0	Ralstonia
1154	51.8	5.2	15231	1	AY166598	AY166598	Burkholde	c1226	51.4	5.2	110000	2	LMFLCHR15_5	LMFLCHR15_5	Continuation (6 of
1155	51.8	5.2	34600	1	AY028431	AY028431	Burkholde	c1227	51.4	5.2	110000	2	LMFLCHR15_6	LMFLCHR15_6	Continuation (7 of
c1156	51.8	5.2	40343	1	AC099831	AC099831	Homo sapi	c1228	51.4	5.2	110000	2	LMFLCHR34_00	LMFLCHR34_00	Leishmani
1156	51.8	5.2	83123	2	AC148294	AC148294	Zea mays	c1229	51.4	5.2	130273	8	OSJN00011	OSJN00011	Oryza sat
1157	51.8	5.2	104190	8	AP004257	AP004257	Oryza sat	c1230	51.4	5.2	152828	8	AC133859	AC133859	Oryza sat
1158	51.8	5.2	110000	2	BX255276_03	BX255276_03	Continuation (4 of	c1231	51.4	5.2	205054	10	AC098712	AC098712	Mus muscu
c1159	51.8	5.2	110000	2	AF357202	AF357202	Streptomy	c1232	51.4	5.2	205054	10	AC098712	AC098712	Mus muscu
1160	51.8	5.2	113193	1	AF357202	AF357202	Streptomy	c1233	51.4	5.2	20524	1	AE016925	AE016925	Chromobac
1161	51.8	5.2	113193	6	AX703543	AX703543	Sequence	c1234	51.4	5.2	301332	1	AE017237	AE017237	Mycobacte
c1162	51.8	5.2	123149	9	AC008655	AC008655	Homo sapi	1235	51.4	5.2	302300	1	AP005034	AP005034	Streptomy
1163	51.8	5.2	185539	2	AC018349	AC018349	Homo sapi	1236	51.4	5.2	343473	1	EX640451	EX640451	Bordetell
c1164	51.8	5.2	190590	2	AC135045	AC135045	Homo sapi	1237	51.2	5.2	699	6	AX412281	AX412281	Sequence
1165	51.8	5.2	202050	1	AL646065	AL646065	Ralstonia	1238	51.2	5.2	699	6	AX507044	AX507044	Sequence
c1166	51.8	5.2	203050	1	AL646071	AL646071	Ralstonia	1239	51.2	5.2	699	6	AX651360	AX651360	Sequence
c1167	51.8	5.2	217514	2	AC145779	AC145779	Sus scrof	1240	51.2	5.2	993	6	BD179823	BD179823	Highly th
c1168	51.8	5.2	298300	1	AP005025	AP005025	Streptomy	1241	51.2	5.2	1182	12	AY659409	AY659409	Synthetic
c1169	51.8	5.2	298450	1	SC0939107	SC0939107	Streptomy	1242	51.2	5.2	1220	8	MZETASSEL5	MZETASSEL5	Zea mays al
c1170	51.8	5.2	298550	1	AP005047	AP005047	Streptomy	1243	51.2	5.2	1683	6	AX697979	AX697979	Sequence
c1171	51.8	5.2	298900	1	AP005937	AP005937	Bradyrhiz	1244	51.2	5.2	2181	8	AX100401	AX100401	Oryza sat
c1172	51.8	5.2	299925	1	AP005042	AP005042	Streptomy	1245	51.2	5.2	2277	6	AP004983	AP004983	Sequence
c1173	51.8	5.2	300550	1	AP005030	AP005030	Streptomy	1246	51.2	5.2	2815	1	SLCUTRS	SLCUTRS	S.lividans
1174	51.8	5.2	301675	1	AP005027	AP005027	Streptomy	c1247	51.2	5.2	3480	1	CFICEND	CFICEND	Cellulomona
c1175	51.8	5.2	305520	1	AE016780	AE016780	Pseudomon	1248	51.2	5.2	3993	8	AE017481	AE017481	Heterosig
c1176	51.8	5.2	349008	1	EX640444	EX640444	Bordetell	1249	51.2	5.2	4467	6	E33370	E33370	NA+-ATPase
c1177	51.8	5.2	349841	1	EX572606	EX572606	Rhodopseu	1250	51.2	5.2	6125	1	PSEPSTD	PSEPSTD	Pseudomonas
1178	51.6	5.2	486	1	AF071792	AF071792	Micromono	1251	51.2	5.2	10375	1	AE004549	AE004549	Pseudomon
1179	51.6	5.2	730	8	AF060180	AF060180	Nicotiana	c1252	51.2	5.2	11334	1	AE004948	AE004948	Pseudomon
1180	51.6	5.2	1584	6	BD180289	BD180289	Highly th	1253	51.2	5.2	12357	1	AE004471	AE004471	Pseudomon
1181	51.6	5.2	2595	6	BD179554	BD179554	Highly th	c1254	51.2	5.2	13802	1	AY2759650	AY2759650	Frankia s
c1182	51.6	5.2	2865	8	AF019296	AF019296	Zea mays	1255	51.2	5.2	22437	1	AY207524	AY207524	Streptomy
c1183	51.6	5.2	4523	14	NNULGENES	NNULGENES	Pseudorabie	1256	51.2	5.2	77457	1	AF210249	AF210249	Streptomy
1184	51.6	5.2	4548	8	AY499410	AY499410	Zea mays	1257	51.2	5.2	103458	8	AC108502	AC108502	Oryza sat
c1185	51.6	5.2	23148	14	AY486470S04	AY486470S04	Human her	1258	51.2	5.2	118018	8	AP005675	AP005675	Oryza sat
c1186	51.6	5.2	39576	3	AC008054	AC008054	Leishmani	1259	51.2	5.2	137651	8	AC130600	AC130600	Oryza sat
c1187	51.6	5.2	93821	2	AC021596	AC021596	Homo sapi	c1260	51.2	5.2	165634	2	CR354375	CR354375	Danio rer

1261	51.2	5.2	185437	8	AP005422	AP005422 Oryza sat	cl334	51	5.2	189050	1	AL646066	AL646066 Ralstonia
1262	51.2	5.2	189370	1	AF010496	AF010496 Rhodobact	cl335	51	5.2	232885	2	AC106163	AC106163 Rattus no
cl263	51.2	5.2	267320	2	AC106562	AC106562 Rattus no	cl336	51	5.2	234888	2	AC102097	AC102097 Mus muscu
1264	51.2	5.2	293050	1	SC0939116	AL939116 Streptomy	cl337	51	5.2	248550	1	SC0939120	SC0939120 Streptomy
cl265	51.2	5.2	298550	1	AP005029	AP005029 Streptomy	1338	51	5.2	299800	1	AP005040	AP005040 Streptomy
cl266	51.2	5.2	300425	1	AP005022	AP005022 Streptomy	1339	51	5.2	299850	1	AP005949	AP005949 Bradyrhiz
cl267	51.2	5.2	301925	1	AP005046	AP005046 Streptomy	cl340	51	5.2	300029	8	AE017104	AE017104 Oryza sat
cl268	51.2	5.2	313200	1	AP005024	AP005024 Streptomy	cl341	50.8	5.1	741	6	AX573720	AX573720 Sequence
1269	51.2	5.2	348997	1	BX640427	BX640427 Corynebact	1342	50.8	5.1	1155	6	AR169160	AR169160 Sequence
1270	51.2	5.2	349028	1	BX640413	BX640413 Bordetell	1343	50.8	5.1	1155	6	BD205825	BD205825 Compounds
cl271	51.2	5.2	349305	1	BX640433	BX640433 Bordetell	1344	50.8	5.1	1155	6	CQ785411	CQ785411 Sequence
cl272	51	5.2	473	1	AB066368	AB066368 Streptomy	1345	50.8	5.1	1155	6	AR182450	AR182450 Sequence
cl273	51	5.2	473	1	AB066369	AB066369 Streptomy	1346	50.8	5.1	1155	6	AR194833	AR194833 Sequence
1274	51	5.2	591	12	AY658503	AY658503 Synthetic	1347	50.8	5.1	1155	6	AR233105	AR233105 Sequence
1275	51	5.2	846	6	BD179798	BD179798 Highly th	1348	50.8	5.1	1155	6	AR353310	AR353310 Sequence
1276	51	5.2	846	6	BD179798	BD179798 Highly th	1349	50.8	5.1	1155	6	AX429604	AX429604 Sequence
1277	51	5.2	959	8	AY513924	AY513924 Zea mays	1350	50.8	5.1	1155	6	AX832589	AX832589 Sequence
1278	51	5.2	1004	8	AY513936	AY513936 Zea mays	1351	50.8	5.1	1155	6	BD006333	BD006333 Compounds
1279	51	5.2	1007	8	AF377762	AF377762 Zea mays	1352	50.8	5.1	1155	6	BD006453	BD006453 Compounds
1280	51	5.2	1008	8	AF377752	AF377752 Zea mays	1353	50.8	5.1	1155	6	BD069293	BD069293 Compounds
1281	51	5.2	1008	8	AF377755	AF377755 Zea mays	1354	50.8	5.1	1173	6	AX653829	AX653829 Sequence
1282	51	5.2	1008	8	AF377763	AF377763 Zea mays	1355	50.8	5.1	1221	6	BD180290	BD180290 Highly th
1283	51	5.2	1012	8	AF377764	AF377764 Zea mays	1356	50.8	5.1	1479	6	AX654603	AX654603 Sequence
1284	51	5.2	1012	8	AF377748	AF377748 Zea mays	1357	50.8	5.1	1494	8	AK109381	AK109381 Oryza sat
1285	51	5.2	1012	8	AF377749	AF377749 Zea mays	1358	50.8	5.1	1502	8	AY187941	AY187941 Oryza sat
1286	51	5.2	1012	8	AF377756	AF377756 Zea mays	1359	50.8	5.1	1897	1	MPUPFMS14	MPUPFMS14 M. olivaste
1287	51	5.2	1012	8	AF377766	AF377766 Zea mays	1360	50.8	5.1	2025	8	AK106761	AK106761 Oryza sat
1288	51	5.2	1012	8	AF377766	AF377766 Zea mays	1361	50.8	5.1	2025	8	AK106761	AK106761 Oryza sat
1289	51	5.2	1014	8	AF377746	AF377746 Zea mays	1362	50.8	5.1	2098	5	GGCYP1A4	GGCYP1A4 Oryza sat
1290	51	5.2	1015	8	AY513919	AY513919 Zea mays	1363	50.8	5.1	2356	8	AK121052	AK121052 Oryza sat
1291	51	5.2	1015	8	AY513926	AY513926 Zea mays	1364	50.8	5.1	2358	1	ABU40823	ABU40823 Azospirillu
1292	51	5.2	1018	8	AF377747	AF377747 Zea mays	1365	50.8	5.1	2445	8	AK072584	AK072584 Oryza sat
1293	51	5.2	1018	8	AF377750	AF377750 Zea mays	1366	50.8	5.1	2490	6	BD179835	BD179835 Highly th
1294	51	5.2	1018	8	AF377750	AF377750 Zea mays	cl367	50.8	5.1	4217	5	AF331669	AF331669 Dromaius
1295	51	5.2	1018	8	AF377757	AF377757 Zea mays	1368	50.8	5.1	5760	6	AX616761	AX616761 Sequence
1296	51	5.2	1018	8	AF377758	AF377758 Zea mays	1369	50.8	5.1	10970	1	AE001869	AE001869 Deinococc
1297	51	5.2	1019	8	AF377760	AF377760 Zea mays	1370	50.8	5.1	12885	1	AE012472	AE012472 Xanthomon
1298	51	5.2	1019	8	AY513915	AY513915 Zea luxur	1371	50.8	5.1	14789	1	AE004916	AE004916 Pseudomon
1299	51	5.2	1019	8	AY513933	AY513933 Zea mays	1372	50.8	5.1	21953	6	CQ792619	CQ792619 Sequence
1300	51	5.2	1021	8	AY513925	AY513925 Zea mays	1373	50.8	5.1	32870	1	AF007101	AF007101 Streptomy
1301	51	5.2	1021	8	AY513922	AY513922 Zea mays	cl374	50.8	5.1	36270	1	SLLINC	X79146 S.lincolnen
1302	51	5.2	1025	8	AF168778	AF168778 Eucalyptu	1375	50.8	5.1	37000	14	BHTIUL	Z78205 Bovine herp
1303	51	5.2	1025	8	AF168778	AF168778 Eucalyptu	1376	50.8	5.1	53951	2	AC148879	AC148879 Chlamydom
1304	51	5.2	1025	8	AF168778	AF168778 Eucalyptu	1377	50.8	5.1	53951	2	AC148879	AC148879 Chlamydom
1305	51	5.2	1025	8	AF168778	AF168778 Eucalyptu	1378	50.8	5.1	63082	2	AC022663	AC022663 Homo sapi
1306	51	5.2	1025	8	AF168778	AF168778 Eucalyptu	1379	50.8	5.1	64259	2	AC136782	AC136782 Homo sapi
1307	51	5.2	1025	8	AF168778	AF168778 Eucalyptu	cl379	50.8	5.1	85268	2	AC022648	AC022648 Homo sapi
1308	51	5.2	1025	8	AF168778	AF168778 Eucalyptu	cl380	50.8	5.1	90348	1	AF497482	AF497482 Micromono
1309	51	5.2	1025	8	AF168778	AF168778 Eucalyptu	1381	50.8	5.1	136687	8	AC136148	AC136148 Oryza sat
1310	51	5.2	1025	8	AF168778	AF168778 Eucalyptu	cl382	50.8	5.1	143266	10	AC121997	AC121997 Mus muscu
1311	51	5.2	1025	8	AF168778	AF168778 Eucalyptu	cl383	50.8	5.1	143266	10	AC121997	AC121997 Mus muscu
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cl134	51	5.2	1025	8	AF168778	AF168778 Eucalyptu	1385	50.8	5.1	160922	2	AC104848	AC104848 Oryza sat
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cl137	51	5.2	1025	8	AF168778	AF168778 Eucalyptu	1388	50.8	5.1	228492	10	AC132058	AC132058 Rattus no
cl138	51	5.2	1025	8	AF168778	AF168778 Eucalyptu	1389	50.8	5.1	300425	1	AP005022	AP005022 Streptomy
cl139	51	5.2	1025	8	AF168778	AF168778 Eucalyptu	1390	50.8	5.1	301146	1	AE017311	AE017311 Desulfuvi
cl140	51	5.2	1025	8	AF168778	AF168778 Eucalyptu	1391	50.8	5.1	301675	1	AP005027	AP005027 Pseudomon
cl141	51	5.2	1025	8	AF168778	AF168778 Eucalyptu	1392	50.8	5.1	301675	1	AP005027	AP005027 Pseudomon
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cl147	51	5.2	1025	8	AF168778	AF168778 Eucalyptu	1398	50.6	5.1	1147	8	AK071797	AK071797 Oryza sat
cl148	51	5.2	1025	8	AF168778	AF168778 Eucalyptu	1399	50.6	5.1	1326	8	AK104577	AK104577 Oryza sat
cl149	51	5.2	1025	8	AF168778	AF168778 Eucalyptu	1400	50.6	5.1	1326	8	AK104577	AK104577 Oryza sat
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cl160	51	5.2	1025	8	AF168778	AF168778 Eucalyptu	1411	50.6	5.1	2255	1	AB001291	AB001291 Thermus t
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cl166	51	5.2	1025	8	AF168778	AF168778 Eucalyptu	1417	50.6	5.1	2255	1	AB001291	AB001291 Thermus t
cl167	51	5.2	1025	8	AF168778	AF168778 Eucalyptu	1418	50.6	5.1	2255	1	AB001291	AB001291 Thermus t
cl168	51	5.2	1025	8	AF168778	AF168778 Eucalyptu	1419	50.6	5.1	2255	1	AB001291	AB001291 Thermus t
cl169	51	5.2	1025	8	AF168778								

1407	50.6	5.1	79677	8	AC090435	Chlamydom	AC090435	1480	50.4	5.1	131049	8	AP005391	AP005391	Oryza sat
1408	50.6	5.1	87817	9	AC079174	Chlamydom	AC079174	c1481	50.4	5.1	155106	8	AC117988	AC117988	Oryza sat
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1410	50.6	5.1	110000	1	AE016822_09	Continuation (23 o	AE016822_09	1483	50.4	5.1	162407	8	AP004121	AP004121	Oryza sat
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1412	50.6	5.1	110000	2	LMFLCHR25_05	Continuation (6 of	LMFLCHR25_05	1485	50.4	5.1	169812	2	AC150169	AC150169	Gallus ga
1413	50.6	5.1	111313	8	AP003685	Oryza sat	AP003685	c1486	50.4	5.1	230138	14	AF232689	AF232689	Rat cytom
1414	50.6	5.1	129506	2	AC136100	Rattus no	AC136100	c1487	50.4	5.1	262048	2	AC109382	AC109382	Rattus no
1415	50.6	5.1	144644	8	AP002818	Oryza sat	AP002818	c1488	50.4	5.1	262998	2	AC109723	AC109723	Rattus no
1416	50.6	5.1	144616	2	AP003305	Oryza sat	AP003305	c1489	50.4	5.1	274676	1	AE017305	AE017305	Thermus t
1417	50.6	5.1	159593	2	AC026302	Homo sapi	AC026302	1490	50.4	5.1	300271	8	AE016901	AE016901	Eremothec
1418	50.6	5.1	162400	8	AP005637	Oryza sat	AP005637	1491	50.4	5.1	300263	1	AE016781	AE016781	Pseudomon
1419	50.6	5.1	164853	8	AC135498	Oryza sat	AC135498	c1492	50.4	5.1	303450	1	SC0939130	SC0939130	Streptomy
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1421	50.6	5.1	179047	8	AP005838	Oryza sat	AP005838	c1494	50.4	5.1	309135	1	AP005946	AP005946	Bradyrhiz
1422	50.6	5.1	183095	8	AP005186	Oryza sat	AP005186	1495	50.4	5.1	348014	1	EX640430	EX640430	Bordetell
1423	50.6	5.1	187336	2	AP005427	Oryza sat	AP005427	1496	50.4	5.1	349442	1	BX640447	BX640447	Bordetell
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1425	50.6	5.1	190452	2	AP079167	Mus muscu	AP079167	1498	50.2	5.1	960	11	PM1204G	PM1204G	Penicilli
1426	50.6	5.1	292400	1	SC0939129	Streptomy	SC0939129	1499	50.2	5.1	981	8	AY513911	AY513911	Zea luxur
1427	50.6	5.1	300343	1	AE017310	Desulfovi	AE017310	1500	50.2	5.1	981	8	AY513921	AY513921	Zea mays
1428	50.6	5.1	302998	1	AE016921	Chromobac	AE016921								
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1430	50.6	5.1	307435	1	AE016914	Chromobac	AE016914								
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1432	50.6	5.1	310550	1	SC0939113	Streptomy	SC0939113								
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1438	50.4	5.1	666	12	AY657499	Synthetic	AY657499								
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1442	50.4	5.1	829	8	AK063046	Oryza sat	AK063046								
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1448	50.4	5.1	1685	9	BC030201	Homo sapi	BC030201								
1449	50.4	5.1	1800	1	ANTRA	Homo sapi	ANTRA								
1450	50.4	5.1	1912	1	SRABPS	Homo sapi	SRABPS								
1451	50.4	5.1	1952	1	SCU42212	Streptomyce	SCU42212								
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1453	50.4	5.1	2826	8	AK110150	Oryza sat	AK110150								
1454	50.4	5.1	2949	8	AK068849	Oryza sat	AK068849								
1455	50.4	5.1	3029	14	AF078728	Caprine h	AF078728								
1456	50.4	5.1	3225	1	SAU29446	Streptomyce	SAU29446								
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1461	50.4	5.1	9302	1	SGR243674	Streptomy	SGR243674								
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ALIGNMENTS

LOCUS	AX201342	989 bp	DNA	linear	PAT 30-AUG-2001
DEFINITION	Sequence 21 from Patent WO0153486.				
ACCESSION	AX201342				
VERSION	AX201342.1	GI:15391164			
KEYWORDS					
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	1				
AUTHORS	Ashkenazi,A.J., Goddard,A., Godowski,P.J., Gurney,A.L., Hillan,K.J., Marsters,S.A., Pan,J., Pitti,R.M., Roy,M.A., Smith,V., Stone,D.M., Watanabe,C.K. and Wood,W.I.				
TITLE	Compositions and methods for the treatment of tumour				
JOURNAL	Patent: WO 0153486-A 21 26-JUL-2001;				
FEATURES	Genetech, Inc. (US)				
source	Location/Qualifiers				
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Qy	181	GGCGTGGCCCGCCCATGGGAGCGCGCGAGAGAGCTGCTGTCTCCCGCGCGAGCGC	240		
Db	181	GGCGTGGCCCGCCCATGGGAGCGCGCGAGAGAGCTGCTGTCTCCCGCGCGAGCGC	240		
Qy	241	GCCTGTGGCAGTATCTTCTGAGCGCTCCATCGCGGAGCACCGCGCTCGGAGCGCTGA	300		

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RESULT 2
AX697237 989 bp DNA linear PAT 02-APR-2003
LOCUS Sequence 305 from Patent WO0078961.
DEFINITION AX697237
ACCESSION AX697237
VERSION AX697237.1 GI:29498404
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Ferrera, N., Stewart, T.A., Williams, P.M., Baker, K.P., Desnoyers, L.,
Eaton, D.L., Gao, W.Q., Pan, J., Betstein, D., Fong, S., Goddard, A.,
Godowski, P.J., Gurney, A.L., Smith, V., Tumas, D., Wood, W.I.,
Grimaldi, C.J., Hillan, K.J., Paoni, N.P., Roy, M.A., and Watanabe, C.K.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL Patent: WO 0078961-A 305 28-DEC-2000;
Genentech Inc. (US)
FEATURES
Location/Qualifiers
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source

/organism="Homo sapiens"
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ORIGIN
Query Match 100.0%; Score 989; DB 6; Length 989;
Best Local Similarity 100.0%; Pred. No. 7.5e-125; Indels 0; Gaps 0;
Matches 989; Conservative 0; Mismatches 0;
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DB 1 GCGGGCCCGGAGTCCGAGACCTGTCCAGGAGCTCCAGCTCACGTGACCTGTCTACTGCG 60
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 KEYWORDS FLI_CDNA
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS
 1 (bases 1 to 989)
 Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J., Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Deuel,B., Dowd,P., Eaton,D., Foster,J., Grimaldi,C., Gu,Q., Haas,P.E., Heidens,S., Huang,A., Kim,H.S., Klimowski,L., Jin,Y., Johnson,S., Lee,J., Lewis,L., Liao,D., Mark,M., Robbie,E., Sanchez,C., Schoenfeld,J., Seshagiri,S., Simmons,L., Singh,J., Smith,V., Stinson,J., Vagts,A., Vandien,R., Watanabe,C., Wisand,D., Woods,K., Xie,M.H., Yansura,D., Yi,S., Yu,G., Yuan,J., Zhang,M., Zhang,Z., Goddard,A., Wood,W.I. and Godowski,P.
 The Secreted Protein Discovery Initiative (SPDI), a Large-Scale Effort to Identify Novel Human Secreted and Transmembrane Proteins: A Bioinformatics Assessment
 JOURNAL
 PUBMED
 12975309
 REFERENCE
 2 (bases 1 to 989)
 Clark,H.F.
 Direct Submission
 TITLE
 Submitted (01-AUG-2003) Department of Bioinformatics, Genentech, Inc., 1 DNA Way, South San Francisco, CA 94080, USA
 JOURNAL
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 ACCESSION AX338454
 VERSION AX338454.1 GI:18128893
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
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 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE
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 Meyers,R.A. and Williamson,M.
 25692, a novel human o-methyltransferase family member and uses

thereof:
JOURNAL Patent: WO 0183719-A 1 08-NOV-2001;
Millennium Pharmaceuticals, Inc. (US)
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ORIGIN
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VERSION BC047774.1 GI:28839536
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ORGANISM Homo sapiens
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REFERENCE 1 (bases 1 to 1041)
AUTHORS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Dietzenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
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Carninci, P., Prange, C., Raha, S., Loquelliano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
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Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., R.A.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Faney, J., Helton, E., Kettman, M., Madan, A.C., Rodriguez, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Green, E.D.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Schmutz, J., Myers, R.M.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalios, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
2 (bases 1 to 1041)
Strausberg, R.
Direct Submission
Submitted (03-MAR-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgabs@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINAL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: <http://www-shgc.stanford.edu>
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,

TITLE
JOURNAL
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL
REMARK
COMMENT

R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAK Plate: 98 Row: g Column: 5
 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 21389376.

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gene

CDS

ORIGIN

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RESULT 6
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 DEFINITION
 ACCESSION BD222712
 VERSION BD222712.1 GI:33032482
 KEYWORDS JP 2002519030-A/58.
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 ORGANISM Homo sapiens
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 L (bases 1 to 985)
 Lal, P., Tang, Y. T., Gorgone, G. A., Corley, N. C., Guegler, K. J., Baughn, M. R., Akerblom, I. E., Young, J. A., Yue, H., Patterson, C., Reddy, R., Hillman, J. L. and Bandman, O.
 Human signal peptide-containing protein
 Patent: JP 2002519030-A 58 02-JUL-2002;
 INCYTE PHARMACEUTICALS INC
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 PN JP 2002519030-A/58
 PD 02-JUL-2002
 PF 25-JUN-1999 JP 2000557363
 PR 26-JUN-1998 US 60/090762 31-JUL-1998 US 60/094983 PR
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 PC CHANDRA PATTERSON, ROOPA REDDY, JENNIFER L HILLMAN, OLGA BANDMAN
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|
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RESULT 8

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BC023663
LOCUS BC023663 913 bp mRNA linear PRI 30-JUN-2004
DEFINITION Homo sapiens catechol-O-methyltransferase domain containing 1, mRNA
(cDNA clone MGC:29637 IMAGE:4897624), complete cds.
ACCESSION BC023663
VERSION BC023663.2 GI:40226187
KEYWORDS MGC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 913)
Straussberg,R.L., Feingold,B.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
```

Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S., Loquellano,N.A., Peters,G.J., Aramisan,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gurnatne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Kettman,M., Madan,A.C., Rodrigues,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smalios,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.

Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

12477932

2 (bases 1 to 913)

Straussberg,R.

Direct Submission

Submitted (05-FEB-2002)

National Institutes of Health, Mammalian

Gene Collection (MGC), Cancer Genomics Office, National Cancer

Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,

USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

On Dec 19, 2003 this sequence version replaced gi:23959051.

Contact: MGC help desk

Email: cgapbs-remail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: Rubin Laboratory

DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: National Institutes of Health Intramural

Sequencing Center (NISC),

Gaithersburg, Maryland;

Web site: <http://www.nisc.nih.gov/>

Contact: nisc_mgc@nhgri.nih.gov

Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,

Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,

DiStreich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,

Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Iaric,P., Legaspi,R.,

Maduro,Q.I., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C.,

McDowell,J., Pearson,R., Stantropop,S., Thomas,P.J., Touchman,J.W.,

Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,

Young,A., Zhang,L.-H. and Green,E.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.llnl.gov>

Series: IRAL Plate: 39 Row: j Column: 6

This clone was selected for full length sequencing because it

passed the following selection criteria: GenomesScan gene

prediction, Similarity but not identity to protein.

Location/Qualifiers

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Query Match      91.8%; Score 907.8; DB 9; Length 913;
Best Local Similarity 99.8%; Pred. No. 7.8e-114;
Matches 909; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy 199 GAGCGCGCGAGAGCAGTGCCTCTTCCCTCCCGAGGACAGCGCTGTGGCAGTATCTTC 258
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Qy 259 TGAGCCGCTCCATGCGGAGACACCGCGCTGCGAAGCCTGAGGCTGTGACCTTGGAGC 318
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Qy 499 CCCGAGCTGGGACCGGCCCTTGTGGAGGACGCGCGAGCGGAGCAAGAATCGACCTCC 558
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Qy 979 AAAAAAAAAA 989
Db 901 AAAAAAAAAA 911

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DEFINITION Sequence 7435 from Patent WO02068579.
ACCESSION   CQ721501
VERSION     CQ721501.1 GI:42282358
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Venter,C.J., Adams,M.C., Li,P.W. and Myers,B.W.
  TITLE     Kits, such as nucleic acid arrays, comprising a majority of
            humanexons or transcripts, for detecting expression and other uses
            thereof
  JOURNAL   Patent: WO 02068579-A 7435 06-SEP-2002;
            PE Corporation (US)
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Best Local Similarity 100.0%; Pred. No. 1e-97;
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Qy 144 CTGGCGCGCGCTTCGCCACTGGCTCTTCTGGGAGGCGGTGCCCGCCATGGGAGGC 203
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LOCUS
DEFINITION
Sequence 3 from Patent WO0183719.
ACCESSION
AX338456
VERSION
AX338456.1 GI:18128895
KEYWORDS
Homo sapiens (human)
SOURCE
Homo sapiens
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
Meyers, R.A. and Williamson, M.
AUTHORS
25692, a novel human o-methyltransferase family member and uses
TITLE
thereof
JOURNAL
Patent: WO 0183719-A 3 08-NOV-2001;
Millennium Pharmaceuticals, Inc. (US)
FEATURES
Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 1e-97;
Matches 789; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      84 ATGACCCAGCGGTGCGCGGCTCTCCGTGCGCGCGGCTGGCCCTGGGCTCAGCCGCA 143
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QY      864 AAGATCTAG 872
Db      781 AAGATCTAG 789

BC049670 946 bp mRNA linear ROD 30-JUN-2004
Mus musculus catechol-O-methyltransferase domain containing 1, mRNA
(cDNA clone MGC:58496 IMAGE:6535487), complete cds.
ACCESSION
BC049670
VERSION
BC049670.1 GI:29612504
KEYWORDS
MGC.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 946)
REFERENCE
Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, P.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
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Abramson, R.D., Mullany, S.J., Bosak, S.A., McEwan, P.J.,
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Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
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Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywicki, M.I., Skalska, U., Smalish, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
2 (bases 1 to 946)
REFERENCE
Strausberg, R.
Direct Submission
Submitted (31-MAR-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
```



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Best Local Similarity 99.7%; Pred. No. 5.8e-33;
Matches 323; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 649 AGAAGTCTCGGCC-TACTACGAGCGCTGCTCGAGCTGCTGCGACCGGAGCATCTCTC 707
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888 AGTGGGCTCGAGGAGGTTGCTCGGAAACCCAGGAATTGACCTGAGTTTAAATTCG 947
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Db 26 AAAATAAGTGGGCTGGGACACA 3

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DEFINITION
unordered pieces.
ACCESSION AC120475
VERSION AC120475.7 GI:25137871
KEYWORDS HTG; HTGS PHASE1; HTGS DRAFT; HTGS FULLTOP.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D.,
Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H.,
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Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P.,
Frazer, C.M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M.,
Gebregorgis, E., Geer, K., Gill, R., Grady, M., Guerra, W., Guevara, W.,
Gunaratne, P., Haaland, W., Hamill, C., Hamilton, C., Hamilton, K.,
Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J.,
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Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C.,
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Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J.,
Lorensuewa, L., Loulseghe, H., Lozada, R.J., Lu, X., Ma, J.,
Maheshwari, M., Mahindaratne, M., Mahmoud, M., Malloy, K., Mangum, A.,
Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E.,
Mawhney, S., McLeod, M.P., McNeill, T.Z., Meenen, E.,
Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S.,
Morgan, M., Morris, K., Morris, S., Munidasa, M., Murphy, M., Nair, L.,
Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S.,

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TITLE JOURNAL
REFERENCE
AUTHORS
TITLE JOURNAL
REFERENCE
AUTHORS
TITLE JOURNAL
COMMENT

Nwaokemeleh, O., Okwuonu, G., Olarnpunsagoon, A., Pal, S., Parks, K.,
Pasternak, S., Paul, H., Perez, L., Perez, L., Pflankoch, C.,
Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pu, L.-L.,
Puazo, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M.A., Reigh, R.,
Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, P.,
Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.J.,
Sanders, W., Savery, G., Scherer, S., Scott, G., Shatman, S., Shen, H.,
Shetty, J., Shivartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D.,
Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Soosa, J.,
Steimle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C.,
Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, B., Umani, K.,
Valas, R., Vera, V., Villasana, D., Waldron, L., Walker, B., Wang, J.,
Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F.,
Williams, G., Willson, R., Wleczky, R., Wooden, H., Worley, K.,
Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V.,
Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von
Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O.,
Weinstock, G. and Gibbs, R.A.

Direct Submission
Unpublished
2 (bases 1 to 237829)
Worley, K.C.
Direct Submission
Submitted (07-MAY-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 237829)
Rat Genome Sequencing Consortium.
Direct Submission
Submitted (20-NOV-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Nov 20, 2002 this sequence version replaced gi:23267656.
The sequence in this assembly is a combination of BAC based reads
and whole genome shotgun sequencing reads assembled using Atlas
(http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described
in the feature table below represents a scaffold in the Atlas
assembly (a 'contig-scaffold'). Within each contig-scaffold,
individual sequence contigs are ordered and oriented, and separated
by sized gaps filled with Ns to the estimated size. The sequence
may extend beyond the ends of the clone and there may be sequence
contigs within a contig-scaffold that consist entirely of whole
genome shotgun sequence reads. Both end sequences and whole genome
shotgun sequence only contigs will be indicated in the feature
table.

----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GXLH
Center clone name: CH230-34D17
----- Summary Statistics
Assembly program: Phrap; version 0.990329
Consensus quality: 218320 bases at least Q40
Consensus quality: 222359 bases at least Q30
Consensus quality: 225092 bases at least Q20
Estimated insert size: 222440; sum-of-contigs estimation
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
-----
* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 2 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 236267: contig of 236267 bp in length
* 236268 236367: gap of unknown length

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* 236368 237829: contig of 1462 bp in length.
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            clone_end:Sp6
            7112..7990
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            complement(233022..233942)
            /note="clone boundary"
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Matches 433; Conservative 0; Mismatches 188; Indels 1; Gaps 1;

QY 53 TCATGCTCCCGCGGCTCTCCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTCTCCGT 112
Db 81826 TTACTGGTCCCGAGTCTGCTGCTCTACTCCAGCACAGTGACCTCTGCTTTGTAAC 81885

QY 113 GCCCGCGCGTGGCGCTGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTTT 172
Db 81886 CGCACATGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTTT 81945

QY 173 CCTGGGAGGCGGCTCCCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 232
Db 81946 CCTGGGAGGCGGCTCCCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 82005

QY 233 GGACAGCGCGTGGGAGTATCTTCTGAGCGGCTCCATGCGGAGGCGGCGGCGGCGGCGG 292
Db 82006 GGACAAATCCCTGTGGGAGTATCTTCTGAGCTGCTCCATGAGGAGGCGGCGGCGGCGG 82065

QY 293 AAGCTGAGGCTGCTGACCTGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 352
Db 82066 GAGCTTGGAGCTGCTGACCTGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 82125

QY 353 GGCCCGAGCTTTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 412
Db 82126 GSCCCAACTTCTGGTCAACCTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 82185

QY 413 CACTTACGGGCTA-CTCCGCGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 471
Db 82186 TACTTTACGGGCTACCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 82245

QY 472 TGGTCACTGCGAGTGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 531
Db 82246 TGGTCACTGCGAGTGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 82305

QY 532 CCGAGCGGAGCACAAGATCGACCTCCGCGTGAAGCCCGGCGGCGGCGGCGGCGGCGGCGG 591
Db 82306 CAGAAGTGGAGCAGAAGATCGAATTCGCGTGCAGCCCGGCGGCGGCGGCGGCGGCGGCGG 82365

QY 592 TCCTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 651
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QY 652 ACTGCTCGGCTTACTACGAGCG 673
Db 82426 CTGCTGCGACTCTTACGCGCG 82447

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```

RESULT 14
AL390034/c
LOCUS
DEFINITION
    Human DNA sequence from clone RP11-375G3 on chromosome 10, complete
    sequence.
ACCESSION
    AL390034
VERSION
    AL390034.23
KEYWORDS
    HTG.
SOURCE
    Homo sapiens (human)
ORGANISM
    Homo sapiens
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
    1 (bases 1 to 38679)
REFERENCE
    Wray, P.
    Direct Submission
    Submitted (01-JAN-2002) Wellcome Trust Sanger Institute, Hinxton,
    Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
    humquery@sanger.ac.uk
    Cloned from request: clonerequest@sanger.ac.uk
    On Jan 2, 2002 this sequence version replaced gi:18032093.
    During sequence assembly data is compared from overlapping clones.
    Where differences are found these are annotated as variations
    together with a note of the overlapping clone name. Note that the
    variation annotation may not be found in the sequence submission
    corresponding to the overlapping clone, as we submit sequences with
    only a small overlap as described above.
    This sequence was finished as follows unless otherwise noted: all
    regions were either double-stranded or sequenced with an alternate
    chemistry or covered by high quality data (i.e., phred quality >=
    30); an attempt was made to resolve all sequencing problems, such
    as compressions and repeats; all regions were covered by at least
    one plasmid subclone or more than one M13 subclone; and the
    assembly was confirmed by restriction digest. The following
    abbreviations are used to associate primary accession numbers given
    in the feature table with their source databases: Em: EMBL; Sw:
    SWISSPROT; Tr: TrEMBL; Wp: WORMPEP; Information on the WORMPEP
    database can be found at
    http://www.sanger.ac.uk/Projects/c_elegans/wormpep
    This sequence
    was generated from part of bacterial clone contigs of human
    chromosome 10, constructed by the Sanger Centre Chromosome 10
    Mapping Group. Further information can be found at
    http://www.sanger.ac.uk/HGP/Chr10
    RP11-375G3 is from the library RP11-11.2 constructed by the group
    of Peter de Jong. For further details see
    http://www.chori.org/bacpac/home.htm
    VECTOR: pBAC3.6
    IMPORTANT: This sequence is not the entire insert of clone
    RP11-375G3 it may be shorter because we sequence overlapping
    sections only once, except for a short overlap.
    The true left end of clone RP11-399K21 is at 36680 in this
    sequence. The true right end of clone RP11-48715 is at 2000 in this
    sequence.
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Query Match      26.0%; Score 256.8; DB 9; Length 38679;
Best Local Similarity 97.4%; Pred. No. 5.2e-26;
Matches 261; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 704 CTGCGCGCTCTCAGAGTCTGTGGCGGCGGAGAGGTGTGCAACCTCCGAAGGGGAGGT 763
Db 7761 CCGCGCGCTCTCAGAGTCTGTGGCGGCGGAGAGGTGTGCAACCTCCGAAGGGGAGGT 7702

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QY 764 GCGGCCGAGTGTGTGCGAAACCTAAACGAACGATCCGGCGGACGTCAGGCTACAT 823
 Db 7701 GCGGCCGAGTGTGTGCGAAACCTAAACGAACGATCCGGCGGACGTCAGGCTACAT 7642
 QY 824 CAGCCTCTCTGCCCCCTGGCGGATGACTACCTTGGCCCTTCAAGATCTAGGCTGCGCCCT 883
 Db 7641 CAGCCTCTCTGCCCCCTGGCGGATGACTACCTTGGCCCTTCAAGATCTAGGCTGCGCCCT 7582
 QY 884 AGTAGTGGCTCGAGGAGGAGGTTCCCTGGGAAACCCCGAGGATTCACCTGAGTTTAAA 943
 Db 7581 AGTAGTGGCTCGAGGAGGAGGTTCCCTGGGAAACCCCGAGGATTCACCTGAGTTTAAA 7522
 QY 944 TTCGAARATTAAGTGGGCTGGACACA 971
 Db 7521 TTCGAARATTAAGTGGGCTGGACACA 7494

RESULT 15
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 DEFINITION Homo sapiens chromosome 10 clone RP11-770D23 map 10, WORKING DRAFT
 SEQUENCE, 28 unordered pieces.
 ACCESSION AC027393
 VERSION AC027393.3 GI:8076860
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 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 169612)
 Birren,B., Linton,L., Nusbaum,C. and Lander,E.
 Homo sapiens chromosome 10, clone RP11-770D23
 Unpublished
 2 (bases 1 to 169612)
 Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
 Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F.,
 Boguslavsky,L., Boukhgalter,B., Brown,A., Burkett,G.,
 Campopiano,A., Castie,A., Choepel,Y., Colangelo,M., Collins,S.,
 Collymore,A., Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S.,
 Dodge,S., Domino,M., Doyle,M., Ferreira,P., FiczHugh,W., Gage,D.,
 Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L.,
 Grand-Pierre,N., Grant,G., Hagos,B., Heaford,A., Horton,L.,
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 Klein,J., LaRocque,K., Lamazares,R., Landers,T., Lehoczy,J.,
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 O'Neil,D., Olivar,T.M., Oliver,J., Peterson,K., Riley,R., Rogov,P.,
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 Vasiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,
 Young,G., Zainoun,J., Zimmer,A. and Zody,M.

TITLE
 JOURNAL
 REFERENCE
 AUTHORS
 3 (bases 1 to 169612)
 Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
 Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F.,
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 Dodge,S., Domino,M., Doyle,M., Ferreira,P., FiczHugh,W., Gage,D.,
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 Klein,J., LaRocque,K., Lamazares,R., Landers,T., Lehoczy,J.,
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 McCarthy,M., McEwan,P., McGurk,A., McKernan,K., McPheeters,R.,
 Meldrim,J., Meneus,L., Mihova,T., Miranda,C., Mlenga,V., Morrow,J.,
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 Tesfaye,S., Theodore,J., Tirrell,A., Travers,M., Trigilio,J.,
 Vasiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,
 Young,G., Zainoun,J., Zimmer,A. and Zody,M.

O'Neil,D., Olivar,T.M., Oliver,J., Peterson,K., Pierre,N.,
 Pibani,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D.,
 Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B.,
 Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamae,J.,
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 Vasiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,
 Young,G., Zainoun,J., Zimmer,A. and Zody,M.

Direct Submission

Submitted (24-AUG-2002) Whitehead Institute/MIT Center for Genome

Research, 320 Charles Street, Cambridge, MA 02141, USA

On May 25, 2000 this sequence version replaced gi:7652066.

All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: http://www-seq.wi.mit.edu

Contact: sequence_submissions@genome.wi.mit.edu

----- Project Information

Center project name: L6572

Center clone name: 770 D 23

----- Summary Statistics

Sequencing vector: M13; M77815; 100% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.960731

Consensus quality: 155213 bases at least Q40

Consensus quality: 162022 bases at least Q30

Consensus quality: 164973 bases at least Q20

Insert size: 179000; agarose-fp

Insert size: 166912; sum-of-contigs

Quality coverage: 4.1 in Q20 bases; agarose-fp

Quality coverage: 4.4 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently

* consists of 28 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.

* 1 1191: contig of 1191 bp in length

* 1192 1291: gap of 100 bp

* 1292 2404: contig of 1113 bp in length

* 2405 2504: gap of 100 bp

* 2505 3705: contig of 1201 bp in length

* 3706 3805: gap of 100 bp

* 3806 4734: contig of 929 bp in length

* 4735 4834: gap of 100 bp

* 4835 6570: contig of 1736 bp in length

* 6571 6570: gap of 100 bp

* 6571 8583: contig of 1313 bp in length

* 8584 8684: gap of 100 bp

* 8684 10290: contig of 1607 bp in length

* 10291 10390: gap of 100 bp

* 10391 11938: contig of 1548 bp in length

* 11939 12038: gap of 100 bp

* 12039 15839: contig of 3801 bp in length

* 15840 15939: gap of 100 bp

* 15940 19203: contig of 3264 bp in length

* 19204 19303: gap of 100 bp

* 19304 22581: contig of 3278 bp in length

* 22582 22681: gap of 100 bp

* 22682 24947: contig of 2266 bp in length

* 24948 25048: gap of 100 bp

* 25048 28167: contig of 3120 bp in length

* 28168 28267: gap of 100 bp

* 28268 32083: contig of 3816 bp in length

* 32084 32183: gap of 100 bp

* 32184 35334: contig of 3350 bp in length

* 35334 41517: contig of 5884 bp in length

TITLE
 JOURNAL
 COMMENT

*	41518	41617: gap of 100 bp
*	41618	47143: contig of 5526 bp in length
*	47143	47243: gap of 100 bp
*	47144	51694: contig of 4451 bp in length
*	47244	51794: gap of 100 bp
*	51695	57570: contig of 5776 bp in length
*	51795	57670: gap of 100 bp
*	57671	63190: contig of 5520 bp in length
*	63191	63290: gap of 100 bp
*	63291	70708: contig of 7418 bp in length
*	70709	78088: gap of 100 bp
*	78089	78988: contig of 8180 bp in length
*	78989	79088: gap of 100 bp
*	79089	86527: contig of 7439 bp in length
*	86528	86627: gap of 100 bp
*	86628	99114: contig of 12487 bp in length
*	99115	99214: gap of 100 bp
*	99215	110221: contig of 11007 bp in length
*	110222	110321: gap of 100 bp
*	110322	123287: contig of 12966 bp in length
*	123288	123387: gap of 100 bp
*	123388	147877: contig of 24490 bp in length
*	147878	147977: gap of 100 bp
*	147978	159612: contig of 21635 bp in length.
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misc_feature	12039. .15839	
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misc_feature	19304. .22581	
	/note="assembly_fragment"	
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misc_feature	41618. .47143	
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misc_feature	47244. .51694	
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 12, 2005, 12:52:52 ; Search time 3040 Seconds
(without alignments)
11854.900 Million cell updates/sec

Title: US-10-017-407A-305

Perfect score: 989

Sequence: 1 gcgggcccggagtcgaga.....caaaaaaaaaaaaaaaaaaaaa 989

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database :

1: gb_est1.*

2: gb_est2.*

3: gb_hic.*

4: gb_est3.*

5: gb_est4.*

6: gb_est5.*

7: gb_est6.*

8: gb_gest1.*

9: gb_gest2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	762.6	77.1	771	6	CB852030 UI-CF-FNO
3	743	75.1	814	4	BM051236 603634191
4	736	74.4	756	6	CA777547 ip21g07.x
5	721	72.9	1006	2	BF663323 602144463
6	716	72.4	921	2	BF664198 602145812
7	707.2	71.5	921	5	BM976177 UI-CF-FNO
8	699.8	70.8	750	6	CB852718 UI-CF-FNO
9	684.4	69.2	772	2	BE796570 601592247
10	669.8	67.7	779	2	BF663695 602145414
11	666.4	67.4	934	5	BQ931589 AGENCOURT
12	630	63.7	1065	5	BQ072503 AGENCOURT
13	625	63.2	625	4	BM768764 K-EST0051
14	621	62.8	912	4	BG339399 602437508
15	609.2	61.6	2243	3	AK054334 Mus muscu
16	607.6	61.4	919	3	AK007659 Mus muscu
17	603.4	61.0	606	2	AW157329 au94f01.x
18	587.8	59.4	910	6	BY707694 BY707694
19	585.8	59.2	589	1	AI692198 wd37h07.x
20	585.6	59.2	1122	4	BG339315 602437607
21	580	58.6	580	4	BM769685 K-EST0052
22	579	58.5	998	5	BQ918468 AGENCOURT
23	578.4	58.5	581	1	AI923559 au95e03.y
24	578.4	58.5	691	2	BE279279 601157608

25	574.6	58.1	904	6	CB194568
26	574.2	58.1	826	5	BP433057
27	564.4	57.1	582	2	AW157252
28	562.8	56.9	886	6	CB181160
29	560.2	56.6	753	5	BP463671
30	557.2	56.3	977	5	BUS41828
31	549.2	55.5	578	1	AW003514
32	548.6	55.5	620	1	AA584408
33	545.4	55.1	1308	3	CR602194
34	542.8	54.9	909	6	CB194405
35	542	54.8	572	1	AI765658
36	540.2	54.6	639	4	BG910899
37	538.4	54.4	566	2	AW163525
38	538.4	54.4	999	3	BC019467
39	535	54.1	564	2	AW163385
40	533.4	53.9	790	4	BI411825
41	526.2	53.2	688	7	CK464189
42	522.6	52.8	546	2	AW157459
43	522	52.8	1035	5	BX339546
44	521.2	52.7	714	2	BF341318
45	519	52.5	725	7	CN157520
46	519	52.5	725	7	CN159458
47	515.6	52.1	575	1	AI810740
48	511.8	51.7	516	4	BG285119
49	509.8	51.5	710	5	BQ746381
50	487.4	49.3	676	2	BB666437
51	482.4	48.8	710	7	CK771494
52	471.8	47.7	638	1	AI924025
53	470.2	47.5	1321	3	CR625911
54	466.4	47.2	666	7	CK463833
55	465.2	47.0	614	7	CK622065
56	460.8	46.6	682	7	CN166896
57	460	46.5	675	7	CN161942
58	460	46.5	675	7	CN163323
59	460	46.5	685	7	CN157439
60	460	46.5	685	7	CN159383
61	456.8	46.2	681	7	CK838500
62	456	46.1	456	5	BQ083301
63	450.2	45.5	622	6	CD674768
64	447.4	45.2	449	2	AW163255
65	446.2	45.1	573	4	BI340505
66	446	45.1	446	4	BM825668
67	445.6	45.1	453	1	AI963924
68	441.4	44.6	459	1	AI925284
69	439.6	44.4	629	1	AI989669
70	439	44.4	1110	4	BI198020
71	438.8	44.4	454	5	BUS00439
72	438.4	44.3	487	7	CK819654
73	438.4	44.3	507	4	BM129438
74	438.4	44.3	519	4	BM141699
75	437.6	44.2	556	2	BE665755
76	437.2	44.2	538	1	AI659582
77	434	43.9	434	4	BM826016
78	427.8	43.3	605	4	BG895491
79	427.4	43.2	549	2	BE014998
80	427.2	43.2	546	2	BE237447
81	426.2	43.1	543	2	BE665750
82	425.6	43.0	550	2	BE684896
83	422.6	42.7	525	4	BM129725
84	419.8	42.4	579	4	BI341406
85	417.4	42.2	460	1	AI340993
86	417	42.2	460	1	AI340993
87	416.2	42.1	970	5	BX422891
88	415.4	42.0	448	1	AI349083
89	413	41.8	413	5	BQ082692
90	411.4	41.6	421	2	AW299522
91	410.8	41.5	422	2	BF593185
92	410.6	41.5	513	2	BF193231
93	406.4	41.1	580	4	BI680796
94	406	41.1	415	2	AW299513
95	404.8	40.9	695	4	BG081244
96	398.2	40.3	1162	2	BE797685
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CB194568	AGENCOURT
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CB181160	AGENCOURT
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AW003514	wq6g010.x
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CR602194	full-leng
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BF341318	602013260
CN157520	946232 MA
CN159458	948536 MA
AI810740	tu04a11.x
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BQ746381	UI-M-ERO-
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CK771494	959788 MA
AI924025	wn73e06.x
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CK463833	934767 MA
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CN163323	952815 MA
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CN159383	948451 MA
CK838500	UI-R-AFI-
BQ083301	K-EST0145
CD674768	fe15a05.y
AW163255	au93e01.y
BI340505	365795 MA
BM825668	K-EST0097
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AI925284	au59e03.x
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BI198020	602762169
BUS00439	AGENCOURT
CK819654	if22d02.x
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BM141699	if24h03.x
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BE014998	126934 MA
BE237447	146741 MA
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AI340993	q082909.x
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AI349083	q083g09.x
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AW299522	x840h01.x
BF593185	7050a03.x
BF193231	244743 MA
BI680796	459974 MA
AW299513	x840g01.x
BG081244	H3062H08-
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BE797685	601584583

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98	397.6	40.2	524	6	CB720369	AMGNNUC:N	171	253	25.6	1292	3	CR681700	Tetraodon
99	397.2	40.2	584	7	CF360100	821402 WA	172	252.8	25.6	1208	3	CR700159	Tetraodon
100	396	40.0	405	1	AI912836	t886c05.x	173	251.4	25.4	1178	3	CR660388	Tetraodon
101	390.2	39.5	516	6	CB716330	AMGNNUC:C	174	251.4	25.4	1201	3	CR633873	Tetraodon
102	387	39.1	411	4	BN768965	K-EST0052	175	251.4	25.4	1205	3	CR692309	Tetraodon
103	385.2	38.9	502	7	CK819655	K-EST0052	176	251.4	25.4	1220	3	CR682032	Tetraodon
104	375.2	37.9	565	4	BN753400	K-EST0030	177	251.4	25.4	1224	3	CR698208	Tetraodon
105	373.8	37.8	517	9	CG651631	OST413096	178	251.4	25.4	1228	3	CR731482	Tetraodon
106	373.2	37.7	476	4	BN141962	BM141962 if24h03.y	179	251.4	25.4	1229	3	CR701700	Tetraodon
107	370	37.4	506	4	BI340371	BI340371 365618 MA	180	250.8	25.4	1215	3	CR676419	Tetraodon
108	365.2	36.9	370	1	AI341293	AI341293 Q85d06.x	181	249.8	25.3	1161	3	CR682009	Tetraodon
109	364	36.8	485	5	EX524890	EX524890	182	249.8	25.3	1226	3	CR695099	Tetraodon
110	361.2	36.5	977	4	BI198073	BI198073 60762269	183	249.8	25.3	1238	3	CR682588	Tetraodon
111	358.2	35.7	732	2	BE287985	BE287985 601093725	184	249.8	25.3	1244	3	CR723230	Tetraodon
112	346.2	35.0	362	2	BF509580	BF509580 UI-H-B14-	185	249.8	25.3	1247	3	CR727683	Tetraodon
113	345.8	35.0	365	6	CB050636	CB050636 NISC g118	186	249.8	25.3	1290	3	CR647544	Tetraodon
114	345.6	34.9	553	2	BE286087	BE286087 601095931	187	249.8	25.3	1572	3	CR693937	Tetraodon
115	344.2	34.8	365	6	CB050637	CB050637 NISC g118	188	249.2	25.2	1218	3	CR727337	Tetraodon
116	343	34.7	1056	5	EX339545	EX339545	189	249	25.2	1216	3	CR732881	Tetraodon
117	342.6	34.6	515	6	CF181537	CF181537 818378 MA	190	248.8	25.2	1218	3	CR687075	Tetraodon
118	339.4	34.3	505	1	AA016453	AA016453 mh40c05.r	191	248.6	25.1	1224	3	CR662508	Tetraodon
119	335	33.9	458	4	BG689814	BG689814 338070 BA	192	248.2	25.1	1198	3	CR695082	Tetraodon
120	332.2	33.6	539	2	BF769048	BF769048	193	248.2	25.1	1231	3	CR687110	Tetraodon
121	329	33.3	442	7	CK457735	CK457735 922062 MA	194	248.2	25.1	1243	3	CR638609	Tetraodon
122	329	33.3	442	7	CK458804	CK458804 923214 MA	195	247.6	25.0	360	5	BY057583	BY057583
123	328.4	33.2	341	1	AI650609	AI650609 w01f04.x	196	247.6	25.0	1186	3	BY057583	BY057583
124	326.4	33.0	470	6	CA777819	CA777819 ip21907.y	197	246.8	25.0	423	2	AW252701	UI-R-BJO-
125	315.4	31.9	499	4	BG995780	BG995780 359409 MA	198	246.6	24.9	1222	3	CR696179	Tetraodon
126	313.4	31.7	528	1	AI548694	AI548694 UI-R-C3-t	199	244.6	24.7	375	5	CR684437	Tetraodon
127	312	31.5	326	2	AA279840	AA279840 z893d02.s	200	244.6	24.7	1143	3	BY041991	BY041991
128	311.8	31.5	426	2	BE233897	BE233897 140418 MA	201	244.4	24.7	1143	3	CR685515	Tetraodon
129	306.6	31.0	414	1	AI325580	AI325580 mm60d11.y	202	243	24.6	1211	3	BI832844	BI832844
130	303.4	30.7	402	6	CB769191	CB769191 AMGNNUC:N	203	243	24.5	401	6	CR698267	Tetraodon
131	301.2	30.5	414	1	AI892364	AI892364 mm60d11.y	204	242.4	24.5	372	5	CR698999	AMGNNUC:N
132	300.2	30.4	458	6	CB739243	CB739243 AMGNNUC:N	205	242.2	24.5	372	5	BY042000	BY042000
133	296	29.9	413	5	BY094423	BY094423	206	241	24.4	1188	3	CR690884	Tetraodon
134	292.2	29.5	398	1	AA132529	AA132529 z020d02.s	207	241	24.4	1263	3	CR727342	Tetraodon
135	292	29.5	382	4	BM856156	BM856156 K-EST0139	208	240.6	24.3	503	3	RG669239	RG669239
136	291.8	29.5	971	4	BG680071	BG680071 602628219	209	238.4	24.1	411	2	AW252346	UI-R-BJO-
137	291.6	29.5	428	5	BY041621	BY041621	210	238	24.0	1188	3	CR698292	Tetraodon
138	291.6	29.5	479	2	BF522579	BF522579 UI-R-BJO-	211	237.8	24.0	1186	3	CR690706	Tetraodon
139	288.8	29.2	379	2	CA480947	CA480947 AGENCOURT	212	237.2	24.0	1200	3	CR698066	Tetraodon
140	288.2	29.1	1074	6	CA518933	CA518933	213	236.8	23.9	740	5	BY074246	BY074246
141	283.2	28.6	375	2	BE653217	BE653217 UI-M-AM0-	214	235.2	23.8	240	1	AI420833	AI420833
142	279	28.2	664	2	BF181707	BF181707 601805520	215	235.2	23.7	292	2	AW074796	AW074796
143	274.8	27.8	683	5	BU615801	BU615801 UI-H-DF0-	216	234.4	23.7	439	5	BY447416	BY447416
144	274.2	27.7	400	5	BY050241	BY050241	217	234.4	23.7	937	6	CA458592	CA458592
145	270	27.3	683	5	BU615801	BU615801 UI-H-DF0-	218	234.4	23.7	1215	3	CR726092	Tetraodon
146	262.8	26.6	434	1	AA068794	AA068794 mm60d11.r	219	234	23.7	273	1	AI307481	AI307481
147	262	26.5	384	1	AA068794	AA068794	220	232.8	23.5	913	3	CR638711	CR638711
148	262	26.5	421	1	AA068794	AA068794	221	232.6	23.5	344	5	BY057551	BY057551
149	262	26.5	473	6	CA395926	CA395926	222	232.4	23.5	583	9	CS567423	OST193749
150	261.8	26.5	1235	5	CR721460	CR721460	223	232.4	23.4	325	2	AW301440	AW301440
151	261.4	26.4	722	5	BO208081	BO208081 UI-R-EP0-	224	231	23.4	871	3	CR653669	CR653669
152	260.2	26.3	1275	3	CR725106	CR725106	225	231	23.3	362	5	BY045218	BY045218
153	260.2	26.3	1194	3	CR722216	CR722216	226	230.8	23.3	419	7	CN542838	CN542838
154	258.6	26.1	1207	3	CR722216	CR722216	227	230	23.3	878	3	CR654482	Tetraodon
155	258.6	26.1	1232	3	CR722216	CR722216	228	229.4	23.2	1181	3	CR692840	Tetraodon
156	258	25.8	1211	3	CR722216	CR722216	229	229.2	23.2	769	6	CA346219	CA346219
157	257	25.6	1211	3	CR722216	CR722216	230	229.2	23.2	336	5	BY048400	BY048400
158	257	25.6	436	2	AW251225	AW251225 UI-R-BJO-	231	229	23.2	885	3	CR633632	Tetraodon
159	256.6	25.9	296	4	BI711000	BI711000 id95h06.y	232	228.4	23.1	360	1	AA279903	AA279903
160	255.8	25.8	1133	3	CR640078	CR640078	233	228	23.1	862	3	CR650550	Tetraodon
161	255.4	25.8	1183	3	CR696893	CR696893	234	225.4	22.8	876	4	CR649975	Tetraodon
162	255	25.7	1156	3	CR685973	CR685973	235	225.2	22.8	406	4	BI288752	UI-R-DK0-
163	254.6	25.7	1163	3	CR685973	CR685973	236	225.2	22.7	881	3	CR656653	Tetraodon
164	253.8	25.7	371	5	BY048974	BY048974	237	224.8	22.6	874	3	CR651698	Tetraodon
165	253.8	25.7	374	5	BY037587	BY037587	238	223.8	22.6	884	3	CR653782	Tetraodon
166	253.8	25.7	1144	3	CR700317	CR700317	239	223.8	22.6	904	3	CR639009	Tetraodon
167	253.8	25.7	1216	3	CR685301	CR685301	240	223.8	22.6	924	3	CR655129	Tetraodon
168	253.2	25.6	298	2	AW664650	AW664650 hi84b01.x	241	223.8	22.5	858	3	CR641707	Tetraodon
169	253	25.6	1162	3	CR683289	CR683289	242	223	22.5	873	3	CR733986	Tetraodon
170	253	25.6	1245	3	CR683190	CR683190	243	222.8	22.5				

244	222.4	22.5	449	1	AA132590	zo20d02.r	317	184.6	18.7	638	4	BJ711589	BJ711589
245	222.4	22.5	860	3	CR656656	Tetraodon	318	184	18.6	670	6	CA355616	CA355616
246	222.2	22.5	910	3	CR637704	Tetraodon	319	184	18.6	678	7	CR974704	CR974704
247	221	22.3	863	3	CR644752	Tetraodon	320	184	18.6	869	7	CR985211	CR985211
248	220	22.2	863	3	CR637158	Tetraodon	321	183.2	18.5	691	4	BJ708514	BJ708514
249	219.4	22.2	866	6	CA374473	648906 NC	322	182.2	18.4	527	5	BQ615750	BQ615750
250	219.4	22.2	740	3	CR655148	Tetraodon	323	180.8	18.3	336	5	BY398227	BY398227
251	219.4	22.2	861	3	CR634105	Tetraodon	324	178.8	18.1	539	6	CA333551	CA333551
252	219.4	22.2	864	3	CR653465	Tetraodon	325	177.6	18.0	617	3	CR647326	CR647326
253	219	22.1	910	3	CR637674	Tetraodon	326	177	17.9	177	7	F36952	F36952
254	217.8	22.0	526	5	BY468703	BY468703	327	175.6	17.8	505	4	BG835402	BG835402
255	217.8	22.0	862	3	CR645383	Tetraodon	328	173.2	17.5	598	7	CR895107	CR895107
256	217.6	22.0	388	5	BY405666	BY405666	329	172.6	17.5	1100	7	CK161647	CK161647
257	217.2	22.0	724	6	CA382012	CA382012	330	172.2	17.4	579	7	CR895655	CR895655
258	217	21.9	386	5	BY394806	BY394806	331	171	17.3	963	7	CK409756	CK409756
259	215.8	21.8	747	6	CA388383	670627 NC	332	170.2	17.2	875	7	CR978664	CR978664
260	215	21.7	715	7	F36954	HSPD34939 H	333	169	17.1	653	4	BM426804	BM426804
261	215	21.7	351	5	BY085557	BY085557	334	169	17.1	907	2	BE412589	BE412589
262	214.8	21.7	370	5	BY398556	BY398556	335	168.6	17.0	749	2	BF626523	BF626523
263	213.4	21.6	678	6	CA353706	CA353706	336	168.6	17.0	864	7	CK195971	CK195971
264	212.4	21.5	582	4	BM574123	BM574123	337	168.4	17.0	587	7	CK896420	CK896420
265	212.2	21.5	596	4	BM574082	fx59d04.y	338	168	17.0	673	5	BO752785	BO752785
266	212	21.4	790	4	BJ719956	BJ719956	339	168	17.0	682	1	AJ612197	AJ612197
267	211.8	21.4	854	3	CR651108	Tetraodon	340	168	17.0	704	2	BF228537	BF228537
268	211.4	21.4	1189	3	CR734171	Tetraodon	341	167.6	16.9	469	4	BJ010311	BJ010311
269	210.2	21.3	264	2	AW477994	18030 MAR	342	167.4	16.9	819	7	CK193277	CK193277
270	209.8	21.2	337	2	AW356352	38646	343	167.2	16.9	881	6	CF250863	CF250863
271	209.4	21.2	213	7	F29823	HSPD19935 H	344	167	16.9	692	6	CD866963	CD866963
272	209	21.1	1206	3	CR641100	Tetraodon	345	167	16.9	794	7	CK193235	CK193235
273	208.6	21.1	576	4	BM529070	BM529070	346	166.4	16.8	499	1	AL919863	AL919863
274	208.2	21.1	765	6	CA341770	CA341770	347	166.2	16.8	836	7	CK195388	CK195388
275	207.6	21.0	582	5	BQ615284	BQ615284	348	166	16.8	208	2	BE853865	BE853865
276	207.2	21.0	371	5	BY404587	BY404587	349	165.8	16.8	713	6	CD869948	CD869948
277	206.6	20.9	581	5	BQ450896	BQ450896	350	165.6	16.7	566	7	CK885643	CK885643
278	206.6	20.9	720	6	CA360096	633318 NC	351	165.6	16.7	816	2	BF064997	BF064997
279	206.4	20.9	569	5	BQ480163	BQ480163	352	165.4	16.7	630	4	BY960166	BY960166
280	205.4	20.8	1002	2	BE785237	BE785237	353	165.2	16.7	1148	7	CN988270	CN988270
281	205.2	20.7	756	4	BJ739050	BJ739050	354	165.2	16.7	694	2	BK214450	BK214450
282	205.2	20.7	764	4	BJ716953	BJ716953	355	165	16.7	694	2	BK214450	BK214450
283	205	20.7	581	5	BQ783563	BQ783563	356	165	16.7	697	2	BK216491	BK216491
284	204.6	20.7	1000	5	BK422892	BK422892	357	165	16.7	700	1	AL503249	AL503249
285	204	20.6	205	7	F36948	HSPD34927 H	358	165	16.7	705	2	BE519617	BE519617
286	203.8	20.6	796	7	CF931709	EST0141 A	359	165	16.7	714	2	BE519891	BE519891
287	203.4	20.6	357	5	BY406134	BY406134	360	165	16.7	737	2	BE559087	BE559087
288	203	20.5	363	5	BY400948	BY400948	361	165	16.7	780	5	BO752940	BO752940
289	202.8	20.5	1205	5	CR652934	CR652934	362	164.6	16.6	673	4	BM370604	BM370604
290	201.2	20.3	688	6	CA350955	621897 NC	363	164.6	16.6	804	2	BF624054	BF624054
291	201	20.3	263	2	AW370022	QV4-BT023	364	163.6	16.5	551	7	CK896911	CK896911
292	200.8	20.3	204	1	AK618529	AK618529	365	163.6	16.5	667	6	CA196132	CA196132
293	200.6	20.3	364	2	AW252050	AW252050	366	163	16.5	649	2	BE216025	BE216025
294	200.4	20.3	555	4	BM154433	BM154433	367	163	16.5	1038	7	CK213384	CK213384
295	200.4	20.3	561	4	BM186124	BM186124	368	162.8	16.5	543	6	C233048	C233048
296	199.8	20.2	614	1	AL180003	AL180003	369	162.6	16.4	600	6	C23352	C23352
297	199.4	20.2	553	4	BM186049	BM186049	370	162.2	16.4	715	6	CD883740	CD883740
298	198.2	20.0	643	6	CB512007	CB512007	371	161.8	16.4	711	6	CD873066	CD873066
299	198.2	20.0	644	6	CA333572	CA333572	372	161.4	16.3	699	1	AJ615461	AJ615461
300	196.6	19.9	407	5	BY395434	BY395434	373	161.4	16.3	706	2	BF625981	BF625981
301	196.6	19.9	635	8	AZ958898	2M0226D22	374	161.4	16.3	714	6	CD864630	CD864630
302	196.4	19.9	365	5	BY079881	BY079881	375	161.4	16.3	1121	7	CK162943	CK162943
303	196.4	19.9	537	4	BM534699	BM534699	376	160.8	16.3	648	4	BY959235	BY959235
304	196.4	19.8	645	4	BM705610	BM705610	377	160.6	16.2	709	5	BQ752659	BQ752659
305	195.6	19.8	660	4	BJ727162	BJ727162	378	160.6	16.2	795	5	BO752791	BO752791
306	194	19.6	202	2	AW299502	AW299502	379	160.6	16.2	807	2	BF065240	BF065240
307	193.4	19.6	352	1	AL1712475	AL1712475	380	160.6	16.2	810	7	CK197247	CK197247
308	192.8	19.5	837	6	C23373	C23373	381	160.6	16.2	930	4	BI956791	BI956791
309	192.6	19.5	302	2	BF605771	BF605771	382	160.4	16.2	802	6	CA158127	CA158127
310	192.4	19.5	429	5	BY412806	BY412806	383	160.4	16.2	869	7	CK409595	CK409595
311	191.8	19.4	629	1	AU179577	AU179577	384	160.4	16.2	1052	7	CK210051	CK210051
312	191.8	19.4	1211	3	CR683715	CR683715	385	160	16.2	642	1	A1477552	A1477552
313	189.6	19.2	439	5	BY599654	BY599654	386	160	16.2	666	1	AL504625	AL504625
314	189.2	19.1	731	4	BU722907	BU722907	387	159.8	16.2	652	4	BI960399	BI960399
315	188.8	19.1	855	7	CN985363	58335_126	388	159.8	16.2	655	5	BQ838311	BQ838311
316	185.4	18.7	513	5	BQ783421	fab29f02.	389	159.8	16.2	669	2	BF474987	BF474987

390	159.8	16.2	694	6	CD937240	OV.106G10	463	150.4	15.2	621	5	BQ743179	BQ743179	WHE4101_C
391	159.8	16.2	729	6	CD885596	G118.0010	464	150.4	15.2	726	5	BQ838107	BQ838107	WHE2906_F
392	159.8	16.2	731	6	CD885623	G118.001P	465	150.4	15.2	733	5	BQ838231	BQ838231	WHE2908_A
393	159.8	16.2	732	6	CD939542	OV.11302A	466	150.4	15.2	776	5	BQ618942	BQ618942	RNOSEQ1F0
394	159.8	16.2	733	6	CD939542	OV.11302A	467	150.2	15.2	596	2	BQ403578	BQ403578	WHE0434_C
395	159.8	16.2	814	7	CK192240	FGAS00773	468	150.2	15.2	631	2	BF473218	BF473218	WHE0922_H
396	159.6	16.1	747	1	CK200458	FGAS00897	469	150.2	15.2	874	2	CK169125	CK169125	WHE0922_H
397	159.6	16.1	1121	6	CA131093	SCBFR106	470	150	15.2	693	6	CA153085	CA153085	SCBFR2202
398	159.4	16.1	661	4	BI468189	EST00596	471	150	15.2	789	7	BN010817	BN010817	WHE3876_E
399	159.4	16.1	868	7	CK406586	AUF Iflvr	472	149.8	15.1	588	2	BE493850	BE493850	WHE1276_H
400	159.4	16.1	943	7	CK409493	AUF Iflvr	473	149.6	15.1	655	7	CF626673	CF626673	zmrws05_0
401	159.2	16.1	683	6	CD930335	GR45.110P	474	149.6	15.1	658	4	BQ510111	BQ510111	BJ510111
402	159.2	16.1	866	6	CB650869	OSMNEB15J	475	149.6	15.1	668	4	BM072891	BM072891	MEST55-D0
403	158.8	16.1	653	4	CB650869	OSMNEB15J	476	149.6	15.1	708	6	CD878344	CD878344	AZOA.1021
404	158.6	16.0	646	6	CB650869	OSMNEB15J	477	149.4	15.1	654	4	BI950057	BI950057	HVSMEN001
405	158.6	16.0	722	5	BQ789135	WHE4158_A	478	149.2	15.1	880	4	BI950057	BI950057	HVSMEN001
406	158.4	16.0	866	7	CK175149	AGVENCOURT	479	149.2	15.1	881	7	CK196097	CK196097	FGAS00454
407	158.2	16.0	647	4	BI960119	HVSMEN002	480	149.2	15.1	1072	3	AY108449	AY108449	Zea may
408	157.6	15.9	612	7	CKN09676	WHE3861_E	481	148.8	15.0	363	2	AW658108	AW658108	93873 MAR
409	157.6	15.9	721	5	BQ838009	WHE2905_E	482	148.8	15.0	398	4	BM573972	BM573972	fx57d11_Y
410	157.4	15.9	639	6	BI959367	HVSMEN001	483	148.4	15.0	640	5	BQ743388	BQ743388	WHE4103_D
411	157.2	15.9	649	6	CD879761	AZOA.106E	484	148.4	15.0	647	7	CK012727	CK012727	WHE3952_B
412	157.2	15.9	731	5	BQ752847	WHE4119_G	485	148.4	15.0	665	8	BZ641948	BZ641948	OGAMK72TM
413	157.2	15.9	1064	7	CK163121	FGAS01573	486	148.4	15.0	899	9	CG297599	CG297599	OG1A080TV
414	156.6	15.8	1142	7	CK162127	FGAS01471	487	148.4	15.0	902	7	CK409572	CK409572	AUF Iflvr
415	156.2	15.8	921	7	CK406607	AUF Iflvr	488	148.4	15.0	934	7	CK406893	CK406893	AUF Iflvr
416	156	15.8	756	6	CB650397	EST00B14N	489	148.4	15.0	956	7	CK406337	CK406337	AUF Iflvr
417	156	15.8	799	7	CF589246	EST00B14N	490	148	15.0	681	4	BI959659	BI959659	HVSMEN002
418	155.8	15.8	1126	7	CK211108	FGAS02294	491	148	15.0	807	2	BF259949	BF259949	HVSMEN002
419	155.6	15.7	918	7	CK409380	AUF Iflvr	492	148	15.0	1146	3	AY104406	AY104406	Zea may
420	155.6	15.7	1080	7	CK213716	FGAS02562	493	147.8	14.9	899	7	CK196097	CK196097	WHE3952_B
421	155.2	15.7	752	5	CKN012179	WHE3893_E	494	147.6	14.9	505	7	CK835885	CK835885	SGP158415
422	155.2	15.7	764	5	BQ804819	WHE3559_C	495	147.6	14.9	659	1	AJ615423	AJ615423	SGP158415
423	155.2	15.7	1138	7	CK163513	FGAS01614	496	147.6	14.9	746	7	CO520722	CO520722	AJ615423
424	155	15.7	797	7	CK193862	FGAS000228	497	147.6	14.9	780	7	CO528134	CO528134	3530_1-18
425	155	15.7	846	7	CK195394	FGAS00383	498	147.4	14.9	465	4	BJ498661	BJ498661	BJ498661
426	154.8	15.7	480	4	BI953501	398267 MA	499	147.4	14.9	499	4	BJ527812	BJ527812	BJ527812
427	154.8	15.7	817	7	CK197928	FGAS00640	500	147.4	14.9	515	4	BJ490344	BJ490344	BJ490344
428	154.6	15.6	905	4	BM439118	IGLVR104	501	147.4	14.9	562	4	BJ496988	BJ496988	BJ496988
429	154.6	15.6	1054	7	CK212315	FGAS02418	502	146.8	14.8	571	7	CKN008321	CKN008321	WHE2939_H
430	154.4	15.6	557	2	BE404145	WHE1201_G	503	146.8	14.8	615	6	CA246946	CA246946	SGP159280
431	154.4	15.6	591	5	BQ753204	WHE4115_D	504	146.8	14.8	737	7	AW012934	AW012934	Ldt -0102
432	154.4	15.6	624	5	BQ744417	WHE4115_D	505	146.8	14.8	739	7	CKN013071	CKN013071	WHE3956_D
433	154.4	15.6	627	5	BQ788936	WHE4115_D	506	146.8	14.8	692	6	CD868552	CD868552	AZ02.109E
434	154.4	15.6	628	5	BQ744183	WHE4112_F	507	146.6	14.8	877	6	CA755835	CA755835	BR0300290
435	154	15.6	646	5	BQ838318	WHE2309_A	508	146.6	14.8	649	6	CD904272	CD904272	G356.112P
436	153.8	15.6	416	5	BQ479917	faa8a07_	509	146.4	14.8	670	6	CA151503	CA151503	SCJFR2201
437	153.6	15.5	629	4	BI959561	HVSMEN002	510	146.4	14.8	896	7	CK407472	CK407472	AUF Iflvr
438	153.6	15.5	643	5	BU977235	HA11B05r	511	146.4	14.8	664	5	BP184560	BP184560	BP184560
439	153.6	15.5	644	6	CD930761	GR45.112E	512	146.2	14.8	923	7	CK407551	CK407551	AUF Iflvr
440	153.6	15.5	823	2	BF264389	HV CBa000	513	146.2	14.8	613	7	CK896516	CK896516	SGP159062
441	153.4	15.5	550	6	CA107671	SCRUR107	514	146	14.8	654	6	CA131555	CA131555	SCBGR104
442	153.4	15.5	617	2	BE405650	WHE1209_G	515	146	14.8	684	2	BF256079	BF256079	HVSMEN000
443	153.4	15.5	630	7	CKN010185	WHE3867_G	516	146	14.8	853	2	BF256079	BF256079	HVSMEN000
444	153.4	15.5	655	4	BI960120	HVSMEN002	517	146	14.8	877	6	CK201455	CK201455	FGAS00397
445	153.2	15.5	636	6	CD902038	HZ36A04r	518	145.8	14.7	851	7	CK215205	CK215205	FGAS02715
446	152.8	15.4	756	2	BF184507	BI960120	519	145.6	14.7	746	7	CA213294	CA213294	SCQGSB113
447	152.8	15.4	638	4	BI957710	WHE1209_G	520	145.6	14.7	915	6	CK213294	CK213294	SCQGSB113
448	152.6	15.4	672	2	BF473981	WHE3867_G	521	145.2	14.7	671	5	EX866474	EX866474	EX866474
449	152.4	15.4	798	7	CK053605	WHE3867_G	522	145.2	14.7	627	5	BQ364974	BQ364974	SL5-0017
450	152.4	15.4	817	7	CK194117	WHE3867_G	523	144.8	14.6	637	5	BQ364974	BQ364974	SL5-0017
451	152.4	15.4	817	7	CK194117	WHE3867_G	524	144.6	14.6	774	6	CA065807	CA065807	SCBGR104
452	151.8	15.3	610	5	BQ467961	WHE3867_G	525	144.4	14.6	616	4	BJ259369	BJ259369	BJ259369
453	151.8	15.3	624	6	CK021273	WHE3867_G	526	144.4	14.6	635	6	CJ23181	CJ23181	C23181 Japa
454	151.6	15.3	666	6	CK021273	WHE3867_G	527	144.4	14.6	649	6	CB870888	CB870888	HC15J04W
455	151.2	15.3	684	1	AL821924	HC12G06W	528	144.4	14.6	803	4	BJ247474	BJ247474	BJ247474
456	151.2	15.3	1141	7	CK210321	FGAS02954	529	144.4	14.6	856	7	CK202105	CK202105	FGAS01062
457	151	15.3	1106	7	CK217545	FGAS02954	530	144.4	14.6	774	9	CK202105	CK202105	FGAS01062
458	150.8	15.2	412	4	BQ608207	H3062H08-	531	144.2	14.6	598	4	CK895980	CK895980	SGP158514
459	150.8	15.2	546	1	AL827353	AL827353	532	144	14.6	648	4	BJ024113	BJ024113	SGP158514
460	150.8	15.2	667	1	BI957447	HVSMEN000	533	143.8	14.5	317	1	AI853323	AI853323	UI-M-BHO-
461	150.8	15.2	720	5	CO532807	3530_1.21	535	143.8	14.5	520	1	AU164541	AU164541	AU164541
462	150.4	15.2	472	5	BQ460884	HE01017r								

682	130.6	13.2	650	1	AJ432275	AJ432275	AJ432275	755	125	12.6	647	6	CA285613	SCZSD107
683	130.6	13.2	654	6	CA175542	SCJLST101	CA175542	c 756	125	12.6	694	4	BK265176	BK265176
684	130.6	13.2	857	7	CN172476	AGCJLST01	CN172476	c 757	125	12.6	1049	7	CK163799	FGA501643
685	130.4	13.2	286	1	AV070774	AV070774	AV070774	758	124.8	12.6	554	6	CA686379	wlm96.pk0
686	130.4	13.2	679	6	CA141617	SCJLRT205	CA141617	759	124.8	12.6	652	4	BI957644	HVSMEN001
687	130.4	13.2	691	6	CA182059	SCBGS310	CA182059	c 760	124.8	12.6	695	6	CA090038	SCSGAM207
688	130.4	13.2	819	7	CN127149	RHOHI_21	CN127149	761	124.6	12.6	448	1	AUI82287	AUI82287
689	130.4	13.2	850	7	CK204382	FGA501291	CK204382	762	124.6	12.6	696	6	CA280310	SCVPLB2C0
690	130.2	13.2	436	7	CK896903	SGP159460	CK896903	763	124.6	12.6	720	7	CN989253	65281_125
691	130.2	13.2	635	5	BUI03556	SCCCHR100	BUI03556	764	124.2	12.6	577	5	BP184433	BP184433
692	130.2	13.2	685	6	CA102750	SCCCHR100	CA102750	765	124.2	12.6	670	7	CF433879	NIT1_30_C
693	130.2	13.2	813	4	BG321263	SCCCHR100	BG321263	766	124.2	12.6	713	6	CA221136	SCZFL404
694	130.2	13.1	319	2	AW670333	114312 MA	AW670333	767	124	12.5	493	4	BG263195	WHE23319_B
c 695	130	13.1	553	5	BQ036499	SL5-0018	BQ036499	768	123.8	12.5	538	5	BQ468035	CA221136
696	130	13.1	720	6	CA221618	SCSGFL403	CA221618	769	123.8	12.5	737	6	CA211695	CA211695
697	130	13.1	973	6	CA136643	SCQGR104	CA136643	770	123.6	12.5	464	2	BE125749	DGI_55_H1
698	125.2	13.1	626	4	EM895773	952065C05	EM895773	771	123.6	12.5	622	6	CA137725	SCCORT200
699	129	13.0	578	6	CB870318	HCL13P20W	CB870318	772	123.6	12.5	702	7	CN123933	CA221136
c 700	129	13.0	624	4	BJ543510	BJ543510	BJ543510	773	123.2	12.5	649	5	BU998774	CA221136
c 701	129	13.0	1090	7	CK216386	FGA502837	CK216386	774	123.2	12.5	1088	4	BG338516	CA221136
702	128.8	13.0	812	6	CA183398	SCQGST312	CA183398	775	123.2	12.5	514	6	CA022538	CA022538
703	128.6	13.0	193	2	BE863348	UI-M-BHO-	BE863348	776	123	12.4	514	6	CA023184	HZ45H18r
704	128.6	13.0	580	7	CK889037	SGP161045	CK889037	777	123	12.4	675	6	CA023184	HZ45H18r
705	128.6	13.0	582	7	CK889567	SGP161045	CK889567	778	122.8	12.4	587	6	CA023184	HZ45H18r
706	128.4	13.0	528	7	CK887538	SGP161045	CK887538	779	122.8	12.4	631	4	BI960531	CA221136
707	128.4	13.0	669	6	CA187131	SCUTST308	CA187131	780	122.8	12.4	632	5	BU977317	HA112D1r
708	128.4	13.0	679	6	CA262688	SCPLB202	CA262688	781	122.8	12.4	635	6	CA025276	HZ51K20r
c 709	128.2	13.0	327	7	CF368954	853716 MA	CF368954	c 782	122.8	12.4	647	6	CD988525	G174_109E
710	128.2	13.0	630	6	CA131650	SCBGR104	CA131650	783	122.8	12.4	803	4	BG837569	Zm10_02f1
711	128.2	13.0	685	6	CA121225	SCBGR104	CA121225	784	122.8	12.4	639	6	CA244742	SCSPFLA08
712	128.2	13.0	696	6	CA085150	SCZAM206	CA085150	785	122.6	12.4	490	2	BF202447	WHE1764_G
713	128.2	13.0	727	6	CA219139	SCRFAD111	CA219139	786	122.4	12.4	274	1	AV074448	AV074448
c 714	128	12.9	597	4	BJ505563	BJ505563	BJ505563	787	122.2	12.4	630	6	CA191567	SCCORT2C0
715	128	12.9	621	6	CA222622	SCZFL404	CA222622	c 788	122.2	12.4	163	2	BF092010	RC0-TN007
716	128	12.9	626	1	AJ615113	AJ615113	AJ615113	789	122	12.3	525	1	AL826716	AL826716
717	128	12.9	673	6	CA220527	SCRFL402	CA220527	790	122	12.3	623	6	CA223020	SCZFL403
c 718	128	12.9	711	4	BJ253542	BJ253542	BJ253542	c 791	122	12.3	623	6	CA223020	SCZFL403
719	127.8	12.9	441	4	BI342114	369789 MA	BI342114	792	122	12.3	648	6	CD936749	OV_105A20
720	127.8	12.9	489	2	BE500470	WHE0987-0	BE500470	793	122	12.3	904	2	BF972265	60240747
721	127.8	12.9	582	6	CD869339	AZ02_111G	CD869339	794	121.4	12.3	802	6	CA180913	SCACST316
722	127.6	12.9	569	5	BQ839423	WHE4163_H	BQ839423	795	121.2	12.3	509	2	BE050599	za67f09_g
723	127.6	12.9	641	1	AL827928	AL827928	AL827928	796	121.2	12.3	531	6	CA018264	HV08B21r
724	127.4	12.9	976	6	CA168547	SCQSB101	CA168547	c 797	121	12.2	635	7	CR292476	CR292476
725	127.2	12.9	446	6	CA190347	SCCORT1C0	CA190347	c 798	121	12.2	654	7	CF575000	MCSA142A0
726	127.2	12.9	561	6	CA019093	HV10M04r	CA019093	c 799	121	12.2	705	4	BJ467041	BJ467041
727	127.2	12.9	567	6	CA187040	SCUTST308	CA187040	c 800	120.8	12.2	641	6	CB651300	OSUNEB16D
728	127.2	12.9	734	9	CG327759	OGXFO38TH	CG327759	c 801	120.8	12.2	681	4	BM267355	MEST365-F
729	127	12.8	425	6	CD969646	SCUTRZ310	CD969646	c 802	120.8	12.2	774	6	CB651301	OSUNEB16D
730	126.6	12.8	425	6	CD969646	SCUTRZ310	CD969646	c 803	120.6	12.2	978	7	CR286455	CR286455
731	126.4	12.8	567	6	CD879591	AZ04_105M	CD879591	c 804	120.2	12.2	1078	4	BG338728	602436489
732	126.4	12.8	636	6	CA183982	SCQST311	CA183982	805	120	12.1	442	7	CN967135	14632_100
733	126.4	12.8	641	6	CA145799	SCVPR207	CA145799	806	119.8	12.1	917	7	CK406909	CK406909
734	126.4	12.8	726	6	CA158055	SCERZ2305	CA158055	c 807	119.8	12.1	295	2	BB020942	BB020942
735	126.2	12.8	742	6	CA146092	SCVPR207	CA146092	808	119.8	12.1	309	1	AV054462	AV054462
736	126	12.7	287	7	F26420	HSPD13893_H	F26420	c 809	119.8	12.1	508	2	BF624013	BF624013
737	126	12.7	318	1	AV212581	AV212581	AV212581	c 810	119.6	12.1	552	6	CA017209	CA017209
738	126	12.7	498	2	BF293046	WHE2159_G	BF293046	c 811	119.6	12.1	587	6	CD899632	CD899632
739	126	12.7	546	7	CK896580	SGP159129	CK896580	c 812	119.4	12.1	360	2	AW070082	AW070082
740	126	12.7	558	7	CK896580	SGP159129	CK896580	c 813	119.2	12.1	468	7	CK895492	CK895492
741	126	12.7	666	3	AY104670	Zea maye	AY104670	814	119	12.0	649	4	BI958809	BI958809
742	126	12.7	976	3	AY104670	Zea maye	AY104670	815	118	12.0	744	6	CD430220	CD430220
743	125.8	12.7	643	9	CL561927	OB_Ba002	CL561927	816	118.6	12.0	309	1	AI427820	AI427820
744	125.8	12.7	692	6	CA168805	SCQSB101	CA168805	817	118.6	12.0	311	1	AI427820	AI427820
c 745	125.6	12.7	637	6	CD904273	G356_112P	CD904273	818	118.6	12.0	571	1	AU246119	AU246119
c 746	125.6	12.7	637	6	CD904273	G356_112P	CD904273	819	118.6	12.0	609	6	CA139015	CA139015
747	125.6	12.7	765	2	BF629072	HVMEB000	BF629072	820	118.4	12.0	807	7	CK201722	CK201722
748	125.4	12.7	519	6	BE215821	HV_CEB000	BE215821	821	118.4	12.0	881	7	CK204040	CK204040
749	125.4	12.7	599	2	BE215821	HV_CEB000	BE215821	822	118.2	12.0	599	2	BF619963	BF619963
750	125.4	12.7	622	6	CA182599	SCCST314	CA182599	823	118.2	12.0	649	6	CA120549	CA120549
751	125.2	12.7	584	2	BF065582	HV_CEB001	BF065582	824	118	11.9	150	7	T24436	EST011_Huma
c 752	125.2	12.7	647	4	BJ2644257	BJ2644257	BJ2644257	825	117.8	11.9	316	2	BB138190	BB138190
753	125.2	12.7	650	2	BF260414	HVMEF002	BF260414	826	117.8	11.9	544	6	CA143610	CA143610
754	125	12.6	470	2	BF484312	WHE2321_G	BF484312	827	117.6	11.9	316	2	BB312938	BB312938

828	117.6	11.9	502	1	AL825598	AL825598	901	108.8	11.0	634	4	BG415448	BG415448	HVSMK000
829	117.4	11.9	501	5	BQ084098	K-EST0147	902	108.6	11.0	629	7	C0523183	3530_1_15	C0523183
830	117.4	11.9	681	6	CD430207	ETH1_17_H	903	108.4	11.0	488	6	CD737778	4023355_1	CD737778
831	117.2	11.9	300	2	BE393514	601310205	c 904	108.2	10.9	583	5	BQ167390	WHE0065_D	BQ167390
832	117.2	11.9	326	7	CF367618	842380_MA	c 905	108.2	10.9	683	2	BB594747	BB594747	BB594747
833	117.2	11.9	326	6	CA133289	SCBORT103	c 906	108.2	10.9	2171	3	AK046931	MUB_muscu	AK046931
834	117	11.8	487	2	BE215905	HV_CEB000	c 907	108	10.9	447	7	CK879029	SGP143200	CK879029
835	117	11.8	500	6	CA017659	HV05N12r	c 908	108	10.9	456	2	BE050598	za67f09.D	BE050598
836	116.6	11.8	259	5	BY044444	BY044444	c 909	107.8	10.9	700	7	CK570273	H015P22W	CK570273
837	116.2	11.7	688	7	CR292950	CR292950	910	107.6	10.9	512	6	CD925726	G750_118G	CD925726
838	116.2	11.7	769	6	CA157738	SCBRT301	911	107.4	10.9	524	6	CA144242	SCBRT201	CA144242
839	116	11.7	646	7	C0529747	3530_1_19	912	107.2	10.8	481	7	CN008201	WHE2638_E	CN008201
c 840	116	11.7	946	6	CA270677	SCBRT206	913	107.2	10.8	487	1	AL819087	AL819087	AL819087
841	115.8	11.7	350	2	BE495474	WHE1287-1	914	107.2	10.8	493	7	CN008123	WHE2637_F	CN008123
842	115.8	11.7	543	6	CA030673	wlein.pk0	915	107.2	10.8	597	4	BI955535	HVSMEM002	BI955535
843	115.6	11.7	654	6	CA069091	SCSBAD105	916	107.2	10.8	674	6	CA131726	SCBRT104	CA131726
844	115.6	11.7	702	6	CA179873	SCCST200	917	106.8	10.8	471	4	BJ464618	BJ464618	BJ464618
845	115.4	11.7	570	6	CA279207	SCBFLB209	918	106.8	10.8	480	5	BQ468043	HR01M03r	BQ468043
846	115.2	11.6	570	5	BQ537567	STEM2_5_B	919	106.8	10.8	536	6	CA186607	CA186607	CA186607
847	115	11.6	515	5	BP184761	BP184761	c 920	106.6	10.8	499	4	BJ515365	BJ515365	BJ515365
848	115	11.6	638	6	CA208994	SCBRT106	c 921	106.2	10.7	600	9	CR180853	Forward_B	CR180853
849	114.8	11.6	521	2	BE490745	WHE0368_H	922	106.2	10.7	640	4	BJ255752	BJ255752	BJ255752
850	114.8	11.6	522	6	CF243853	3530_1_24	923	106.2	10.7	713	7	CN146262	WOUN1_39	CN146262
851	114.8	11.6	592	4	BM660366	952037B06	924	106.2	10.7	810	6	CF213611	CGF10079	CF213611
852	114.6	11.6	573	2	AW257987	687065002	c 925	106.2	10.7	819	7	CF517012	CAP0004_I	CF517012
853	114.6	11.6	635	7	CN984292	53247_126	926	106.2	10.7	942	7	CF516928	CAP0004_I	CF516928
854	114.4	11.6	509	4	BG314500	WHE2495_E	927	105.8	10.7	662	4	BI954845	HVSMEM002	BI954845
855	113.8	11.5	312	6	CD809071	LCA03N04c	928	105.4	10.7	595	6	CB616815	CB616815	CB616815
856	113.8	11.5	656	4	BG836117	Zm06_08f1	929	105.4	10.7	599	4	BG836020	Zm06_10b0	BG836020
857	113.6	11.5	486	4	BM443304	EBEm09_SQ	930	105.4	10.7	653	6	CD229208	CCC1_13_F	CD229208
858	113.6	11.5	504	1	AL822404	AL822404	931	105.4	10.7	842	7	CK201404	FGAS00992	CK201404
859	113.6	11.5	869	6	CA130757	SCBRT106	932	105.4	10.6	483	1	AL829858	AL829858	AL829858
860	113.4	11.5	599	1	AI981881	pat.pk006	c 933	105.2	10.6	832	6	CF215096	CAST0001	CF215096
861	113.2	11.4	516	4	BM402624	SLA006D04	934	105.2	10.6	833	6	CF215293	CAST0001	CF215293
862	113.2	11.4	577	6	CD933864	GR45_122E	935	105	10.6	260	1	AV062880	AV062880	AV062880
863	113.2	11.4	614	6	CA137607	SCAGRT304	936	104.6	10.6	658	1	AJ805285	AJ805285	AJ805285
864	113.2	11.4	738	6	CA146644	SCVPT208	937	104.6	10.6	762	1	AJ792459	AJ792459	AJ792459
c 865	113	11.4	116	1	AI915440	tr28B04_X	938	104.4	10.6	471	2	B8639039	946018DD08	B8639039
c 866	113	11.4	718	6	CD888511	G118_108E	939	104.4	10.6	505	1	AV438086	AV438086	AV438086
c 867	112.8	11.4	622	6	CA170058	SCQGSB108	940	104.2	10.6	507	6	CA719362	wkm2n.pk0	CA719362
868	112.8	11.4	316	2	BM490687	BB490687	941	104.2	10.5	568	6	CA615505	wr1.pk172	CA615505
869	112.6	11.4	712	7	CN975952	25862_125	942	104.2	10.5	604	6	CD429608	ETH1_14_C	CD429608
870	112.6	11.4	829	4	BG323539	602422001	943	104.2	10.5	629	7	CA139894	SCEZRT201	CA139894
871	112.6	11.4	596	6	CA077827	SCRFAM102	944	104.2	10.5	631	7	CF432712	NIT1_18_A	CF432712
c 872	112.4	11.4	636	6	CD932185	GR45_117C	945	104.2	10.5	656	6	CA080098	SCSGAM109	CA080098
873	112.4	11.4	634	4	BI959396	HVSMEM001	946	104	10.5	593	6	CA727938	wdi1c.pk0	CA727938
874	112.2	11.3	649	6	CA180857	SCACST316	947	104	10.5	616	4	BI956207	HVSMEM000	BI956207
875	112	11.3	489	7	CF931812	EST0244_A	c 948	104	10.5	648	6	CD878345	AZ04_102I	CD878345
876	111.8	11.3	387	1	AU179319	AU179319	c 949	104	10.5	789	8	BH022213	GH_WB0000	BH022213
877	111.6	11.3	387	1	AU179319	AU179319	950	103.8	10.5	501	6	CB605514	5529_1_67	CB605514
878	111.6	11.3	517	4	BG935465	SL1-0818	951	103.8	10.5	603	7	CF432761	NIT1_18_G	CF432761
879	111.4	11.3	442	7	CN966263	13760_100	c 952	103.6	10.5	343	1	AA899498	UI-R-E0-d	AA899498
880	111.2	11.2	402	7	D22878	RICCI705A_R	953	103.6	10.5	896	6	CF215012	CAST0001	CF215012
881	111.2	11.2	650	6	CA120618	SCCCLR107	954	103.6	10.5	1041	6	CA207625	SCBRSB1C1	CA207625
c 882	111.2	11.2	785	4	BG320047	Zm03_01c0	c 955	103.2	10.4	510	4	BM895774	952065C05	BM895774
c 883	111	11.2	543	5	BQ660910	HM01A23w	956	103.2	10.4	658	6	CA172349	SCSGSB100	CA172349
884	111	11.2	638	6	CA070754	SCUTAD103	957	103	10.4	405	3	CR653216	Tetraodon	CR653216
885	110.8	11.2	259	1	AV261882	AV261882	958	103	10.4	583	1	AL504534	AL504534	AL504534
886	110.8	11.2	670	6	CA298654	SCSPFL804	959	103	10.4	584	6	CD898524	G174_109E	CD898524
887	110.6	11.2	489	4	BM444060	EBEm09_SQ	c 960	102.8	10.4	645	5	BQ752825	WHE4119_E	BQ752825
888	110.6	11.2	613	6	CA276256	SCBPSD200	961	102.6	10.4	593	4	BI140992	IP1_41_G1	BI140992
889	110.4	11.2	488	6	CB095964	1e98b07_b	962	102.6	10.4	595	4	BI141003	IP1_41_H1	BI141003
890	110.4	11.2	496	4	BJ246686	BJ246686	963	102.6	10.4	600	7	CF427278	PH1_4_H04	CF427278
891	110	11.1	516	5	BP184412	BP184412	c 964	102.2	10.3	551	6	CA039685	aaInwh01	CA039685
c 892	109.6	11.1	668	6	CD939543	OV_113024	965	102.2	10.3	552	6	CA193113	SCRLAD104	CA193113
893	109.4	11.1	500	1	AL505702	AL505702	966	102.2	10.3	680	6	CA130734	SCBRT106	CA130734
894	109.4	11.1	594	7	C0531897	3530_1_20	967	102	10.3	617	6	CA270275	SCQSLB205	CA270275
895	109.4	11.1	598	6	CD884471	FL116L20	968	101.8	10.3	441	6	CA007423	HU07017r	CA007423
c 896	109.2	11.0	477	4	BI468157	EST00564	969	101.8	10.3	1068	7	CK162448	FGAS01504	CK162448
897	109.2	11.0	648	5	BQ743293	WHE4102_D	970	101.4	10.3	455	4	BI956370	HVSMEM000	BI956370
898	109	11.0	533	2	BE637000	WHE1808_A	971	101.4	10.3	467	4	BI957989	HVSMEM001	BI957989
899	108.8	11.0	486	2	BE215236	HV_CEB000	972	101.4	10.3	508	5	BQ239349	TaE05032B	BQ239349
900	108.8	11.0	491	2	BF6233901	HVSMEM000	973	101.4	10.3	684	6	CB091578	he94a09_g	CB091578

974	101	10.2	632	6	CA157288	SCFQRZ309	1047	94.6	9.6	636	6	CB090660	CB090660
975	100.8	10.2	338	4	B0259370	B0259370	1048	94.6	9.6	709	7	CA0165605	CA0165605
976	100.6	10.2	634	6	CA124374	SCQGLR108	1049	94.4	9.5	466	6	CA704504	CA704504
c 977	100.2	10.1	261	9	CB5675240	tigr-988-	1050	94.4	9.5	516	2	BR429250	BR429250
978	100.2	10.1	553	7	CN135765	OXI 38 G0	1051	94.2	9.5	353	5	BY401495	BY401495
979	100.2	10.1	651	7	CF479933	POI1 62 E	1052	94.2	9.5	501	1	CO524755	CO524755
980	10.1	10.1	689	7	CN991252	67764.125	1053	94.2	9.5	737	7	CF397756	CF397756
c 981	100.1	10.1	900	7	CO488021	Q0255.B3	1054	94.2	9.5	762	7	CF472622	CF472622
c 982	99.8	10.1	227	1	A1614596	mm33c06.Y	1055	94	9.5	658	7	CK240496	CK240496
c 983	99.6	10.1	504	4	B0531649	B0531649	1056	93.8	9.5	614	1	AU101479	AU101479
c 984	99.4	10.1	500	4	B0511906	B0511906	c1057	93.6	9.5	617	1	AI477667	AI477667
c 985	98.4	10.1	592	6	CA020122	HV14G11r	1058	93.6	9.5	766	7	AI477667	AI477667
986	98.2	10.0	520	5	BR436475	604144737	c1059	93.4	9.4	547	6	CD933865	CD933865
987	98.2	10.0	530	6	CA068263	SCRUAD106	1060	93.2	9.4	462	1	AJ434313	AJ434313
c 988	98.1	10.0	526	6	CA151587	CA151587	1061	93.2	9.4	648	7	CN192437	CN192437
989	98.8	10.0	801	2	BF254803	HVSMF000	1062	93.2	9.4	708	7	CN184479	CN184479
990	98.4	9.9	542	6	CA112745	SCQOLB106	1063	93.2	9.4	745	7	CN192437	CN192437
991	98.4	9.9	452	6	CB093002	CB093002	1064	93.2	9.4	788	7	CN184479	CN184479
992	98.2	9.9	494	6	CA207983	CA207983	1065	93.2	9.4	787	7	CF835276	CF835276
993	98.2	9.9	538	6	CA186909	CA186909	1066	93.2	9.4	812	9	CF838445	CF838445
994	98.2	9.9	609	6	CB093108	CB093108	1067	93.2	9.4	856	7	CF838788	CF838788
995	98.2	9.9	679	6	CA191740	CA191740	1068	93.2	9.4	880	7	CG847727	CG847727
996	98.2	9.9	583	2	BE360219	DGL 62 C1	1069	93.2	9.4	236	1	CO117389	CO117389
997	97.6	9.9	586	6	CA248579	CA248579	1070	93.2	9.4	286	1	CN151185	CN151185
998	97.6	9.9	610	6	CA254903	CA254903	c1071	93	9.4	447	4	AV141679	AV141679
999	97.6	9.9	708	6	CA083641	CA083641	c1072	93	9.4	447	4	BG842772	BG842772
1000	97.6	9.9	735	6	CA082691	CA082691	1073	93	9.4	447	4	CG907078	CG907078
1001	97.6	9.9	735	6	CA082691	CA082691	1074	93	9.4	591	5	BJ611537	BJ611537
1002	97.4	9.8	564	6	CB087866	CB087866	1075	93	9.4	695	5	BX252395	BX252395
1003	97.4	9.8	643	7	CF518411	CF518411	1076	93	9.4	843	7	CA016496	CA016496
1004	97	9.8	582	6	CA734194	CA734194	1077	92.6	9.4	592	6	CA082157	CA082157
1005	96.8	9.8	264	1	AV323544	AV323544	1078	92.4	9.3	436	6	BE498018	BE498018
1006	96.8	9.8	666	6	CB091902	CB091902	1079	92.4	9.3	436	6	CB092484	CB092484
1007	96.8	9.8	685	5	BX253301	BX253301	1080	92.2	9.3	666	6	CB085655	CB085655
1008	96.8	9.8	692	6	CB653599	CB653599	1081	92	9.3	731	1	AJ803420	AJ803420
1009	96.6	9.8	724	4	BI960633	BI960633	1082	92	9.3	521	2	BE493244	BE493244
1010	96.6	9.8	635	6	CA221355	CA221355	1083	91.8	9.3	701	7	CN975504	CN975504
1011	96.6	9.8	744	7	CF478537	CF478537	1084	91.8	9.3	798	7	CR288023	CR288023
c1012	96.6	9.8	794	7	CO174177	CO174177	1085	91.6	9.3	551	4	BJ257751	BJ257751
1013	96.4	9.7	809	7	CO165036	CO165036	1086	91.6	9.3	655	7	CK987647	CK987647
1014	96.2	9.7	569	4	BJ463342	BJ463342	1087	91.6	9.3	675	7	CF932162	CF932162
c1015	96.2	9.7	589	6	CA453183	CA453183	1088	91.6	9.3	833	7	CK934159	CK934159
1016	96.2	9.7	745	5	BQ699842	BQ699842	1089	91.6	9.3	595	6	CA160253	CA160253
1017	96.2	9.7	782	7	CF669736	CF669736	1090	91.4	9.2	625	6	CA083727	CA083727
1018	96.2	9.7	792	7	CO363528	CO363528	1091	91.4	9.2	283	1	AV325538	AV325538
1019	96.2	9.7	817	7	CO364800	CO364800	1092	91.2	9.2	393	9	CG085800	CG085800
c1020	96.2	9.7	822	7	CO364711	CO364711	1093	91.2	9.2	559	6	CD864258	CD864258
c1021	96.2	9.7	854	7	CO363617	CO363617	1094	91.2	9.2	565	4	BJ252030	BJ252030
1023	96.2	9.7	219	1	AA079945	AA079945	c1096	91.2	9.2	569	4	BJ246116	BJ246116
c1024	96	9.7	349	7	CR464258	CR464258	c1098	91.2	9.2	584	6	CD454107	CD454107
c1025	96	9.7	212	5	BX632080	BX632080	1099	91	9.2	625	4	BI953755	BI953755
1026	95.8	9.7	520	1	AL450922	AL450922	c1100	90.8	9.2	519	4	BJ263171	BJ263171
1027	95.6	9.7	520	1	AL450922	AL450922	1101	90.8	9.2	674	6	CA165465	CA165465
1028	95.6	9.7	671	4	BI954074	BI954074	1102	90.8	9.2	818	6	CF203341	CF203341
1029	95.6	9.7	747	7	CF396117	CF396117	1103	90.6	9.2	522	4	BG604615	BG604615
1030	95.4	9.6	555	7	CN133810	CN133810	c1104	90.6	9.2	600	7	CN008603	CN008603
1031	95.2	9.6	542	4	BJ551247	BJ551247	1105	90.4	9.1	635	1	AJ560090	AJ560090
1032	95.2	9.6	673	6	CB082763	CB082763	1106	90.4	9.1	638	7	CN975309	CN975309
1033	95.2	9.6	712	7	CF389766	CF389766	1107	90.4	9.1	580	5	BU977318	BU977318
1034	95.2	9.6	712	7	CF473897	CF473897	c1108	90.2	9.1	632	4	BM079242	BM079242
1035	95.2	9.6	718	8	BZ635220	BZ635220	c1109	90.2	9.1	789	5	BX250520	BX250520
1036	95.2	9.6	729	8	CF478998	CF478998	1110	90.2	9.1	628	7	CF418067	CF418067
c1037	95.2	9.6	777	7	CO172079	CO172079	1111	90.2	9.1	728	7	CF418067	CF418067
c1038	95.2	9.6	787	9	CC626240	CC626240	1112	90	9.1	552	4	BG605452	BG605452
c1039	95.2	9.6	841	9	CG367905	CG367905	1113	90	9.1	650	7	CK987645	CK987645
c1040	95.2	9.6	852	9	CG320079	CG320079	1114	90	9.1	652	7	CF836276	CF836276
c1041	95.2	9.6	880	9	CG367832	CG367832	1115	90	9.1	726	7	CF836276	CF836276
c1042	95.2	9.6	880	9	CG322953	CG322953	1116	90	9.1	739	7	CK932528	CK932528
1043	95.2	9.6	919	9	CG235840	CG235840	c1117	90	9.1	848	7	CN191778	CN191778
1044	95.2	9.6	453	4	BI956521	BI956521	1118	89.8	9.1	242	1	AV341874	AV341874
1045	94.6	9.6	590	6	CA080520	CA080520	1119	89.8	9.1	242	1	AV341874	AV341874

1120	89.8	9.1	537	6	CA215379	SCRLAD113	1193	86	8.7	751	6	CD821098	BN25.040N
1121	89.8	9.1	599	6	CA242898	SCSFFL309	1194	86	8.7	776	7	CN987035	62721.125
1122	89.8	9.1	660	7	CF418675	USDA-PP 1	1195	86	8.7	854	2	BF260683	HVSMF002
1123	89.8	9.1	674	5	BX251216	BX251216	1196	86	8.7	882	7	CG605765	gmrlrww6-
1124	89.6	9.1	417	5	BQ539085	MEST611-B	1197	86	8.7	986	4	BG838133	Gc01.06d0
1125	89.4	9.0	439	2	BF145727	WHB1840 A	1198	85.8	8.7	788	4	BF1971175	GM830012B
1126	89.4	9.0	518	6	CA271127	SCRUB206	1199	85.8	8.7	789	2	BF860393	963016801
1127	89.4	9.0	848	2	AN982228	HVSMF000	1200	85.6	8.7	484	4	BJ246483	BJ246483
1128	89.2	9.0	627	6	CB910128	VVD174D02	1201	85.6	8.7	498	1	AL824727	AL824727
1129	89	9.0	564	8	BZ628758	ih62b02.b	1202	85.6	8.7	506	1	AL808335	AL808335
1130	89	9.0	644	2	BB635220	BB635220	1203	85.6	8.7	635	5	BU044203	PP LEa001
1131	89	9.0	707	7	CN988152	CN988152	1204	85.6	8.7	677	7	CF806867	peH8016M
1132	89	9.0	3835	3	AK079754	Mus muscu	1205	85.6	8.7	689	4	BG544230	E2031 Chi
1133	88.8	9.0	507	7	CF972935	PSU 2blon	1206	85.6	8.7	760	4	BG934808	SLI--0074
1134	88.8	9.0	673	7	CF389114	RTDR2_13	1207	85.6	8.7	960	2	BE213939	HV CEB000
1135	88.8	9.0	747	7	CF474427	RTWM2_20	1208	85.4	8.6	400	2	BF221093	NXCI 163
1136	88.8	9.0	750	7	CF198619	CF198619	1209	85.4	8.6	714	1	AJ778942	AJ778942
1137	88.8	9.0	775	7	CF390634	CF390634	1210	85.4	8.6	840	7	CN191650	UCRCS06 0
1138	88.8	9.0	817	7	CF831643	CF831643	1211	85.2	8.6	501	1	AL818819	AL818819
1139	88.8	9.0	864	6	CB822986	CB822986	1212	85.2	8.6	742	5	BQ634193	NXR0064 H
1140	88.4	8.9	637	7	CN189395	UCRCS06 0	1213	85	8.6	266	6	CF075267	EST00106
1141	88.4	8.9	775	6	CD576142	CD576142	1214	84.8	8.6	637	5	BQ623195	USDA-PP 0
1142	88.2	8.9	414	4	BZ281814	BZ281814	1215	84.8	8.6	693	2	BE208866	GF-FV-P3C
1143	88.2	8.9	549	6	CD429497	ETH1 4 H0	1216	84.8	8.6	704	6	CD817128	BN20.040N
1144	88.2	8.9	608	7	CK750439	pan01-fms	1217	84.8	8.6	715	7	CN183738	UCRCS04 0
1145	88.2	8.9	671	6	CA160341	CA160341	1218	84.8	8.6	721	7	CF833360	UCRCS02 0
1146	88.2	8.9	829	2	BF260105	BF260105	1219	84.8	8.6	730	7	CF833321	UCRCS02 0
1147	88	8.9	454	7	CF887520	CF887520	1220	84.8	8.6	731	7	CN190617	UCRCS06 0
1148	88	8.9	769	6	CA784719	sat88a11	1221	84.8	8.6	730	7	CF833684	UCRCS02 0
1149	87.8	8.9	534	6	CA701924	CA701924	1222	84.8	8.6	752	7	CN128863	RHOH1_32
1150	87.8	8.9	750	7	CF921444	CF921444	1223	84.8	8.6	826	7	CN128942	RHOH1_32
1151	87.6	8.9	785	6	CB346952	CB346952	1224	84.8	8.6	830	7	CF838016	UCRCS03 0
1152	87.6	8.9	1105	8	BZ549226	BZ549226	1225	84.8	8.6	394	2	BE996908	NXCI 097
1153	87.4	8.8	250	1	AV080674	AV080674	1226	84.6	8.6	486	6	CA688073	wlm96.pk0
1154	87.4	8.8	404	7	CF573768	CF573768	1227	84.6	8.6	534	6	CA630115	wlm96.pk0
1155	87.4	8.8	449	4	BG559195	BG559195	1228	84.6	8.6	544	4	BM527684	sal64f09
1156	87.4	8.8	470	1	AV929789	AV929789	1229	84.6	8.6	550	6	CA178809	SCSFT106
1157	87.2	8.8	452	6	CB863482	CB863482	1230	84.6	8.6	510	7	CF971448	AUB IfHrt
1158	87.2	8.8	484	1	AL809451	AL809451	1231	84.4	8.5	534	6	CD932184	GM45.117C
1159	87.2	8.8	628	6	CB914191	CB914191	1232	84.4	8.5	684	5	BU875316	V005C03 P
1160	87.2	8.8	724	7	CF921036	CF921036	1233	84.4	8.5	694	5	BU877332	V032G08 P
1161	87	8.8	580	1	AL691472	AL691472	1234	84.4	8.5	696	6	CD832570	BN40.063N
1162	87	8.8	598	4	BJ321639	BJ321639	1235	84.4	8.5	716	5	BU874994	V001B12 P
1163	87	8.8	610	4	BJ728276	BJ728276	1236	84.4	8.5	808	6	CD827397	BN25.067F
1164	86.8	8.8	661	7	CK987646	CK987646	1237	84.4	8.5	492	6	CA686271	wlm96.pk0
1165	86.8	8.8	696	6	CA113262	SCB2L8101	1238	84.2	8.5	669	7	CF507287	USDA-PP 1
1166	86.8	8.8	757	2	CF395287	CF395287	1239	84.2	8.5	763	7	CK121692	202c15.p1
1167	86.6	8.8	487	2	BE356694	BE356694	1240	84	8.5	789	7	CK119117	214b16.p1
1168	86.6	8.8	550	6	CD462624	CD462624	1241	84	8.5	818	6	CD575294	UCRPT01 0
1169	86.6	8.8	575	2	BE405628	BE405628	1242	84	8.5	924	3	CF652643	68-L02013
1170	86.6	8.8	575	6	CB617031	CB617031	1243	84	8.5	1003	3	CNS0A315	Arabidops
1171	86.6	8.8	594	6	CB874255	CB874255	1244	84	8.5	1024	6	CA594498	Arabidops
1172	86.6	8.8	674	5	BX254999	BX254999	1245	83.6	8.5	484	6	CA594498	wpalc.pk0
1173	86.4	8.7	409	2	BF200550	BF200550	1246	84	8.5	645	5	CF471822	UTDS1_6 C
1174	86.4	8.7	432	2	BE499371	BE499371	1247	84	8.5	535	7	BQ624278	USDA-PP 0
1175	86.4	8.7	577	6	CA030887	CA030887	1248	84	8.5	580	7	CNS17425	Q00092.B3
1176	86.4	8.7	589	6	CB870901	CB870901	1249	84	8.5	582	7	CN495499	MDfW20201
1177	86.4	8.7	589	6	CB874266	CB874266	1250	83.6	8.4	601	6	CD877326	AZ04.100B
1178	86.4	8.7	609	1	AU069930	AU069930	1251	83.6	8.4	606	2	BB021597	sm60a04.y
1179	86.4	8.7	673	7	CN190619	CN190619	1252	83.4	8.4	633	7	CF418893	USDA-PP 1
1180	86.2	8.7	414	2	BF474477	BF474477	1253	83.4	8.4	672	6	CD825507	BN25.060P
1181	86.2	8.7	473	4	BM497443	BM497443	1254	83.4	8.4	675	1	AU299511	AU299511
1182	86.2	8.7	484	1	AL809743	AL809743	1255	83.4	8.4	708	6	CF213537	CF213537
1183	86.2	8.7	614	1	AV916275	AV916275	1256	83.4	8.4	797	7	CF838015	UCRCS03 0
1184	86.2	8.7	624	6	CB873498	CB873498	1257	83.4	8.4	800	7	CF833359	UCRCS02 0
1185	86.2	8.7	627	6	CB895488	CB895488	1258	83.4	8.4	807	7	CF833320	UCRCS02 0
1186	86.2	8.7	630	4	BU468176	BU468176	1259	83.4	8.4	522	7	CF577081	MCSA208D0
1187	86.2	8.7	762	7	CO171539	CO171539	1260	83.4	8.4				
1188	86.2	8.7	927	7	CO480346	CO480346	1261	83.4	8.4				
1189	86	8.7	319	1	AJ605122	AJ605122	1262	83.4	8.4				
1190	86	8.7	442	4	BI953073	BI953073	1263	83.4	8.4				
1191	86	8.7	511	7	CF603338	CF603338	1264	83.2	8.4				
1192	86	8.7	751	6	CD820878	BN25.040B	1265	83.2	8.4				

1266	83.2	8.4	531	4	BI426741	BI426741	8906909.	1339	79	8.0	560	6	CD236225	CD236225	SS1_32_B0
1267	83.2	8.4	744	7	CF838018	CF838018	UCRCS03_0	1340	79	8.0	731	8	CC348296	CC348296	GMU456TH
1268	83	8.4	544	6	CA015838	CA015838	HV05N12U	1341	79	8.0	737	7	AW348485	AW348485	GM210002B
1269	82.8	8.4	224	1	AV043940	AV043940	AV043940	1342	79	8.0	815	7	CO083019	CO083019	GR_Ea470
1270	82.8	8.4	534	1	AI443130	AI443130	884601.Y	1343	78.8	8.0	486	5	BQ661501	BQ661501	HM03L08u
1271	82.8	8.4	662	2	BE610562	BE610562	8Q77H11.Y	1344	78.8	8.0	539	7	CO415038	CO415038	MdFw2041m
1272	82.8	8.4	686	1	AU162815	AU162815	AU162815	1345	78.8	8.0	584	5	BQ6223631	BQ6223631	USDA-PP_0
1273	82.8	8.4	699	5	BX251392	BX251392	BX251392	1346	78.8	8.0	618	2	BE801899	BE801899	Wdrf.pko
1274	82.8	8.4	529	6	CA642958	CA642958	wreln.pko	1347	78.6	7.9	436	6	CA723695	CA723695	WHF2226.D
1275	82.6	8.4	624	6	CR293091	CR293091	CR293091	1348	78.6	7.9	443	4	BQ274261	BQ274261	EST_4685
1276	82.6	8.4	672	6	CA216151	CA216151	SCSFFL401	1349	78.6	7.9	859	6	CB823461	CB823461	wdrf.pko
1277	82.6	8.4	772	6	CF233249	CF233249	PrAJX002	1350	78.4	7.9	643	5	CA723044	CA723044	UMATB11
1278	82.6	8.4	772	6	CF233114	CF233114	PrAJX001	1351	78.4	7.9	803	7	CA723044	CA723044	UMATB11
1279	82.4	8.3	552	6	CB859954	CB859954	HI12C04W	1352	78.4	7.9	366	6	CA2020280	CA2020280	RTD52_10_
1280	82.4	8.3	878	7	CO366616	CO366616	RTKL_29_A	1353	78.2	7.9	399	4	BF482619	BF482619	WHE2301-2
1281	82.4	8.3	911	7	CO239360	CO239360	WS00725.B	1354	78.2	7.9	401	2	BF482619	BF482619	WHE2301-2
1282	82.2	8.3	316	7	D48033	D48033	RTCS13955A	1355	78.2	7.9	426	6	CA017891	CA017891	HV06L01r
1283	82.2	8.3	317	7	D48033	D48033	RTCS13955A	1356	78.2	7.9	427	6	CA017891	CA017891	HV06L01r
1284	82.2	8.3	437	6	CB863741	CB863741	HH04N16V	1357	78.2	7.9	571	2	BE803196	BE803196	sr53a11.Y
1285	82.2	8.3	599	1	AI855419	AI855419	603018E02	1358	78.2	7.9	630	2	AW757356	AW757356	sl33c10.Y
1286	82	8.3	123	6	CA533969	CA533969	CO409801-	1359	78.2	7.9	630	2	AW757356	AW757356	sl33c10.Y
1287	81.8	8.3	365	2	BE996909	BE996909	NXCI_097	1360	78	7.9	249	2	BI133157	BI133157	BB133157
1288	81.8	8.3	471	6	CA691259	CA691259	wlm96.pko	1361	78	7.9	468	1	AU057943	AU057943	AU057943
1289	81.8	8.3	622	6	CB092238	CB092238	hf03a08.G	1362	78	7.9	619	4	BG045242	BG045242	aaa39d08.
1290	81.8	8.3	667	4	BI958598	BI958598	HVSMEN001	1363	78	7.9	629	7	CF629443	CF629443	zmrwE48_0
1291	81.6	8.3	506	5	BQ654778	BQ654778	NXR085_E	1364	78	7.9	692	7	CK099634	CK099634	A078P58-5
1292	81.6	8.3	882	7	CN201625	CN201625	Tori690_G	1365	78	7.9	837	3	CNS0A6PN	CNS0A6PN	ArabiDops
1293	81.4	8.2	327	7	CF649137	CF649137	3530_1_64	1366	78	7.9	837	3	CNS0A6PN	CNS0A6PN	ArabiDops
1294	81.2	8.2	968	7	CO083020	CO083020	GR_Ea470	1367	77.8	7.9	515	2	BE362957	BE362957	DGL_92_G0
1295	81	8.2	321	9	CE459357	CE459357	tIGF-ges-	1368	77.8	7.9	607	7	CK439808	CK439808	Q00021B.B
1296	81	8.2	374	6	CA333620	CA333620	haa87b04.	1369	77.8	7.9	625	5	BQ633731	BQ633731	NKR0056_B
1297	81	8.2	509	6	BU979265	BU979265	HA15T2r	1370	77.8	7.9	711	5	BQ633731	BQ633731	NKR0056_B
1298	81	8.2	549	5	CB859935	CB859935	HI12A24W	1371	77.8	7.9	789	5	BU894945	BU894945	X017B10-P
1299	81	8.2	591	4	BI960325	BI960325	HVSMEN002	1372	77.8	7.9	912	7	CK185418	CK185418	X017B10-P
1300	81	8.2	593	5	BU979082	BU979082	HA15B18r	1373	77.8	7.9	915	2	BF266762	BF266762	HV6_C5a001
1301	81	8.2	686	7	CF833210	CF833210	UCRCS02_0	1374	77.6	7.8	401	6	CA029054	CA029054	H264504r
1302	81	8.2	719	7	CF833209	CF833209	UCRCS02_0	1375	77.6	7.8	584	1	AJ802385	AJ802385	AJ802385
1303	81	8.2	872	7	CO064791	CO064791	est_k_bfe	1376	77.6	7.8	588	4	BM520677	BM520677	sak97b12.
1304	80.8	8.2	598	2	AW071192	AW071192	sk22a02.Y	1377	77.6	7.8	621	2	AW306951	AW306951	sf50h03.Y
1305	80.8	8.2	598	5	BU994274	BU994274	HM06H04r	1378	77.6	7.8	636	7	CK060552	CK060552	gmhrHw6-
1306	80.8	8.2	764	1	AO070794	AO070794	GO0258.B3	1379	77.6	7.8	753	6	CA782445	CA782445	8at28h08.
1307	80.6	8.1	261	7	CF653377	CF653377	PTAXM0026	1380	77.6	7.8	770	4	BI967327	BI967327	GM830001B
1308	80.6	8.1	699	7	CF229531	CF229531	PTAXM0026	1381	77.6	7.8	783	2	BE413688	BE413688	SCU002.A0
1309	80.6	8.1	772	6	CF229531	CF229531	PTAXM0026	1382	77.4	7.8	586	3	CF419317	CF419317	USDA-PP_1
1310	80.4	8.1	221	1	AV127873	AV127873	AV127873	1383	77.4	7.8	1045	3	CNS0A6EG	CNS0A6EG	AL509899
1311	80.4	8.1	375	5	BQ244891	BQ244891	TaE15033H	1384	77.2	7.8	561	1	AL509899	AL509899	AL509899
1312	80.4	8.1	511	6	CA707767	CA707767	wk2c.pko	1385	77.2	7.8	668	5	BU887057	BU887057	R054A07_P
1313	80.4	8.1	908	9	CG323583	CG323583	OGWIE57TH	1386	77.2	7.8	712	7	CD933370	CD933370	GR45.L20M
1314	80	8.1	640	2	BE427259	BE427259	PSR6177_I	1387	77	7.8	485	6	CA194169	CA194169	SCFPR3313
1315	80	8.1	676	5	BQ655308	BQ655308	NXR092_G	1388	77	7.8	681	6	CF213698	CF213698	CGF100079
1316	80	8.1	690	6	CF233271	CF233271	PrAJX002	1389	77	7.8	716	7	CN137990	CN137990	OX1_61_C0
1317	80	8.1	731	7	CK240495	CK240495	VRJ324_V1	1390	77	7.8	354	2	BE429121	BE429121	MTD014.F0
1318	80	8.1	766	6	CD909627	CD909627	G468.L13C	1391	76.8	7.8	391	5	BQ606397	BQ606397	BRY_2256
1319	79.8	8.1	503	6	BE427259	BE427259	PSR6177_I	1392	76.8	7.8	543	4	BI788368	BI788368	sag6909.
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BM451059
BM451059.1 GI:18500099
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ORGANISM Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Bases 1 to 889)
NTH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strauberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM12121 Row: d Column: 08
High quality sequence stop: 665.
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Average insert size 1.75 kb. Library constructed by Life
Technologies."

Query Match 80.6%; Score 797.4; DB 4; Length 889;
Best Local Similarity 99.5%; Pred. No. 2.5e-150;
Matches 821; Conservative 0; Mismatches 1; Indels 3; Gaps 2;

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Oy 132 GGCTCAGCCGACATGGGCGCGGCTTCGCCACTTCCTCTTCTGGGAGCGGTGCC 191
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```

2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
Tel: 319 356 4866
Fax: 319 356 7171
Email: paul-mccray@uiowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com).
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES
source

Location/Qualifiers
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UI-CF-FNO is a subtracted cDNA library derived from two
normalized human lung epithelial cell libraries (EN1 and
DU1). The library was subtracted according to according to
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. For additional information, contact:
bento-soares@uiowa.edu
TAG_SEQ=None found"

ORIGIN

Query Match 77.1%; Score 762.6; DB 6; Length 771;
Best Local Similarity 99.5%; Pred. No. 2.6e-143;
Matches 765; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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591 GCTGACCTGGGCACCTTTCACGGCTACTCCGCGCTTGGCCCTTGGCGCTTGGCCGC 532
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471 GTGAGGCGAGCGCGAGCGGAGCAAGATCGACTCCGGCTGAAGCCCGCTTTGGAGAC 412
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641 GACAGAGAGAACTGCTCGGCTACTAGAGCGCTCTGAGCGCTGTGCGACCCCGGAGG 700
351 GGACAGAGAGAACTGCTCGGCTACTAGAGCGCTCTGAGCGCTGTGCGACCCCGGAGG 292
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LOCUS
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UI-CF-FNO-aes-j-02-0-UI.s1 UI-CF-FNO Homo sapiens cDNA clone
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CB852030
VERSION
CB852030.1 GI:30046884
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 771)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)
JOURNAL
MEDLINE
PUBMED
889548
Contact; McCray, PB
McCray Lab
University of Iowa


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Db      231  |||||||CTGTGCGGCGGAGTGTGCGGAAACCTAAACGACATCCGCGGGACGTCAGGGTCTA 172
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VERSION   BM051236.1 GI:16780503
KEYWORDS EST.
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 814)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LCM1886 row: e column: 23
High quality sequence stop: 811.
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    in the laboratory of Gerald M. Rubin (University of
    California, Berkeley) using ZAP-cDNA synthesis kit
    (Stratagene) and Superscript II RT (Life Technologies).
    Note: this is a NIH_MGC Library. |"

FEATURES
source

ORIGIN
Query Match 75.1%; Score 743; DB 4; Length 814;
Best Local Similarity 98.6%; Pred. No. 2,3e-139;
Matches 802; Conservative 0; Mismatches 5; Indels 6; Gaps 5;

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Qy      508  |||||||TGGGACGCGCCCTGTGGAGGCGAGCGCGAGGCGGAGCACAAGATCGACCTCGGGCTGAAGC 567
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Qy      568  |||||||CCGCTTGGAGACCTTGGACCGAGCTGTGTGGCGGGGGC--GAGGCGCGGACCTTGCAGCT 625
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Qy      626  |||||||GGCGTGTGTGATGCGGACGAGGAGACTGCTCGGCTTACTACGAGCGCTGCTGCGCAGC- 684
Db      542  |||||||GGCGTGTGTGATGCGGACGAGGAGACTGCTCGGCTTACTACGAGCGCTGCTGCGCAGCT 601
Qy      685  |||||||TGCTGCGACCGCGAGGACATCTCTCGCGCTCTCAGAGTCTCTGTGGCGCGGAGGTGCTGC 744
Db      602  |||||||TGCTGCGACCGCGAGGACATCTCTCGCGCTCTCAGAGTCTCTGTGGCGCGGAGGTGCTGC 661
Qy      745  |||||||AACCTCCGAAAGGGAGCTGTGGCGCGCGAGTG-TGTGCGAAACCTTAAACGAAAC-GCATCG 802
Db      662  |||||||AACCTCCGAAAGGGAGCTGTGGCGCGCGAGTG-TGTGCGAAACCTTAAACGAAACGCGATCG 721
Qy      803  |||||||GCGGAGCTGAGGCTTACATCAGCCTCTGCGGCTGCGCGATGAGTACCTTGGCGCTT 862
Db      722  |||||||GCGGAGCTGAGGCTTACATCAGCCTCTGCGGCTGCGCGATGAGTACCTTGGCGCTT 781
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DEFINITION ip21907.x1 HR85 islet Homo sapiens cDNA clone IMAGE:6217933 3',
similar to tr:O85769 O85769 HYPOTHETICAL 24.8 KD PROTEIN. ;, mRNA
sequence.
ACCESSION CA777547
VERSION   CA777547.1 GI:26015422
KEYWORDS EST.
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 756)
AUTHORS Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
Lemishka,I., Searce,M., Brestelli,J., Gradwohl,G., Clifton,S.,
Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blisfain,A.,
Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J.,
Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagarishvili,R.,
Williams,T., Jackson,Y. and Bowers,Y.
Endocrine Pancreas Consortium
Unpublished (2000)
COMMENT Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue

```


Endocrine Pancreas Consortium
 Harvard University, Howard Hughes Medical Institute
 Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
 MA 02138
 Tel: 617-495-1812
 Fax: 617-495-8557
 Email: dmeitton@biohp.harvard.edu
 Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
 Washington University Genome Sequencing Center For information on
 obtaining a clone please contact: Dr. Hiroshi Inoue
 (hinoue@im.wustl.edu)
 Seq primer: -40UP from Gibco
 High quality sequence stop: 462.
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 Size-selected on agarose gel. Average insert size ~1kb. 5'
 XhoI site was destroyed after directional cloning.
 Amplified once. Contact information: Hiroshi Inoue, MD,
 Metabolism Div. (Alan Permutt Lab), Washington University
 School of Medicine, Box 8127, 660 South Euclid Ave., St.
 Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:
 314-362-1916, Fax: 314-747-2692."

FEATURES

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 NotI; Site_2: XhoI; cDNA made by oligo-dT priming.
 Size-selected on agarose gel. Average insert size ~1kb. 5'
 XhoI site was destroyed after directional cloning.
 Amplified once. Contact information: Hiroshi Inoue, MD,
 Metabolism Div. (Alan Permutt Lab), Washington University
 School of Medicine, Box 8127, 660 South Euclid Ave., St.
 Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:
 314-362-1916, Fax: 314-747-2692."

ORIGIN

Query Match 74.4%; Score 736; DB 6; Length 756;
 Best Local Similarity 99.2%; Pred. No. 5.9e-138;
 Matches 750; Conservative 0; Mismatches 5; Indels 1; Gaps 1;
 222 CTTCCCGCCGACAGCCGCTGTGCGAGTATCTTCTGAGCGCTCCATCGCGGAGCAC 281
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 282 CCGCGCTGCGAAGCCTGAGGCTGCTGACCTCGAGCAGCGGAGGATTTATGATG 341
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 342 ACTGCGAGCAGGCGGCTGTTGGCCAACTGCGCGGCTCATCCAGCCAGAGGCG 401
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 702 ATCTCTGCGCTCTCAGAGTCTGTGGCGGCGGAGGTTGCTGCAACTCTCGAAAGGGGAC 761
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QY 762 GTGGCGGCGAGTGTGTGCGAAACCTAAACGAAACCATCCGCGGAGCTCAGGCTCTAC 821
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 QY 822 ATCAGCTCTCTCCCTGGCGATGAGTCACTTTGGCTTCAAGATCTAGGGCTGGGCC 881
 DB 156 ATCAGCTCTCTCCCTGGCGATGAGTCACTTTGGCTTCAAGATCTAGGGCTGGGCC 97
 QY 882 -CTAGTGTAGTGGCTGCGAGGAGGTTGCTTGGGAACCCAGGAATTGACCTGAGTTT 940
 DB 96 GATAGTGTAGTGGCTGCGAGGAGGTTGCTTGGGAACCCAGGAATTGACCTGAGTTT 37
 QY 941 AATATCGAAATAAAGTGGGCTGGGACACAAAAA 976
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 LOCUS 602144463F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4297911 5',
 DEFINITION mRNA sequence.

ACCESSION BF663323 GI:11937218
 VERSION BF663323.1
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 1006)
 NIH-MGC http://mgs.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 CONTACT: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
 cDNA Library Preparation: Ling Hong/Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
 Plate: L1CM1152 row: m column: 16
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FEATURES

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 Site_2: EcoRI; cDNA made by oligo-dT priming.
 Directionally cloned into EcoRI/XhoI sites using the
 following 5' adaptor: GGCACGAG(G). Size-selected >500bp
 for average insert size 1.8kb. Library constructed by Ling
 Hong in the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH_MGC Library."

ORIGIN

Query Match 72.9%; Score 721; DB 2; Length 1006;
 Best Local Similarity 90.9%; Pred. No. 6.3e-135;
 Matches 835; Conservative 0; Mismatches 75; Indels 9; Gaps 6;
 QY 79 GGGCCATGACCCAGCGGTCGCCGCTCTCCGTGCCCGCGCTGCGCTGAG 138
 DB 2 GGGCCATGACCCAGCGGTCGCCGCTCTCCGTGCCCGCGCTGCGCTGAG 61
 QY 139 CGGACTGGGCGCGCTTCCGCACTTCTTCTGGGAGGCGGTCGCCCATGCG 198

Db 62 CCGCACTGGGCGCCCTTGGCACTGGCTTCTTCTGGGAGGCGGTGCCCCCATGGC 121
Qy 199 GAGGCGCGGAGAGAGAGTCCCTGCTTCCCTCCCGAGGACAGCGCGCTGTGGCAGTATCTTC 258
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Db 182 TGAGCGCGTCCATGCGGAGAGACCCCGGCGCTGCGAAGCTGAGGCTGTGACCTTGAGC 241
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Db 242 AGCGCAGGCGGATCTATGATGACCTGCGAGCAGCGCGAGCTTTGSCCAACCTGGCGC 301
Qy 379 GGCTCATCCAGGCCAAGAGCGCTGGACCTTGGGCACCTTTCACGGGCTACTCCCGCCCTGG 438
Db 302 GGCTCATCCAGGCCAAGAGCGCTGGACCTTGGGCACCTTTCACGGGCTACTCCCGCCCTGG 361
Qy 439 CCTGGCGCTGGCGTGGCGGAGCGCGGCGGTGGTACCTGCGAGTGAGCGCGAGC 498
Db 362 CCTGGCGCTGGCGTGGCGGAGCGCGGCGGTGGTACCTGCGAGTGAGCGCGAGC 421
Qy 499 CCCGAGCTGGGACGCGCCCTGTGGAGCGAGCGCGGCGAGCACAAAGATCGACCTCC 558
Db 422 CCCGAGCTGGGACGCGCCCTGTGGAGCGAGCGCGGCGAGCACAAAGATCGACCTCC 481
Qy 559 GGCTGAAGCCCGCTTGGAGACCTTGGAGAGCTGCTGGCGCGGCGAGCGCGCACCT 618
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VERSION BF664198.1 GI:11938093
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SOURCE Homo sapiens (human)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 921)

AUTHORS
TITLE
JOURNAL
COMMENT

NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/ILNL at:
<http://image.llnl.gov>
Plate: LICM1182 row: h column: 03
High quality sequence stop: 726.

FEATURES
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1. 921
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/mol_type="mRNA"
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/clones="IMAGE:4309298"
/tissue_type="Primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_48"
/note="Organ: B-cells; Vector: pOTB7; Site:1: XhoI;
Site:2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

ORIGIN

Query Match 72.4%; Score 716; DB 2; Length 921;
Best Local Similarity 97.4%; Pred. No. 6.3e-134; Indels 6; Gaps 5;
Matches 781; Conservative 0; Mismatches 15;
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Qy 139 CCGCACTGGGCGCGCTTGGCCACTGGCTCTTCTTGGGAGGCGGTGCCCCCATGGC 198
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Qy 199 GAGCGCGGAGAGCAGTGTCTTCCCGGAGGAGCAGCGCTGTGGCAGTATCTTC 258
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Qy 259 TGAGCCCTCTCATGCGGAGCACCGCGGCTTCCGAAAGCTGAGGCTGTGACCTGGAGC 318
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Qy 319 AGCGCAGGCGGATCTATGATGACCTGCGAGCAGCGCGAGCTTGGGCCAACCTGGCGC 378
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Qy 379 GGCTCATCCAGGCCAAGAGCGCTGGACCTTGGGACCTTCCAGGGCTACTCCGCCCTGG 438
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 ACCESSION
 VERSION
 KEYWORDS
 EST.
 ORGANISM
 Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 714)
 Bonaldo,M.F., Lennon,G. and Soares,M.B.
 Normalization and subtraction: two approaches to facilitate gene
 discovery
 Genome Res. 6 (9), 791-806 (1996)
 97044477
 8889548
 Contact: McCray, PB
 McCray Lab
 University of Iowa
 2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
 Tel: 319 356 4866
 Fax: 319 356 7171
 Email: paul.mccray@uiowa.edu
 Tissue Procurement: Dr. M. J. Welsh, University of Iowa
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Researchers may obtain clones from Research
 Genetics (www.resgen.com) or from Open Biosystems
 (www.openbiosystems.com).
 Seq primer: M13 FORWARD
 POLYA=Yes.

FEATURES
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ORIGIN

Query Match 71.5%; Score 707.2; DB 5; Length 714;
 Best Local Similarity 99.6%; Pred. No. 3.7e-132;
 Matches 709; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 278 GCACCCGGCGCTGCGAAGCTGAGGCTGTGACCTCTGCGGAGCGCGGAGGATCTAT 337
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 QY 638 TCGCGACGAGGAGCTGCTCCGCTTACTAGAGCGCTGCTGCGCTGCTGCGACCGCG 697
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CB852718 750 bp mRNA linear EST 22-APR-2003
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 UI-CF-FNO-afl-p-08-0-UI 3', mRNA sequence.

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              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 750)
AUTHORS      Ronaldo,M.F., Lennon,G. and Soares,M.B.
TITLE        Normalization and subtraction: two approaches to facilitate gene
              discovery
JOURNAL        Genome Res. 6 (9), 791-806 (1996)
MEDLINE       9704477
PubMed        889548
COMMENT       Contact: McCray, PB
              University of Iowa
              2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
              Tel: 319 356 4866
              Fax: 319 356 7171
              Email: paul-mccray@uiowa.edu
              Tissue Procurement: Dr. M. J. Welsh, University of Iowa
              cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
              cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
              DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
              Clone Distribution: Researchers may obtain clones from Research
              Genetics (www.resgen.com) or from Open Biosystems
              (www.openbiosystems.com).
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              DU1) The library was subtracted according to according to
              Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
              1996. For additional information, contact:
              bento-soares@uiowa.edu
              TAG_SEQ=None found"

ORIGIN
Query Match      70.8%; Score 699.8; DB 6; Length 750;
Best Local Similarity 97.3%; Pred. No. 1.1e-130;
Matches 732; Conservative 0; Mismatches 18; Indels 2; Gaps 2;

Qy 148 GCGCGCTTGCACACTGGCTCTTCCCTGGGGAGCGGTGCCCCCATATGGCGAGCGCGC 207
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Qy 208 GAGGACGTGCTGCTTCCCCCGGAGGACCGCGCTGTGGCAGTATCTTCTGAGCGCT 267
Db 61 GAGGACGTGCTGCTTCCCCCGGAGGACCGCGCTGTGGCAGTATCTTCTGAGCGCT 120

Qy 268 CCATCGCGGAGCACCGCGCTGCGAAGCCTGAGGCTGTGACCTGAGGAGCGCGCAGG 327
Db 121 CCATCGCGGAGCACCGCGCTGCGAAGCCTGAGGCTGTGACCTGAGGAGCGCGCAGG 180

Qy 328 GGGATTCTATGATGACCTCGAGCAGGCGCCAGCTTTGGCCAACTGGCGCGGCTCATCC 387
Db 181 GGGATTCTATGATGACCTCGAGCAGGCGCCAGCTTTGGCCAACTGGCGCGGCTCATCC 240

Qy 398 AGGCCAAGAGCGCTGACCTGGGACCTTCACGGGCTACTCCGCCCTGGCCCTGGCCC 447
Db 241 AGGCCAAGAGCGCTGACCTGGGACCTTCACGGGCTACTCCGCCCTGGCCCTGGCCC 300

448 TGGCGCTCCCGCGGACCGGCGCGCTGTGTGTAAGTGGAGGTGGAACGCGCAGCCCCCGGAGC 507
301 TGGCGCTCCCGCGGACCGGCGCGCTGTGTGTAAGTGGAGGTGGAACGCGCAGCCCCCGGAGC 360
508 TGGGACGCGCCCTGTGGAGGCGAGCCGAGGCGGAGCACAAGATCGACCTCCGGCTGAAGC 567
361 TGGGACGCGCCCTGTGGAGGCGAGCCGAGGCGGAGCACAAGATCGACCTCCGGCTGAAGC 420
568 CCGCTTTGGAGACCTCGACGAGCTGTGTGGCGGGCGGAGCGCGCAGCTTTCGACGTGG 627
421 CCGCTTTGGAGACCTCGACGAGCTGTGTGGCGGGCGGAGCGCGCAGCTTTCGACGTGG 480
628 CCGTGTGTGATGCGGACAAAGGAGAACTCTCTCCGCCCTACTAGAGCGCTGCTTGCAGCTGC 687
481 CCGTGTGTGATGCGGACAAAGGAGAACTCTCTCCGCCCTACTAGAGCGCTGCTTGCAGCTGC 540
688 TGGCAGCCCGGAGGACCTCTCCCGCTCCTCAGAGTCTGTGGCGGGAGGAGTGTGCAAC 747
541 TGGCAGCCCGGAGGACCTCTCCCGCTCCTCAGAGTCTGTGGCGGGAGGAGTGTGCAAC 600
748 CTCCGAAAGGGGACGCTGGCGGCGGAGTGTGTGCGAAACCTAAACGAAACGCAATCCGCGCGG 807
601 CTCCGAAAGGGGACGCTGGCGGCGGAGTGTGTGCGAAACCTAAACGAAACGCAATCCGCGCGG 660
808 ACGTACAGGCTTACATCAGCCTCTCTGCCCCCTGGGCGATGAGCTACCTTGGCTTTCAAGA 867
661 ACGTACAGGCTTACATCAGCCTCTCTGCCCCCTGGGCGATGAGCTACCTTGG-CTTCAAGA 719
868 TCTAGGCTGGCGCCCTAGTGTGAGTGGCTCGAG 899
720 TCTAGGCTGG-CCCTAGTGTGAGTGGCTCGAG 750

RESULT 9
LOCUS      BE796570
DEFINITION BE796570 772 bp mRNA linear EST 20-SEP-2000
              601592247F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3946546 5',
              mRNA sequence.
ACCESSION  BE796570
VERSION     BE796570.1  GI:10217768
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1 (bases 1 to 772)
AUTHORS      NIH-MGC http://mgi.nci.nih.gov/.
TITLE        National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL      Unpublished (1999)
COMMENT      Contact: Robert Strausberg, Ph.D.
              Email: cgapbs-remail.nih.gov
              Tissue Procurement: DCTD/DTP
              cDNA Library Preparation: Ling Hong/Rubin Laboratory
              cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
              DNA Sequencing by: Incyte Genomics, Inc.
              Clone distribution: MGC clone distribution information can be
              found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
              Plate: L1CM806 row: m column: 11
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              /clone_lib="NIH_MGC_7"
              /note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2:
              EcoRI; cDNA made by oligo-dr priming. Directionally
              cloned into EcoRI/XhoI sites using the following 5'

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adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).

ORIGIN

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Query Match      69.2%; Score 684.4; DB 2; Length 772;
Best Local Similarity 97.4%; Pred. No. 1.5e-127;
Matches 760; Conservative 0; Mismatches 11; Indels 9; Gaps 6;

QY 83 CATGACCCAGCGGTGCCCGCGCTTCCGTCCCGCGCGCTGACCTTGGGCTCAGCGC 142
DB 1 CATGACCCAGCGGTGCCCGCGCTTCCGTCCCGCGCGCTGACCTTGGGCTCAGCGC 60

QY 143 ACTGGGCGCGCTTGGCACTGGCTTCTTCTGGGAGGCGGTGCCCGCATGGCGAGG 202
DB 61 ACTGGGCGCGCTTGGCACTGGCTTCTTCTGGGAGGCGGTGCCCGCATGGCGAGG 120

QY 203 CCGGCGAGCAGTGCCTTCTTCCCGCGAGCAGCGCGCTGTGGCAGTATCTTCTGAG 262
DB 121 CCGGCGAGCAGTGCCTTCTTCCCGCGAGCAGCGCGCTGTGGCAGTATCTTCTGAG 180

QY 263 CGCTTCCATGCGGGAGCACCGCGGCTCGAAGCTGAGGCTGTGACCTTGGAGCGC 322
DB 181 CGCTTCCATGCGGGAGCACCGCGGCTCGAAGCTGAGGCTGTGACCTTGGAGCGC 240

QY 323 CGAGGGGATTTATGATGACTGCGAGCGGCGGCTTCTTGGCCACCTTGGCGGCT 382
DB 241 CGAGGGGATTTATGATGACTGCGAGCGGCGGCTTCTTGGCCACCTTGGCGGCT 300

QY 383 CATTCAGGCGCAAGAGGCGCTGACCTTGGGCACTTACGGGCTACTCGGCGCT 442
DB 301 CATTCAGGCGCAAGAGGCGCTGACCTTGGGCACTTACGGGCTACTCGGCGCT 360

QY 443 GGCCTTGGCGTCCCGCGGAGCGGCGGTGTGACTCTGCGAGGTGAGCGGCGGCT 502
DB 361 GGCCTTGGCGTCCCGCGGAGCGGCGGTGTGACTCTGCGAGGTGAGCGGCGGCT 420

QY 503 GAGCTGGGACGCGGCTTGTGAGCGCGGCGGCGGAGCACAAGATCGACCTCGGCT 562
DB 421 GAGCTGGGACGCGGCTTGTGAGCGCGGCGGCGGAGCACAAGATCGACCTCGGCT 480

QY 563 GAAAGCCCGCTTGGAGACCTTGGACGAGCTGTGCGGCGGCGGAGCGGCACTTGA 622
DB 481 GAAAGCCCGCTTGGAGACCTTGGACGAGCTGTGCGGCGGCGGAGGCGGCACTTGA 538

QY 623 CTTGGCGGTGGTGGATGCGGCAAGAGAACTGTCTCGGCTTACTAGAGCGCTGCTGA 682
DB 539 CTTGGCGGTGGTGGATGCGGCAAGAGAACTGTCTCGGCTTACTAGAGCGCTGCTGA 598

QY 683 GCTGCTGCGACCGGAGGCGATCTCGCGCTCTCAGAGTCTTGTGGCGGGAAGTGT 742
DB 599 GCTGCTGCGACCGGAGGCGATCTCTCGCGCTCTCAGAGTCTTGTGGCGGGAAGTGT 658

QY 743 GC-AACTCTCGAAAGGGGACGTGGCGCGGAGTGTGTGCGAAACCTTAAACGACATCC 801
DB 659 GC-AACTCTCGAAAGGGGACGTGGCGCGGAGTGTGTGCGAAAC--TAAAGAACGAT-C 715

QY 802 GCGGGAAGTCAAGGTCTTACATCAGGCTCTCGGCGCTTGGCGCATGAGTCACTTGGCT 861
DB 716 GCGGGAAGTCAAGGTCTTACATCAGGCTCTCGGCGCTTGGCGCATGAGTCACTTGGCT 772
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RESULT 10

BF663695 779 bp mRNA linear EST 21-DEC-2000
LOCUS 602145414F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4309010 5',
DEFINITION mRNA sequence.
ACCESSION BF663695
VERSION BF663695.1 GI:11937590
KEYWORDS EST.
SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 779)

AUTHORS

NIH-MGC <http://mgi.nci.nih.gov/>.

TITLE

National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL

Unpublished (1999)

COMMENT

Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LMC181 row: 1 column: 03
High quality sequence stop: 761.

FEATURES

Location/Qualifiers

source

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/clone="IMAGE:4309010"
/tissue_type="primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_48"
/note="Organ: B-cells; Vector: pOTB7; Site: 1: XhoI;
Site 2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

ORIGIN

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Query Match      67.7%; Score 669.8; DB 2; Length 779;
Best Local Similarity 98.1%; Pred. No. 1.3e-124;
Matches 762; Conservative 0; Mismatches 7; Indels 8; Gaps 8;

QY 79 GCGCATGACCCAGCGGTGCCCGCTTCCGTCCCGCGCGCTGCGGCTGCGGCTCAG 138
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QY 139 CCGCACTGGGCGCGGCTTCCGCACTGCGCTTCTTCTGGGAGGCGGTGCCCATGGC 198
DB 62 CCGCACTGGGCGCGGCTTCCGCACTGCGCTTCTTCTGGGAGGCGGTGCCCATGGC 121

QY 199 GAGCGCGCGAGAGAGTGCCTGCTTCCCCCGAGGACAGCGGCTGTGGCAGTATCTTC 258
DB 122 GAGCGCGCGAGAGAGTGCCTGCTTCCCCCGAGGACAGCGGCTGTGGCAGTATCTTC 181

QY 259 TGAGCGGCTCCATGCGGAGCACCGCGCTGCGAAGCTGAGGCTGTGACCTTGGAGC 318
DB 182 TGAGCGGCTCCATGCGGAGCACCGCGGCTGTGCGAAGCTGTGACCTTGGAGC 241

QY 319 AGCGCGAGGGGATTTATGATGACTCTCGAGCA-GGCGGAGCTTGGCGAACTGGC- 376
DB 242 AGCGCGAGGGGATTTATGATGACTCTCGAGCAAGCTGTGAGCTTGGCGAACTGGC 301

QY 377 GCGGCTCATCCAGGCAAGAGGCGCTGACCTGGGCACTTCCAC-GGGCTACTCCGCC 435
DB 302 GCGGCTCATCCAGGCAAGAGGCGCTGACCTGGGCACTTCCACTGGGCTACTCCGCC 361

QY 436 TGGGCTTCCGCTTGC-GCTGCCCGGACCGGCGCGCTGTGACCTGGAGGTGACGCG 494
DB 362 TGGGCTTCCGCTTGCCTGCTGCTGCCCGGACCGGCGCGTGGTGGCTGTGGAGTGC 421

QY 495 CAGCCCCCGGAGCTGGGACGCGGCTTGTGGAGGACAGCGCGGAGGACAGATCGAC 554
DB 422 CAGCCCCCGGAGCTGGGACGCGGCTTGTGGAGGACAGCGCGGAGGACAGATCGAC 481
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QY 555 CTCGGCTGAAGCCCGCTTGGAGACCTTGGACGAGCTGCTGGCGCGGCGGAGCCGGC 614
 DB 482 CTCGGCTGAAGCCCGCTTGGAGACCTTGGACGAGCTGCTGGCGCGGCGGAGCCGGC 541
 QY 615 ACCTTCGAGCTGGCGCTGGT-CGATCGCGACCAAGGAGAACTGCTCGGCTACTAGAGCG 573
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 QY 674 CTCGCTGCAAGCTGCTGGACCGCGGAGCA-TCTCGCGCTCTCAGAGTCTGTGTGGCGG 732
 DB 602 CTCGCTGCAAGCTGCTGGACCGCGGAGCA-TCTCGCGCTCTCAGAGTCTGTGTGGCGG 661
 QY 733 GGAAGTGTGCAACTCTCGAAGGAGAC-GTGGCGCGCGAGTGTGTGCGAAGAACTTAAAC 791
 DB 662 GGAAGTGTGCAACTCTCGAAGGAGACGCTGGCGCGAGTGTGTGCGAAGAACTTAAAC 721
 QY 792 GAAAGCATCGCGCGGGA-CGTGAGGTCTACATCAGCTTCTGGCGCTTGGCGGATGG 847
 DB 722 GACCGATCCGCGGAGCGTCAGGCTCTACATCAGCTTCTGGCGCTTGGCGGATGG 778

RESULT 11
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 LOCUS
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 5', mRNA sequence.
 B0931589
 VERSION B0931589.1 GI:22346620
 KEYWORDS
 SOURCE EST.
 ORGANISM Homo sapiens (human)
 REFERENCE
 AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-romail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Rubin Laboratory
 DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
 Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
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 /note="Organ: lung; Vector: pOTB7; Site:1: EcoRI; Site:2: XhoI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

FEATURES

source
 Query Match 67.4%; Score 666.4; DB 5; Length 934;
 Best Local Similarity 95.8%; Pred. No. 6.2e-124;
 Matches 751; Conservative 0; Mismatches 21; Indels 12; Gaps 6;
 QY 87 ACCGAGCCGGTCCCGGCTCTCCGTCGCGCGGCTGGCCCTGGGCTCAGCGCACTG 146

ORIGIN

Query Match 67.4%; Score 666.4; DB 5; Length 934;
 Best Local Similarity 95.8%; Pred. No. 6.2e-124;
 Matches 751; Conservative 0; Mismatches 21; Indels 12; Gaps 6;
 QY 87 ACCGAGCCGGTCCCGGCTCTCCGTCGCGCGGCTGGCCCTGGGCTCAGCGCACTG 146

DB 1 ACCGAGCCGGTCCCGCTCTCCGTCGCGCGGCTGGCCCTGGGCTCAGCGCACTG 60
 QY 147 GCGCGCGCTTCCGCACTGGCTCTTCTGGGAGGCGGTGCCCTCCCAATGGCGAGCCGG 206
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 QY 207 CGAGAGCAGTGCCTGCTTCCCGGAGCAAGCCGCTGTGGCAGTATCTTCTGAGCCGC 266
 DB 121 CGAGAGCAGTGCCTGCTTCCCGGAGCAAGCCGCTGTGGCAGTATCTTCTGAGCCGC 180
 QY 267 TCCATGCGGAGCACCCGCGCTGCGAGCCTGAGGCTGCTGACCTGGAGCAGCGGAG 326
 DB 181 TCCATGCGGAGCACCCGCGCTGCGAGCCTGA----GCTGACCTGGAGCAGCGGAG 236
 QY 327 GGGGATTTATGATGACCTGGAGCAGCCGCTTCTGGCCAACTGGCGGCTCATC 386
 DB 237 GGGGATTTATGATGACCTGGAGCAGCCGCTTCTGGCCAACTGGCGGCTCATC 296
 QY 387 CAGGCCAAGAGGCGCTGGAACCTGGGCACTTACGGGCTACTCGGCTCTGGCCCTGGCC 446
 DB 297 CAGGCCAAGAGGCGCTGGAACCTGGGCACTTACGGGCTACTCGGCTCTGGCCCTGGCC 356
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 QY 507 CTGGAGCGGCGCTTGTGAGGCGAGCCGAGCGGAGCAAGATCGACTCGCGCTGAAG 566
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 DB 777 CCTT 780
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 B0972503
 VERSION B0972503.1 GI:19901549
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 SOURCE EST.
 ORGANISM Homo sapiens (human)
 REFERENCE
 AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgabs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at:
http://image.lnl.gov
Plate: LLAM12810 row: 1 column: 17
High quality sequence stop: 489.
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/note="Organ: pooled lung and spleen; Vector: pCMV-SPORT6;
Site 1: NotI; Site 2: EcoRV (destroyed); RNA source
anonymous pool of 24 week female lung, 16 week female
spleen, and 20-22 week male spleens. Library is oligo-dT
primed and directionally cloned (EcoRV site is destroyed
upon cloning). Average insert size 1.4 kb, insert size
range 1-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 026. Note:
this is a NIH MGC Library."

FEATURES
source

i. 1065
Location/Vdu...
/organism="Homo sapiens"
/mol_type="mRNA"
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/clone="IMAGE:5761696"
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/clone_lbl="NIH_MGC_122"
/notes="Organ: pooled lung and spleen; Vector: pCMV-SPORTS;
Site 1: NotI; Site 2: EcoRV (destroyed); RNA source
anonymous pool of 24 week female lung, 16 week female
spleen, and 20-22 week male spleens. Library is oligo-dT
primed and directionally cloned (EcoRV site is destroyed
upon cloning). Average insert size 1.4 kb, insert size
range 1-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 026. Note:
this is a NIH MGC library."

ORIGIN

ch	63.7%;	Score 630;	DB 5;	Length 1065;
1	Similarity 96.7%;	Pred. No. 1.3e-116;	Indels 3;	Gaps 3;
675;	Conservative 0;	Mismatches 20;		
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61	TCC	CGCGCGCTCTTGGCCGCGCGCATGACCCAGCCGGTGCCTCCCGGCTCTCCGTGCCGCGCG	120	
121	CGCT	TGGCCCTGGGCTCAGCCGCACTTGGCGCGCTTTCGGCACTGGGCTCTTCTCTGGGGA	180	
121	CGCT	TGGCCCTGGGCTCAGCCGCACTTGGCGCGCTTTCGGCACTGGGCTCTTCTCTGGGGA	180	
181	GGCG	TGCCCCCTATGGCGAGCCGGCGGAGAGCAGTGCCTGTCTCCCGCCGAGGACAGCC	240	
181	GGCG	TGCCCCCTATGGCGAGCCGGCGGAGAGCAGTGCCTGTCTCCCGCCGAGGACAGCC	240	
241	GCCT	TGGCAGTATCTTCTGAGCCGCTCATTCGGGGAGACCCGGCGCTTGGAGAGCTTGA	300	
241	GCCT	TGGCAGTATCTTCTGAGCCGCTCATTCGGGGAGACCCGGCGCTTGGAGAGCTTGA	300	
301	GGCT	CTGACCTGAGAGACCGCGAGGGGGAATCTATGATGACCTTCGGAGCAGGCCACAC	360	
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361	TCTT	TGGCCAACTGGCGGGCTCATTCAGGCCAAGAGCGCTGGACCTGGGCACTTCA	420	
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421	CGGG	CTACTTCCGCCCTTGGCCCTTGGCCCTTGGCCCTTGGCCCTTGGCCCTTGGCTGACCT	480	
481	GGAG	TGAGACGGCGAGCCCGCGAGCTGGAGCGGCCCTTGTGGAGCGCAGGCCGAGCGCG	540	
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541	AGCA	CAAGATCGACCTCCGGCTGAAGCCCGCTTGGAGA- CCTTGAACGAGCTGCTGGCG	599	
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QY 600 G-CGGCGAGCGCGGCA-CCTTCGACGTGCCCTGTGTGATCGGACAGAGCAACTGCT 657

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QY 658 CCGCTACTACGAGCGCTGCTGGAGCTGTGTGCAGCCC 695

Db 661 CCCCTACTACAACGCACTCCTGCACCTGTGCGAACC 698

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+ CCHC

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LOCUS	K-EST0051789	S14K402	Homo sapiens	cDNA clone S14K402-11-A01 5',
DEFINITION	mRNA sequence.			
ACCESSION	BM768764	Homo sapiens (human)		
VERSION	BM768764.1	GI:19098379		
KEYWORDS	EST.			
SOURCE	Homo sapiens			
ORGANISM	Homo sapiens			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.			
REFERENCE	1 (bases 1 to 625)			
AUTHORS	Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.			
TITLE	21C Frontier Korean EST Project 2001			
JOURNAL	Unpublished (2002)			
COMMENT	Contact: Kim YS			

FEATURES

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/cell_line="K402"
/lab_host="Top10P"
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/note="Organ: Stomach; Vector: pTZ18RP1; Site 1: EcoRI;
Site 2: NotI; The poly (A)+ RNA was dephosphorylated with
bacterial alkaline phosphatase (BAP) and then decapped
with tabacco acid pyrophosphatase (TAP). The decapped
intact mRNA was ligated with DNA-RNA linker including EcoRI
I site by treatment of T4 RNA ligase and the first strand
cDNA was synthesised from oligo dT-selected mRNA by
priming with dT-tailed vector. The dT-tailed vector was
adjusted to have about 60nt. The cDNA vector was
circularized with E. coli DNA ligase after digestion of
EcoRI which site is also included in vector. An RNA strand
converted to a DNA strand by Okayama-Berg method. The
obtained cDNA vectors were used for transformation of
competent cells E. coli top10P by electroporation method
The cDNA libraries constructed by this method are
full-length enriched cDNA library."

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ORIGIN

[illegible]

	Db	 61	GGCCTGGGCTCAGCCGCACCTGGGCGCGCTTGCCACTGGCCCTTCCTCTGGGAGGGC	120
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	Qy	 245	GTGGCAGTATCTTTCTGAGCCGCTCCATCGGGGAGCACCGGGGCTTCGNAGCCTGAGGCT	304
	Db	 181	GTGGCAGTATCTTTCTGAGCCGCTCCATCGGGGAGCACCGGGGCTTCGCAAGCTGAGGCT	240
	Qy	 305	GCTGACCTTGAGACAGCCGAGGGGATCTTATGATGACCTGCGAGCAGGCCACCAGCTTT	364
	Db	 241	GCTGACCTTGAGCAGCCGCGAGGGGATCTTATGATGACCTGCGAGCAGGCCACCAGCTTT	300
	Qy	 365	GGCCAACTGTGGCGGCTCATCCAGGCCAAGAAGCGCTGACCTGGGCACCTTCACGGG	424
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	Db	 481	CAAGATGACCTTCGCGTGAAGCCCGCTTGGAGACCTTGACGAGCTGTCTGGCGGCGGG	540
	Qy	 605	CGAGGCGGCACTTTCGACGTGGCGTGGTGGATGCGGACAAGGAGAACTGCTCCGCGCTTA	664
	Db	 541	CGAGGCGGCACTTTCGACGTGGCGTGGTGGATGCGGACAAGGAGAACTGCTCCGCGCTTA	600
	Qy	 665	CTACGAGCGCTGCTTCGACGTGCTG	689
	Db	 601	CTACGAGCGCTGCTTCGAGCTGCTG	625

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LOCUS	602437508F1	NIH_MGC_46	Homo sapiens	CDNA clone	IMAGE:4555609 5',
DEFINITION			mRNA		

ACCESSION BG339399
VERSION BG339399.1 GI:13145837

KEYWORDS EST.

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM	Homo sapiens
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CREATININ nomlo baprens
Eukaryota: Metazoa: Chordata: Vertebrata: Euteleostomi:

Eukaryota; Metazoa;
Mammalia: Eutheria:

1. (1955) 14. 11. 1955

Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE 1 (bases 1 to 912)

AUTHORS NIH-MGC <http://mgc>

TITLE National Institutes of Health, Man

JOURNAL Unpublished (1999)

COMMENT
Contact: Robert Strausberg
Conference (1995)

CONTACT: ROBERT STRAUBERG, PH.D.
Email: cstraubg-r@mail.nih.gov

Email: csarob-r@mail.nih.gov
 Telephone: 301-401-9700

Tissue Procurement: ATCC

cdNA Library Preparation: Ling Hong/Rubin Laboratory

cdNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

clone distribution: MGC clone distribution information can be

found through the T.M.A.G.E. Consortium/I.I.N.T. at:

found through the I.M.A.G.E.E. Consortium/LEND at:
<http://image.lni.gov>

<http://image.llnl.gov>

Plate: LLCM1256 row: 0 column: 02

High quality sequence stop: 719.

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204200      /organism="Homo sapiens"
204300

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RESULT 15
AK054334

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/clone_lib="NIH_MGC_46"
/notes="Organ: uterus; Vector: pOTB7; Site 1: XhoI; Site 2:
ECORI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
Library."

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ORIGIN

Query Match	62.8%;	Score 621;	DB 4;	Length 912;
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Db	2	CTGCCGCGCGCATGACCCAGACCGGTGCCCGGCTCTCCGTCGCCCGCGCGCTGGCCCTTGG	61	
QY	133	GCTCAGCCGCACTGGGCGCGGCTTCGCGCACTGGGCTCTTCCTGGGAGAGCGGTCGCCCC	192	
Db	62	GCTCAGCCGCACTGGGCGCGGCTTCGCGCACTGGGCTCTTCCTGGGAGAGCGGTCGCCCC	121	
QY	193	CATGGCGAGGCGCGGAGAGCAGTGCCTGCTTCCCCCGAGGACAGCCGCTGTGGCAGT	252	
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QY	253	ATCTTCTGAGCCGCTCCATGCGGAGACACCGGCGCTGCGAAGCCCTGAGGCTGTGACCC	312	
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QY	313	TGAGCAGCCGCGAGGGGATTTCTATGATGACCTGGAGCAGGCCCAAGCTTGGGCCAAC	372	
Db	242	TGAGCAGCCGCGAGGGGATTTCTATGATGACCTGGAGCAGGCCCAAGCTTGGGCCAAC	301	
QY	373	TGCGCGGCTCATCCAGGCCAAGAGGCGCTGACCTGGGCACTTTCAGGGGCTACTCCG	432	
Db	302	TGCGCGGCTCATCCAGGCCAAGAGGCGCTGACCTGGGCACTTTCAGGGGCTACTCCG	361	
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QY	613	GCACTTTCGACGTGGCCGCTGGTGGATGCGGACAAGAGAACTGTCTCCGCTACTACGAGC	672	
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QY	673	GCTGCTGCACTGTGCGACCGGAGGACATCCTCGCGCTCTCAGAGTCTGTGGCGCG	732	
Db	597	GCTGCTGCACTGTGCGACCGGAGGACATCCTCGCGCTCTCAGAGTCTGTGGCGCG	654	
QY	733	GGAGGTGTGCAACTCTCGAAGGGGAGCTGGCGGCGGAGTGTGTGCGAAACCTTAAGC	792	
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RESULT 15
AK054334

LOCUS AK054334 2243 bp mRNA linear HTC 03-APR-2004
DEFINITION Mus musculus 2 days pregnant adult female ovary cDNA, RIKEN full-length enriched library, clone:E330016L21 product:weakly similar to PUTATIVE O-METHYLTRANSFERASE (FRAGMENT) [Rhodothermus marinus], full insert sequence.

ACCESSION AK054334 GI:26344156
VERSION AK054334.1
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
10349636

2
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
20493374
11042159

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Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsumi, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsumura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
20530913
11076861

4
The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)

5
The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)

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(bases 1 to 2243)
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, M., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imetani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Satoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akaira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.
Direct Submission
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gs.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

COMMENT
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken

Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site for further details.
URL: http://genome.gsc.riken.jp/
URL: http://fantom.gsc.riken.jp/.

FEATURES
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12: Geneseqn2004s:*

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PD 09-MAR-2000.
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PA (GETH ) GENENTECH INC.
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ID ABK40264 standard; cDNA; 989 BP.
DE cDNA encoding human PRO1558 polypeptide.
FN WO200153486-A1.
PD 26-JUL-2001.
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Best Local Similarity 100.0%; Pred. No. 4.5e-156;
RESULT 4
ID AC68458 standard; cDNA; 989 BP.
DE Novel human secreted and transmembrane protein PRO1558 cDNA.
FN US2003073130-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 989; DB 9; Length 989;
Best Local Similarity 100.0%; Pred. No. 4.5e-156;
RESULT 5
ID ACH04560 standard; cDNA; 989 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1558.
FN US2003044841-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 989; DB 9; Length 989;
Best Local Similarity 100.0%; Pred. No. 4.5e-156;

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Best Local Similarity 100.0%; Pred. No. 4.5e-156;
RESULT 6
ID AC68104 standard; cDNA; 989 BP.
DE Novel human secreted and transmembrane protein PRO1558 cDNA.
FN US2003073129-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 989; DB 9; Length 989;
Best Local Similarity 100.0%; Pred. No. 4.5e-156;
RESULT 7
ID ADC18174 standard; cDNA; 989 BP.
DE Human PRO polynucleotide #86.
FN US2003064925-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 989; DB 10; Length 989;
Best Local Similarity 100.0%; Pred. No. 4.5e-156;
RESULT 8
ID ADD70820 standard; cDNA; 989 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1558.
FN US2003099625-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 989; DB 10; Length 989;
Best Local Similarity 100.0%; Pred. No. 4.5e-156;
RESULT 9
ID ADD39897 standard; cDNA; 989 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1558.
FN US2003083462-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 989; DB 10; Length 989;
Best Local Similarity 100.0%; Pred. No. 4.5e-156;
RESULT 10
ID ADD70343 standard; cDNA; 989 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1558.
FN US2003054406-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 989; DB 10; Length 989;
Best Local Similarity 100.0%; Pred. No. 4.5e-156;
RESULT 11
ID ADD38464 standard; cDNA; 989 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1558.
FN US2003096955-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 989; DB 10; Length 989;
Best Local Similarity 100.0%; Pred. No. 4.5e-156;
RESULT 12
ID ADD39420 standard; cDNA; 989 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1558.
FN US2003096954-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 989; DB 10; Length 989;
Best Local Similarity 100.0%; Pred. No. 4.5e-156;
RESULT 13
ID ADD38943 standard; cDNA; 989 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1558.
FN US2003092061-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 989; DB 10; Length 989;
Best Local Similarity 100.0%; Pred. No. 4.5e-156;
RESULT 14
ID ADD40374 standard; cDNA; 989 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1558.
FN US2003082627-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 989; DB 10; Length 989;
Best Local Similarity 100.0%; Pred. No. 4.5e-156;

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RESULT 15
ID ADE50595 standard; cDNA; 989 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1558.
PN US2003069179-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 989; DB 10; Length 989;
Best Local Similarity 100.0%; Pred. No. 4.5e-156;
RESULT 16
ID ADE20207 standard; cDNA; 989 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1558.
PN US2003092883-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 989; DB 10; Length 989;
Best Local Similarity 100.0%; Pred. No. 4.5e-156;
RESULT 17
ID ADE50118 standard; cDNA; 989 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1558.
PN US2003082626-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 989; DB 10; Length 989;
Best Local Similarity 100.0%; Pred. No. 4.5e-156;
RESULT 18
ID ADE21676 standard; cDNA; 989 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1558.
PN US2003082628-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 989; DB 10; Length 989;
Best Local Similarity 100.0%; Pred. No. 4.5e-156;
RESULT 19
ID ADF30101 standard; cDNA; 989 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1558.
PN US2003204053-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 989; DB 10; Length 989;
Best Local Similarity 100.0%; Pred. No. 4.5e-156;
RESULT 20
ID ADF55994 standard; cDNA; 989 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1558.
PN US2003204054-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 989; DB 10; Length 989;
Best Local Similarity 100.0%; Pred. No. 4.5e-156;
RESULT 21
ID ADH99498 standard; cDNA; 989 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1558.
PN US2003065142-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 989; DB 10; Length 989;
Best Local Similarity 100.0%; Pred. No. 4.5e-156;
RESULT 22
ID ADJ37302 standard; cDNA; 989 BP.
DE Human tumour therapy associated PRO1558 cDNA.
PN US2003211096-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 989; DB 10; Length 989;
Best Local Similarity 100.0%; Pred. No. 4.5e-156;
RESULT 23
ID ADE96678 standard; cDNA; 989 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1558.
PN US2003195347-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 989; DB 12; Length 989;
Best Local Similarity 100.0%; Pred. No. 4.5e-156;
RESULT 24
ID ADE50595 standard; cDNA; 989 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1558.
PN US2003069179-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 989; DB 10; Length 989;
Best Local Similarity 100.0%; Pred. No. 4.5e-156;
RESULT 25
ID ADF24888 standard; cDNA; 989 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1558.
PN US2003198993-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 989; DB 12; Length 989;
Best Local Similarity 100.0%; Pred. No. 4.5e-156;
RESULT 26
ID ADF29624 standard; cDNA; 989 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1558.
PN US2003203401-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 989; DB 12; Length 989;
Best Local Similarity 100.0%; Pred. No. 4.5e-156;
RESULT 27
ID ADE97155 standard; cDNA; 989 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1558.
PN US2003195334-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 989; DB 12; Length 989;
Best Local Similarity 100.0%; Pred. No. 4.5e-156;
RESULT 28
ID ADH03193 standard; cDNA; 989 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1558.
PN US2003216562-A1.
PD 20-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 989; DB 12; Length 989;
Best Local Similarity 100.0%; Pred. No. 4.5e-156;
RESULT 29
ID ADH04147 standard; cDNA; 989 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1558.
PN US2003220471-A1.
PD 27-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 989; DB 12; Length 989;
Best Local Similarity 100.0%; Pred. No. 4.5e-156;
RESULT 30
ID ADH03670 standard; cDNA; 989 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1558.
PN US2003224478-A1.
PD 04-DEC-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 989; DB 12; Length 989;
Best Local Similarity 100.0%; Pred. No. 4.5e-156;
RESULT 31
ID ADG68226 standard; cDNA; 989 BP.
DE Human PRO polypeptide cDNA #11.
PN US2003170228-A1.
PD 11-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 989; DB 12; Length 989;
Best Local Similarity 100.0%; Pred. No. 4.5e-156;
RESULT 32
ID ADH04624 standard; cDNA; 989 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1558.
PN US2004005626-A1.
PD 08-JAN-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 989; DB 12; Length 989;
Best Local Similarity 100.0%; Pred. No. 4.5e-156;
RESULT 33
ID ADH61625 standard; cDNA; 989 BP.
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DE Human cDNA encoding secreted/transmembrane protein PRO1558.
PN US2004014130-A1.
PD 22-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 989; DB 12; Length 989;
Best Local Similarity 100.0%; Pred. No. 4.5e-156;
RESULT 34
ID ADL94824 standard; cDNA; 989 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1558.
PN US2004073015-A1.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 989; DB 12; Length 989;
Best Local Similarity 100.0%; Pred. No. 4.5e-156;
RESULT 35
ID ADO42276 standard; cDNA; 989 BP.
DE Human NOVX polynucleotide #63.
PN US2004058338-A1.
PD 25-MAR-2004.
PA (AGEE/) AGEE M L.
PA (ALSO/) ALSOBROOK J P.
PA (ANDE/) ANDERSON D W.
PA (BERG/) BERGHS C.
PA (BOLD/) BOLDOG F L.
PA (BURG/) BURGESS C E.
PA (CATT/) CATTERTON E.
PA (DIPI/) DIPIPPO V A.
PA (EDIN/) EDINGER S R.
PA (EISE/) EISEN A.
PA (ELLE/) ELLERMAN K.
PA (GANG/) GANGOLLI E A.
PA (GERL/) GERLACH V.
PA (GORM/) GORMAN L.
PA (ROTH/) ROTHBERG B G.
PA (GUOX/) GUO X S.
PA (HERR/) HERMANN J L.
PA (HALV/) HALVORSEN Y.
PA (JIWW/) JI W.
PA (KEKU/) KEKUDA R.
PA (KHRA/) KHRAMTSOV N V.
PA (LARO/) LAROCHELLE W J.
PA (LEPL/) LEFLEY D M.
PA (LILL/) LI L.
PA (MACD/) MACDOUGALL J R.
PA (MILL/) MILLER C E.
PA (ORTT/) ORT T.
PA (PADI/) PADIGARU M.
PA (PATT/) PATTURAJAN M.
PA (PENA/) PENA C E A.
PA (PEYM/) PEYMAN J A.
PA (RIEG/) RIEGER D K.
PA (ROTH/) ROTHENBERG M E.
PA (SHEN/) SHENOY S G.
PA (SMIT/) SMITHSON G.
PA (SPAD/) SPADERNA S K.
PA (SPYT/) SPYTEK K A.
PA (STON/) STONE D J.
PA (TAUP/) TAUPIER R J.
PA (VERN/) VERNET C A M.
PA (VOSS/) VOSS E Z.
PA (ZHON/) ZHONG M.
Query Match 100.0%; Score 989; DB 12; Length 989;
Best Local Similarity 100.0%; Pred. No. 4.5e-156;
RESULT 36
ID ABA05419 standard; cDNA; 1037 BP.
DE Human O-methyltransferase family member 25692 encoding cDNA.
PN WO200183719-A2.
PD 08-NOV-2001.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 99.7%; Score 985.8; DB 6; Length 1037;
Best Local Similarity 99.8%; Pred. No. 1.5e-155;
RESULT 37
ID AA298166 standard; cDNA; 985 BP.

DE Human signal peptide containing protein HSPP-58 cDNA SEQ ID NO:192.
PN WO200006010-A2.
PD 06-JAN-2000.
PA (INCY-) INCYTE PHARM INC.
Query Match 99.3%; Score 981.8; DB 3; Length 985;
Best Local Similarity 99.8%; Pred. No. 7.1e-155;
RESULT 38
ID ABQ61039 standard; cDNA; 1100 BP.
DE Human PRO1558 protein encoding sequence.
PN WO200231111-A2.
PD 18-APR-2002.
PA (HYSE-) HYSEQ INC.
Query Match 99.3%; Score 981.8; DB 6; Length 1100;
Best Local Similarity 99.8%; Pred. No. 7.1e-155;
RESULT 39
ID ADO42272 standard; cDNA; 988 BP.
DE Human NOVX polynucleotide #61.
PN US2004058338-A1.
PD 25-MAR-2004.
PA (AGEE/) AGEE M L.
PA (ALSO/) ALSOBROOK J P.
PA (ANDE/) ANDERSON D W.
PA (BERG/) BERGHS C.
PA (BOLD/) BOLDOG F L.
PA (BURG/) BURGESS C E.
PA (CATT/) CATTERTON E.
PA (DIPI/) DIPIPPO V A.
PA (EDIN/) EDINGER S R.
PA (EISE/) EISEN A.
PA (ELLE/) ELLERMAN K.
PA (GANG/) GANGOLLI E A.
PA (GERL/) GERLACH V.
PA (GORM/) GORMAN L.
PA (ROTH/) ROTHBERG B G.
PA (GUOX/) GUO X S.
PA (HERR/) HERMANN J L.
PA (HALV/) HALVORSEN Y.
PA (JIWW/) JI W.
PA (KEKU/) KEKUDA R.
PA (KHRA/) KHRAMTSOV N V.
PA (LARO/) LAROCHELLE W J.
PA (LEPL/) LEFLEY D M.
PA (LILL/) LI L.
PA (MACD/) MACDOUGALL J R.
PA (MILL/) MILLER C E.
PA (ORTT/) ORT T.
PA (PADI/) PADIGARU M.
PA (PATT/) PATTURAJAN M.
PA (PENA/) PENA C E A.
PA (PEYM/) PEYMAN J A.
PA (RIEG/) RIEGER D K.
PA (ROTH/) ROTHENBERG M E.
PA (SHEN/) SHENOY S G.
PA (SMIT/) SMITHSON G.
PA (SPAD/) SPADERNA S K.
PA (SPYT/) SPYTEK K A.
PA (STON/) STONE D J.
PA (TAUP/) TAUPIER R J.
PA (VERN/) VERNET C A M.
PA (VOSS/) VOSS E Z.
PA (ZHON/) ZHONG M.
Query Match 98.8%; Score 977; DB 12; Length 988;
Best Local Similarity 99.9%; Pred. No. 4.5e-154;
RESULT 40
ID AAH33455 standard; cDNA; 967 BP.
DE Human colon cancer antigen encoding cDNA SEQ ID NO:511.
PN WO200122920-A2.
PD 05-APR-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 94.9%; Score 938.2; DB 4; Length 967;
Best Local Similarity 99.4%; Pred. No. 1.3e-147;
RESULT 41
ID AAC76634 standard; cDNA; 812 BP.

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DE Human OREX ORF2189 polynucleotide sequence SEQ ID NO:4377.
PN WO200058473-A2.
PD 05-OCT-2000.
PA (CURA-) CURAGEN CORP.
Query Match 80.9%; Score 799.8; DB 3; Length 812;
Best Local Similarity 99.1%; Pred. No. 1.6e-124;
RESULT 42
ID ABA05420 standard; cDNA; 789 BP.
DE Human O-methyltransferase family member 25692 coding sequence.
PN WO200183719-A2.
PD 08-NOV-2001.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 79.8%; Score 789; DB 6; Length 789;
Best Local Similarity 100.0%; Pred. No. 1e-122;
RESULT 43
ID AAD56372 standard; DNA; 876 BP.
DE Human secreted protein-encoding gene 11 cDNA clone HTAQ018, SEQ ID NO:32.
PN WO2003038038-A2.
PD 08-MAY-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 71.0%; Score 701.8; DB 9; Length 876;
Best Local Similarity 86.5%; Pred. No. 3.4e-108;
RESULT 44
ID AAD56361 standard; DNA; 885 BP.
DE Human secreted protein-encoding gene 11 cDNA clone HTAQ018, SEQ ID NO:21.
PN WO2003038038-A2.
PD 08-MAY-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 70.9%; Score 701; DB 9; Length 885;
Best Local Similarity 86.2%; Pred. No. 4.7e-108;
RESULT 45
ID ADO42274 standard; cDNA; 787 BP.
DE Human NOVX polynucleotide #62.
PN US2004058338-A1.
PD 25-MAR-2004.
PA (AGEE/) AGEE M L.
PA (ALSO/) ALSOBROOK J P.
PA (ANDE/) ANDERSON D W.
PA (BERG/) BERGHS C.
PA (BOLD/) BOLDIG F L.
PA (BURG/) BURGESS C E.
PA (CATT/) CATTERTON E.
PA (DIPI/) DIPIPO V A.
PA (EDIN/) EDINGER S R.
PA (EISE/) EISEN A.
PA (ELLE/) ELLERMAN K.
PA (GANG/) GANGOLLI E A.
PA (GERL/) GERLACH V.
PA (GORM/) GORMAN L.
PA (ROTH/) ROTHBERG B G.
PA (GUOX/) GUO X S.
PA (HERR/) HERRMANN J L.
PA (HALV/) HALVORSEN Y.
PA (JIWW/) JI W.
PA (KEKU/) KEKUDA R.
PA (KIRA/) KIRAMTSOV N V.
PA (LARO/) LAROCHELLE W J.
PA (LEPL/) LEFLEY D M.
PA (LILL/) LI L.
PA (MACD/) MACDOUGALL J R.
PA (MILL/) MILLER C E.
PA (ORTT/) ORT T.
PA (PADI/) PADIGARU M.
PA (PATI/) PATTURAJAN M.
PA (PENA/) PENA C E A.
PA (PEYM/) PEYMAN J A.
PA (RIEG/) RIEGER D K.
PA (ROTH/) ROTHENBERG M E.
PA (SHEN/) SHENOY S G.
PA (SMIT/) SMITHSON G.
PA (SPAD/) SPADERNA S K.
PA (SPYT/) SPYTEK K A.
PA (STON/) STONE D J.

PA (TAUP/) TAUPIER R J.
PA (VERN/) VERNET C A M.
PA (VOSS/) VOSS E Z.
PA (ZHON/) ZHONG M.
Query Match 59.0%; Score 583.6; DB 12; Length 787;
Best Local Similarity 90.1%; Pred. No. 1.8e-88;
RESULT 46
ID ACH35195 standard; cDNA; 474 BP.
DE Human endothelial cell cDNA #3328.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Query Match 42.7%; Score 422; DB 9; Length 474;
Best Local Similarity 100.0%; Pred. No. 1.6e-61;
RESULT 47
ID ACH35890 standard; cDNA; 458 BP.
DE Human endothelial cell cDNA #4023.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Query Match 41.8%; Score 413; DB 9; Length 458;
Best Local Similarity 100.0%; Pred. No. 4.9e-60;
RESULT 48
ID ADD34178 standard; DNA; 770 BP.
DE Mouse mitochondrial DNA sequence SEQ ID NO:1956.
PN WO2003020220-A2.
PD 13-MAR-2003.
PA (UTEM-) UNIV EMORY.
Query Match 40.9%; Score 404.4; DB 10; Length 770;
Best Local Similarity 80.4%; Pred. No. 1.3e-58;
RESULT 49
ID ABN94134 standard; DNA; 326 BP.
DE Gene #632 used to diagnose liver cancer.
PN WO200229103-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 31.5%; Score 312; DB 6; Length 326;
Best Local Similarity 99.7%; Pred. No. 3.4e-43;
RESULT 50
ID ADM80035 standard; DNA; 11171 BP.
DE Spiramycin biosynthesis related DNA, SEQ ID 2.
PN FR2845394-A1.
PD 09-APR-2004.
PA (AVET) AVENTIS PHARMA SA.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 19.7%; Score 194.8; DB 12; Length 11171;
Best Local Similarity 55.1%; Pred. No. 1.1e-23;
RESULT 51
ID ADN97551 standard; DNA; 11171 BP.
DE S ambotaciens spiramycin biosynthetic enzyme genomic region #2.
PN WO2004033689-A2.
PD 22-APR-2004.
PA (AVET) AVENTIS PHARMA SA.
PA (CNRS) CNRS.
Query Match 19.7%; Score 194.8; DB 12; Length 11171;
Best Local Similarity 55.1%; Pred. No. 1.1e-23;
RESULT 52
ID ADM80044 standard; DNA; 675 BP.
DE Spiramycin biosynthesis orf5*, SEQ ID 11.
PN FR2845394-A1.
PD 09-APR-2004.
PA (AVET) AVENTIS PHARMA SA.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 19.6%; Score 193.8; DB 12; Length 675;
Best Local Similarity 58.1%; Pred. No. 1.7e-23;

RESULT 53
ID ADN97560 standard; DNA; 675 BP.
DE S ambotaciens spiramycin biosynthetic gene ORFs*.
PN WO2004033689-A2.
PD 22-APR-2004.
PA (AVET) AVENTIS PHARMA SA.
PA (CNRS) CNRS.
Query Match 19.6%; Score 193.8; DB 12; Length 675;
Best Local Similarity 58.1%; Pred. No. 1.7e-23;
RESULT 54
ID ABD04592 standard; DNA; 846 BP.
DE Pseudomonas aeruginosa polynucleotide #3196.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 19.1%; Score 189; DB 11; Length 846;
Best Local Similarity 56.0%; Pred. No. 1.1e-22;
RESULT 55
ID AAQ4449 standard; DNA; 2381 BP.
DE 3-acylating enzyme coding sequence.
PN JP06038750-A.
PD 15-FEB-1994.
PA (MEIJ) MEIJI SEIKA KAISHA.
Query Match 18.8%; Score 185.8; DB 2; Length 2381;
Best Local Similarity 57.3%; Pred. No. 3.6e-22;
RESULT 56
ID ADM45913 standard; DNA; 84428 BP.
DE Streptomyces mycarofaciens midcamycin polyketide synthetase DNA.
PN JP2004049100-A.
PD 19-FEB-2004.
PA (MEIJ) MEIJI SEIKA KAISHA LTD.
Query Match 18.8%; Score 185.8; DB 12; Length 84428;
Best Local Similarity 57.3%; Pred. No. 3.2e-22;
RESULT 57
ID ADI39159 standard; DNA; 85692 BP.
DE Streptomyces hygroscopicus geldanamycin gene cluster, SEQ ID NO:1.
PN WO2003106653-A2.
PD 24-DEC-2003.
PA (KOSA-) KOSAN BIOSCIENCES INC.
PA (REID/) REID R C.
Query Match 18.4%; Score 182.4; DB 12; Length 85692;
Best Local Similarity 57.4%; Pred. No. 1.2e-21;
RESULT 58
ID ADI39160 standard; DNA; 86941 BP.
DE Streptomyces hygroscopicus herbimycin gene cluster, SEQ ID NO:2.
PN WO2003106653-A2.
PD 24-DEC-2003.
PA (KOSA-) KOSAN BIOSCIENCES INC.
PA (REID/) REID R C.
Query Match 18.1%; Score 179.2; DB 12; Length 86941;
Best Local Similarity 57.9%; Pred. No. 4.1e-21;
RESULT 59
ID AAC89765 standard; CDNA; 953 BP.
DE Human Gastrointestinal inflammation-related CDNA, SEQ ID NO: 34.
PN WO200073324-A2.
PD 07-DEC-2000.
PA (DIGI-) DIGITAL GENE TECHNOLOGIES INC.
Query Match 17.7%; Score 174.8; DB 4; Length 178;
Best Local Similarity 98.9%; Pred. No. 2.6e-20;
RESULT 60
ID ABS63429 standard; CDNA; 953 BP.
DE DNA encoding wheat caffeoyl-CoA O-methyltransferase (CCOMT).
PN US2002081693-A1.
PD 27-JUN-2002.
PA (CAHO/) CAHOON R E.
PA (FADE/) FADER G M.
PA (RAFA/) RAFALSKI J A.
Query Match 16.4%; Score 161.8; DB 6; Length 953;
Best Local Similarity 55.1%; Pred. No. 3.7e-18;
RESULT 61
ID ABS63428 standard; CDNA; 1049 BP.
DE DNA encoding wheat caffeoyl-CoA O-methyltransferase (CCOMT).
PN US2002081693-A1.

PD 27-JUN-2002.
PA (CAHO/) CAHOON R E.
PA (FADE/) FADER G M.
PA (RAFA/) RAFALSKI J A.
Query Match 16.1%; Score 159.2; DB 6; Length 1049;
Best Local Similarity 54.8%; Pred. No. 9.9e-18;
RESULT 62
ID ABS63413 standard; CDNA; 997 BP.
DE DNA encoding rice caffeoyl-CoA O-methyltransferase (CCOMT).
PN US2002081693-A1.
PD 27-JUN-2002.
PA (CAHO/) CAHOON R E.
PA (FADE/) FADER G M.
PA (RAFA/) RAFALSKI J A.
Query Match 16.0%; Score 158.6; DB 6; Length 997;
Best Local Similarity 54.2%; Pred. No. 1.2e-17;
RESULT 63
ID ADA71076 standard; DNA; 1338 BP.
DE Rice gene, SEQ ID 4399.
PN WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 15.0%; Score 158.6; DB 8; Length 1338;
Best Local Similarity 55.2%; Pred. No. 1.2e-17;
RESULT 64
ID ABS63427 standard; CDNA; 1078 BP.
DE DNA encoding wheat caffeoyl-CoA O-methyltransferase (CCOMT).
PN US2002081693-A1.
PD 27-JUN-2002.
PA (CAHO/) CAHOON R E.
PA (FADE/) FADER G M.
PA (RAFA/) RAFALSKI J A.
Query Match 15.9%; Score 157.2; DB 6; Length 1078;
Best Local Similarity 57.1%; Pred. No. 2.1e-17;
RESULT 65
ID ABS63424 standard; CDNA; 1018 BP.
DE DNA encoding wheat caffeoyl-CoA O-methyltransferase (CCOMT).
PN US2002081693-A1.
PD 27-JUN-2002.
PA (CAHO/) CAHOON R E.
PA (FADE/) FADER G M.
PA (RAFA/) RAFALSKI J A.
Query Match 15.7%; Score 155.6; DB 6; Length 1018;
Best Local Similarity 56.6%; Pred. No. 3.9e-17;
RESULT 66
ID ABS63407 standard; CDNA; 891 BP.
DE DNA encoding corn caffeoyl-CoA O-methyltransferase (CCOMT).
PN US2002081693-A1.
PD 27-JUN-2002.
PA (CAHO/) CAHOON R E.
PA (FADE/) FADER G M.
PA (RAFA/) RAFALSKI J A.
Query Match 15.6%; Score 154; DB 6; Length 891;
Best Local Similarity 56.7%; Pred. No. 7.3e-17;
RESULT 67
ID AAA14651 standard; DNA; 77536 BP.
DE Nucleotide sequence of the FK-520 biosynthetic gene cluster.
PN WO2003000906-A2.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 15.4%; Score 152.8; DB 9; Length 1112;
Best Local Similarity 58.3%; Pred. No. 1.2e-16;
RESULT 68
ID ADA49019 standard; DNA; 1112 BP.
DE Wheat gene conferring disease resistance in plants.
PN WO2003000906-A2.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 15.4%; Score 152.8; DB 9; Length 1112;
Best Local Similarity 58.3%; Pred. No. 1.2e-16;
RESULT 69
ID AAX25215 standard; CDNA; 1218 BP.
DE Maize caffeoyl-CoA 3-O-methyltransferase cDNA.
PN WO9910498-A2.
PD 04-MAR-1999.
PA (PION-) PIONEER HI-BRED INT INC.

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Query Match 15.4%; Score 152.4; DB 2; Length 1218;
 Best Local Similarity 56.5%; Pred. No. 1.3e-16;
 RESULT 70
 ID AAD05742 standard; cDNA; 1218 BP.
 DE Maize caffeoyl-CoA-3-O-methyltransferase (CCoA-OMT) cDNA.
 PN WO200134817-A2.
 PD 17-MAY-2001.
 PA (PION-) PIONEER HI-BRED INT INC.
 Query Match 15.4%; Score 152.4; DB 5; Length 1218;
 Best Local Similarity 56.5%; Pred. No. 1.3e-16;
 RESULT 71
 ID AAL61224 standard; DNA; 82746 BP.
 DE Actinosynnema pretiosum aneamtocin biosynthetic gene cluster I.
 PN WO2003045312-A2.
 PD 05-JUN-2003.
 PA (UNIW) UNIV WASHINGTON.
 Query Match 15.3%; Score 151.4; DB 8; Length 82746;
 Best Local Similarity 57.3%; Pred. No. 1.8e-16;
 RESULT 72
 ID ABZ40101 standard; DNA; 666 BP.
 DE N. gonorrhoeae nucleotide sequence SEQ ID 4791.
 PN WO200275243-A2.
 PD 10-OCT-2002.
 PA (CHIR-) CHIRON SPA.
 Query Match 15.1%; Score 149.2; DB 10; Length 666;
 Best Local Similarity 53.5%; Pred. No. 4.7e-16;
 RESULT 73
 ID AX25210 standard; cDNA; 1003 BP.
 DE Maize caffeoyl-CoA 3-O-methyltransferase cDNA.
 PN WO9910498-A2.
 PD 04-MAR-1999.
 PA (PION-) PIONEER HI-BRED INT INC.
 Query Match 15.1%; Score 149.2; DB 2; Length 1003;
 Best Local Similarity 58.0%; Pred. No. 4.6e-16;
 RESULT 74
 ID ADM49212 standard; DNA; 798 BP.
 DE Maize gene conferring disease resistance in plants.
 PN WO2003000906-A2.
 PD 03-JAN-2003.
 PA (SYNG) SYNGENTA PARTICIPATIONS AG.
 Query Match 15.0%; Score 148; DB 9; Length 798;
 Best Local Similarity 53.7%; Pred. No. 7.3e-16;
 RESULT 75
 ID ABS63425 standard; cDNA; 1118 BP.
 DE DNA encoding wheat caffeoyl-CoA O-methyltransferase (CCOMT).
 PN US2002081693-A1.
 PD 27-JUN-2002.
 PA (CAHO/) CAHOON R. E.
 PA (FADE/) FADER G. M.
 PA (RAFA/) RAFALSKI J. A.
 Query Match 15.0%; Score 148; DB 6; Length 1118;
 Best Local Similarity 53.7%; Pred. No. 7.3e-16;
 RESULT 76
 ID ABS63408 standard; cDNA; 1146 BP.
 DE DNA encoding corn caffeoyl-CoA O-methyltransferase (CCOMT).
 PN US2002081693-A1.
 PD 27-JUN-2002.
 PA (CAHO/) CAHOON R. E.
 PA (FADE/) FADER G. M.
 PA (RAFA/) RAFALSKI J. A.
 Query Match 15.0%; Score 148; DB 6; Length 1146;
 Best Local Similarity 53.7%; Pred. No. 7.3e-16;
 RESULT 77
 ID ADD34177 standard; DNA; 407 BP.
 DE Mouse mitochondrial DNA sequence SEQ ID NO:1955.
 PN WO2003020220-A2.
 PD 13-MAR-2003.
 PA (UYEM-) UNIV EMORY.
 Query Match 14.9%; Score 147.4; DB 10; Length 407;
 Best Local Similarity 73.3%; Pred. No. 9.4e-16;
 RESULT 78
 ID AAA81501 standard; DNA; 48275 BP.
 DE N. meningitidis partial DNA sequence gnm_48 SEQ ID NO:48.

PN WO20022430-A2.
 PD 20-APR-2000.
 PA (CHIR) CHIRON CORP.
 Query Match 14.8%; Score 146.8; DB 3; Length 48275;
 Best Local Similarity 53.1%; Pred. No. 1e-15;
 RESULT 79
 ID AAA81489 standard; DNA; 837096 BP.
 DE N. meningitidis partial DNA sequence gnm_37 SEQ ID NO:37.
 PN WO20022430-A2.
 PD 20-APR-2000.
 PA (CHIR) CHIRON CORP.
 Query Match 14.8%; Score 146.8; DB 3; Length 110000;
 Best Local Similarity 53.1%; Pred. No. 1e-15;
 RESULT 80
 ID RAF21610 standard; DNA; 349980 BP.
 DE Neisseria meningitidis B nucleotide sequence SEQ ID NO:111.
 PN WO200066791-A1.
 PD 09-NOV-2000.
 PA (CHIR) CHIRON CORP.
 PA (GENO-) INST GENOMIC RES.
 Query Match 14.8%; Score 146.8; DB 3; Length 349980;
 Best Local Similarity 53.1%; Pred. No. 9.8e-16;
 RESULT 81
 ID AAL61190 standard; DNA; 504 BP.
 DE Actinosynnema pretiosum O-methyltransferase gene.
 PN WO2003045312-A2.
 PD 05-JUN-2003.
 PA (UNIW) UNIV WASHINGTON.
 Query Match 14.8%; Score 146.6; DB 8; Length 504;
 Best Local Similarity 57.7%; Pred. No. 1.3e-15;
 RESULT 82
 ID AAX25208 standard; cDNA; 1160 BP.
 DE Maize caffeoyl-CoA 3-O-methyltransferase cDNA.
 PN WO9910498-A2.
 PD 04-MAR-1999.
 PA (PION-) PIONEER HI-BRED INT INC.
 Query Match 14.8%; Score 146.4; DB 2; Length 1160;
 Best Local Similarity 53.5%; Pred. No. 1.3e-15;
 RESULT 83
 ID ABS63409 standard; cDNA; 1057 BP.
 DE DNA encoding corn caffeoyl-CoA O-methyltransferase (CCOMT).
 PN US2002081693-A1.
 PD 27-JUN-2002.
 PA (CAHO/) CAHOON R. E.
 PA (FADE/) FADER G. M.
 PA (RAFA/) RAFALSKI J. A.
 Query Match 14.6%; Score 144.4; DB 6; Length 1057;
 Best Local Similarity 57.3%; Pred. No. 2.9e-15;
 RESULT 84
 ID ADA71075 standard; DNA; 783 BP.
 DE Rice gene, SEQ ID 4398.
 PN WO2003000898-A1.
 PD 03-JAN-2003.
 PA (SYNG) SYNGENTA PARTICIPATIONS AG.
 Query Match 14.3%; Score 141.8; DB 8; Length 783;
 Best Local Similarity 57.4%; Pred. No. 7.9e-15;
 RESULT 85
 ID ACL23248 standard; DNA; 509 BP.
 DE DNA clone originating in barley containing SNP encoding sequence #13239.
 PN WO2003057877-A1.
 PD 17-JUL-2003.
 PA (UYNI-) UNIV JAPAN OKAYAMA.
 Query Match 14.2%; Score 140.8; DB 9; Length 509;
 Best Local Similarity 60.3%; Pred. No. 1.2e-14;
 RESULT 86
 ID ABS63412 standard; cDNA; 1058 BP.
 DE DNA encoding rice caffeoyl-CoA O-methyltransferase (CCOMT).
 PN US2002081693-A1.
 PD 27-JUN-2002.
 PA (CAHO/) CAHOON R. E.
 PA (FADE/) FADER G. M.
 PA (RAFA/) RAFALSKI J. A.
 Query Match 14.2%; Score 140.6; DB 6; Length 1058;

Best Local Similarity 50.6%; Pred. No. 1.2e-14;
 RESULT 87
 ID ADA70823 standard; DNA; 783 BP.
 DE Rice gene, SEQ ID 4146.
 PN WO200300089-A1.
 PD 03-JAN-2003.
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 Query Match 14.2%; Score 140; DB 8; Length 783;
 Best Local Similarity 52.9%; Pred. No. 1.6e-14;
 RESULT 88
 ID ABN87118 standard; cDNA; 1103 BP.
 DE Lolium perenne LpCCoAMTB nucleotide sequence SEQ ID NO:12.
 PN WO200226994-A1.
 PD 04-APR-2002.
 PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.
 PA (AGRE-) AGRESEARCH LTD.
 Query Match 13.7%; Score 135.6; DB 6; Length 1103;
 Best Local Similarity 57.0%; Pred. No. 8.5e-14;
 RESULT 89
 ID ABN87121 standard; cDNA; 773 BP.
 DE Lolium perenne LpCCoAMTB partial nucleotide sequence SEQ ID NO:16.
 PN WO200226994-A1.
 PD 04-APR-2002.
 PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.
 PA (AGRE-) AGRESEARCH LTD.
 Query Match 13.7%; Score 135; DB 6; Length 773;
 Best Local Similarity 56.9%; Pred. No. 1.1e-13;
 RESULT 90
 ID ABN87122 standard; cDNA; 789 BP.
 DE Lolium perenne LpCCoAMTB partial nucleotide sequence SEQ ID NO:17.
 PN WO200226994-A1.
 PD 04-APR-2002.
 PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.
 PA (AGRE-) AGRESEARCH LTD.
 Query Match 13.7%; Score 135; DB 6; Length 789;
 Best Local Similarity 56.9%; Pred. No. 1.1e-13;
 RESULT 91
 ID ABN87120 standard; cDNA; 693 BP.
 DE Lolium perenne LpCCoAMTB partial nucleotide sequence SEQ ID NO:15.
 PN WO200226994-A1.
 PD 04-APR-2002.
 PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.
 PA (AGRE-) AGRESEARCH LTD.
 Query Match 13.3%; Score 131.6; DB 6; Length 693;
 Best Local Similarity 56.9%; Pred. No. 4e-13;
 RESULT 92
 ID AAS08693 standard; DNA; 109519 BP.
 DE Micromonospora DNA encoding biosynthetic enzymes for Evernimycin.
 Query Match 12.9%; Score 127.4; DB 5; Length 109519;
 Best Local Similarity 55.8%; Pred. No. 1.7e-12;
 RESULT 93
 ID ABN87126 standard; cDNA; 689 BP.
 DE Lolium perenne LpCCoAMTB nucleotide sequence SEQ ID NO:21.
 PN WO200226994-A1.
 PD 04-APR-2002.
 PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.
 PA (AGRE-) AGRESEARCH LTD.
 Query Match 12.8%; Score 126.8; DB 6; Length 689;
 Best Local Similarity 57.1%; Pred. No. 2.5e-12;
 RESULT 94
 ID ABS63410 standard; cDNA; 923 BP.
 DE DNA encoding corn caffeoyl-CoA O-methyltransferase (CCOMT).
 PN US2002081693-A1.
 PD 27-JUN-2002.
 PA (CAHO/) CAHOON R E.
 PA (FADE/) FADER G M.
 PA (RAPA/) RAPALSKI J A.
 Query Match 12.7%; Score 126; DB 6; Length 923;
 Best Local Similarity 56.6%; Pred. No. 3.4e-12;
 RESULT 95
 ID AAX25209 standard; cDNA; 944 BP.
 DE Maize caffeoyl-CoA 3-O-methyltransferase cDNA.
 PN WO9910498-A2.

PD 04-MAR-1999.
 PA (PION-) PIONEER HI-BRED INT INC.
 Query Match 12.7%; Score 126; DB 2; Length 944;
 Best Local Similarity 56.6%; Pred. No. 3.4e-12;
 RESULT 96
 ID ADA48371 standard; DNA; 835 BP.
 DE Rice gene conferring disease resistance in plants.
 PN WO2003000906-A2.
 PD 03-JAN-2003.
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 Query Match 12.7%; Score 125.4; DB 9; Length 835;
 Best Local Similarity 55.0%; Pred. No. 4.3e-12;
 RESULT 97
 ID ADC68436 standard; cDNA; 1051 BP.
 DE Lolium perenne lignin biosynthesis protein cDNA SEQ ID NO:146.
 PN WO2003040306-A2.
 PD 15-MAY-2003.
 PA (GENE-) GENESIS RES & DEV CORP LTD.
 PA (WRIG-) WRIGHTSON SEEDS LTD.
 Query Match 12.6%; Score 125; DB 10; Length 1051;
 Best Local Similarity 54.0%; Pred. No. 5e-12;
 RESULT 98
 ID ADC68544 standard; cDNA; 1059 BP.
 DE Lolium perenne lignin biosynthesis protein cDNA SEQ ID NO:36.
 PN WO2003040306-A2.
 PD 15-MAY-2003.
 PA (GENE-) GENESIS RES & DEV CORP LTD.
 PA (WRIG-) WRIGHTSON SEEDS LTD.
 Query Match 12.5%; Score 123.4; DB 10; Length 1059;
 Best Local Similarity 53.9%; Pred. No. 9.2e-12;
 RESULT 99
 ID ADC68545 standard; cDNA; 1063 BP.
 DE S. arundinaceus lignin biosynthesis protein cDNA SEQ ID NO:37.
 PN WO2003040306-A2.
 PD 15-MAY-2003.
 PA (GENE-) GENESIS RES & DEV CORP LTD.
 PA (WRIG-) WRIGHTSON SEEDS LTD.
 Query Match 12.4%; Score 122.6; DB 10; Length 1063;
 Best Local Similarity 54.2%; Pred. No. 1.3e-11;
 RESULT 100
 ID ABN87112 standard; cDNA; 765 BP.
 DE Lolium perenne LpCCoAMTB partial nucleotide sequence SEQ ID NO:6.
 PN WO200226994-A1.
 PD 04-APR-2002.
 PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.
 PA (AGRE-) AGRESEARCH LTD.
 Query Match 12.0%; Score 118.4; DB 6; Length 765;
 Best Local Similarity 53.7%; Pred. No. 6.3e-11;
 RESULT 101
 ID AAQ14978 standard; DNA; 1810 BP.
 DE ACYA gene.
 PN EP459525-A.
 PD 04-DEC-1991.
 PA (SAOC) MERCIAN CORP.
 Query Match 11.9%; Score 118; DB 2; Length 1810;
 Best Local Similarity 57.8%; Pred. No. 7.2e-11;
 RESULT 102
 ID ABN87245 standard; cDNA; 1161 BP.
 DE Lolium perenne CCoAMTB cDNA sequence SEQ ID NO:168.
 PN WO200226994-A1.
 PD 04-APR-2002.
 PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.
 PA (AGRE-) AGRESEARCH LTD.
 Query Match 11.9%; Score 117.8; DB 6; Length 1161;
 Best Local Similarity 53.7%; Pred. No. 7.9e-11;
 RESULT 103
 ID ABN87110 standard; cDNA; 758 BP.
 DE Lolium perenne LpCCoAMTB partial nucleotide sequence SEQ ID NO:4.
 PN WO200226994-A1.
 PD 04-APR-2002.
 PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.
 PA (AGRE-) AGRESEARCH LTD.
 Query Match 11.7%; Score 115.6; DB 6; Length 758;
 Best Local Similarity 53.7%; Pred. No. 7.9e-11;

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Best Local Similarity 52.8%; Pred. No. 1.9e-10;
 RESULT 104
 ID ABN87115 standard; cDNA; 793 BP.
 DE Lolium perenne LpCCoAMTa partial nucleotide sequence SEQ ID NO:9.
 PN WO200226994-A1.
 PD 04-APR-2002.
 PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.
 PA (AGRE-) AGRESEARCH LTD.
 Query Match 11.7%; Score 115.6; DB 6; Length 793;
 Best Local Similarity 52.8%; Pred. No. 1.9e-10;
 RESULT 105
 ID ABN87108 standard; cDNA; 1113 BP.
 DE Lolium perenne LpCCoAMTa nucleotide sequence SEQ ID NO:1.
 PN WO200226994-A1.
 PD 04-APR-2002.
 PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.
 PA (AGRE-) AGRESEARCH LTD.
 Query Match 11.6%; Score 115; DB 6; Length 1113;
 Best Local Similarity 52.8%; Pred. No. 2.3e-10;
 RESULT 106
 ID ABN87246 standard; cDNA; 1199 BP.
 DE Lolium perenne CCoAMT2 cDNA sequence SEQ ID NO:170.
 PN WO200226994-A1.
 PD 04-APR-2002.
 PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.
 PA (AGRE-) AGRESEARCH LTD.
 Query Match 11.6%; Score 115; DB 6; Length 1199;
 Best Local Similarity 52.8%; Pred. No. 2.3e-10;
 RESULT 107
 ID ABN87111 standard; cDNA; 774 BP.
 DE Lolium perenne LpCCoAMTa partial nucleotide sequence SEQ ID NO:5.
 PN WO200226994-A1.
 PD 04-APR-2002.
 PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.
 PA (AGRE-) AGRESEARCH LTD.
 Query Match 11.5%; Score 113.8; DB 6; Length 774;
 Best Local Similarity 53.0%; Pred. No. 3.7e-10;
 RESULT 108
 ID ABN87113 standard; cDNA; 777 BP.
 DE Lolium perenne LpCCoAMTa partial nucleotide sequence SEQ ID NO:7.
 PN WO200226994-A1.
 PD 04-APR-2002.
 PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.
 PA (AGRE-) AGRESEARCH LTD.
 Query Match 11.4%; Score 113.2; DB 6; Length 777;
 Best Local Similarity 52.2%; Pred. No. 4.7e-10;
 RESULT 109
 ID ABN87114 standard; cDNA; 792 BP.
 DE Lolium perenne LpCCoAMTa partial nucleotide sequence SEQ ID NO:8.
 PN WO200226994-A1.
 PD 04-APR-2002.
 PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.
 PA (AGRE-) AGRESEARCH LTD.
 Query Match 11.1%; Score 110; DB 6; Length 792;
 Best Local Similarity 51.9%; Pred. No. 1.6e-09;
 RESULT 110
 ID AA24153 standard; cDNA to mRNA; 111 BP.
 DE Human gene signature HUMG06156.
 PN WO9514772-A1.
 PD 01-JUN-1995.
 PA (MATS/) MATSUBARA K.
 PA (OKUB/) OKUBO K.
 Query Match 10.8%; Score 106.8; DB 2; Length 111;
 Best Local Similarity 97.3%; Pred. No. 5.7e-09;
 RESULT 111
 ID ABK62368 standard; cDNA; 343 BP.
 DE Rat sequence differentially expressed in response to a hepatotoxin #275.
 PN WO200210453-A2.
 PD 07-FEB-2002.
 PA (GENE-) GENE LOGIC INC.
 Query Match 10.5%; Score 103.6; DB 6; Length 343;
 Best Local Similarity 68.7%; Pred. No. 1.9e-08;
 RESULT 112

ID ADB55662 standard; DNA; 343 BP.
 DE Toxicity-related gene, SEQ ID 688.
 PN WO2003064624-A2.
 PD 07-AUG-2003.
 PA (GENE-) GENE LOGIC INC.
 Query Match 10.5%; Score 103.6; DB 10; Length 343;
 Best Local Similarity 68.7%; Pred. No. 1.9e-08;
 RESULT 113
 ID ABT40596 standard; DNA; 343 BP.
 DE Toxicity modelling related rat gene SEQ ID NO 298.
 PN WO200295000-A2.
 PD 28-NOV-2002.
 PA (GENE-) GENE LOGIC INC.
 Query Match 10.5%; Score 103.6; DB 10; Length 343;
 Best Local Similarity 68.7%; Pred. No. 1.9e-08;
 RESULT 114
 ID AAA68001 standard; DNA; 1012 BP.
 DE Pinus radiata OMT nucleotide sequence SEQ ID NO:94.
 PN WO200022099-A1.
 PD 20-APR-2000.
 PA (GENE-) GENESIS RES & DEV CORP LTD.
 PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.
 Query Match 9.8%; Score 96.8; DB 3; Length 1012;
 Best Local Similarity 50.8%; Pred. No. 2.5e-07;
 RESULT 115
 ID ADD41751 standard; DNA; 1012 BP.
 DE O-methyl transferase DNA #9.
 PN US2003131373-A1.
 PD 10-JUL-2003.
 PA (BLOK/) BLOKSBERG L N.
 PA (HAVU/) HAVUKKALA I.
 Query Match 9.8%; Score 96.8; DB 10; Length 1012;
 Best Local Similarity 50.8%; Pred. No. 2.5e-07;
 RESULT 116
 ID AAV23912 standard; DNA; 1026 BP.
 DE Plant OMT enzyme DNA sequence.
 PN WO9811205-A2.
 PD 19-MAR-1998.
 PA (GENE-) GENESIS RES & DEV CORP LTD.
 PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.
 Query Match 9.8%; Score 96.8; DB 2; Length 1026;
 Best Local Similarity 50.8%; Pred. No. 2.5e-07;
 RESULT 117
 ID AA206875 standard; cDNA; 1026 BP.
 DE Pine O-methyl transferase (OMT) partial cDNA 1.
 PN US952486-A.
 PD 14-SEP-1999.
 PA (GENE-) GENESIS RES & DEV CORP LTD.
 PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.
 Query Match 9.8%; Score 96.8; DB 2; Length 1026;
 Best Local Similarity 50.8%; Pred. No. 2.5e-07;
 RESULT 118
 ID AAA67913 standard; DNA; 1026 BP.
 DE Pinus radiata OMT nucleotide sequence SEQ ID NO:6.
 PN WO200022099-A1.
 PD 20-APR-2000.
 PA (GENE-) GENESIS RES & DEV CORP LTD.
 PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.
 Query Match 9.8%; Score 96.8; DB 3; Length 1026;
 Best Local Similarity 50.8%; Pred. No. 2.5e-07;
 RESULT 119
 ID ADD41663 standard; DNA; 1026 BP.
 DE O-methyl transferase DNA #1.
 PN US2003131373-A1.
 PD 10-JUL-2003.
 PA (BLOK/) BLOKSBERG L N.
 PA (HAVU/) HAVUKKALA I.
 Query Match 9.8%; Score 96.8; DB 10; Length 1026;
 Best Local Similarity 50.8%; Pred. No. 2.5e-07;
 RESULT 120
 ID ABN87119 standard; cDNA; 628 BP.
 DE Lolium perenne LpCCoAMTb partial nucleotide sequence SEQ ID NO:14.
 PN WO200226994-A1.

PD 04-APR-2002.
PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.
PA (AGRE-) AGRESEARCH LTD.
Query Match 9.6%; Score 95.4; DB 6; Length 628;
Best Local Similarity 53.7%; Pred. No. 4.4e-07;
RESULT 121
ID AC123249 standard; DNA; 542 BP.
DE DNA clone originating in barley containing SNP encoding sequence #13240.
PN WO2003057877-A1.
PD 17-JUL-2003.
PA (UTYNI-) UNIV JAPAN OKAYAMA.
Query Match 9.6%; Score 95.2; DB 9; Length 542;
Best Local Similarity 50.9%; Pred. No. 4.7e-07;
RESULT 122
ID ADK69906 standard; DNA; 1180 BP.
DE Maize P4 CCoAOMT2 gene, seq id 3.
PN FR2833615-A1.
PD 20-JUN-2003.
PA (GENO-) GENOPLANTE-VALOR SAS.
Query Match 9.6%; Score 95.2; DB 10; Length 1180;
Best Local Similarity 58.5%; Pred. No. 4.6e-07;
RESULT 123
ID ADK69926 standard; DNA; 1199 BP.
DE Maize W64A CCoAOMT2 gene insertion mutant #4.
PN FR2833615-A1.
PD 20-JUN-2003.
PA (GENO-) GENOPLANTE-VALOR SAS.
Query Match 9.6%; Score 95.2; DB 10; Length 1199;
Best Local Similarity 58.5%; Pred. No. 4.6e-07;
RESULT 124
ID AB000975 standard; DNA; 675 BP.
DE Klebsiella pneumoniae polynucleotide seqid 6750.
PN US6610836-B1.
PD 26-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 9.4%; Score 93.4; DB 11; Length 675;
Best Local Similarity 52.3%; Pred. No. 9.4e-07;
RESULT 125
ID ADK69918 standard; DNA; 1172 BP.
DE Maize W64A CCoAOMT2 gene deletion mutant #1.
PN FR2833615-A1.
PD 20-JUN-2003.
PA (GENO-) GENOPLANTE-VALOR SAS.
Query Match 9.4%; Score 93; DB 10; Length 1172;
Best Local Similarity 59.7%; Pred. No. 1.1e-06;
RESULT 126
ID ADK69927 standard; DNA; 1178 BP.
DE Maize W64A CCoAOMT2 gene deletion mutant #2.
PN FR2833615-A1.
PD 20-JUN-2003.
PA (GENO-) GENOPLANTE-VALOR SAS.
Query Match 9.4%; Score 93; DB 10; Length 1178;
Best Local Similarity 59.7%; Pred. No. 1.1e-06;
RESULT 127
ID ADK69919 standard; DNA; 1181 BP.
DE Maize W64A CCoAOMT2 gene substitution mutant #1.
PN FR2833615-A1.
PD 20-JUN-2003.
PA (GENO-) GENOPLANTE-VALOR SAS.
Query Match 9.4%; Score 93; DB 10; Length 1181;
Best Local Similarity 59.7%; Pred. No. 1.1e-06;
RESULT 128
ID ADK69920 standard; DNA; 1181 BP.
DE Maize W64A CCoAOMT2 gene substitution mutant #2.
PN FR2833615-A1.
PD 20-JUN-2003.
PA (GENO-) GENOPLANTE-VALOR SAS.
Query Match 9.4%; Score 93; DB 10; Length 1181;
Best Local Similarity 59.7%; Pred. No. 1.1e-06;
RESULT 129
ID ADK69928 standard; DNA; 1181 BP.
DE Maize W64A CCoAOMT2 gene substitution mutant #7.
PN FR2833615-A1.

PD 20-JUN-2003.
PA (GENO-) GENOPLANTE-VALOR SAS.
Query Match 9.4%; Score 93; DB 10; Length 1181;
Best Local Similarity 59.7%; Pred. No. 1.1e-06;
RESULT 130
ID ADK69923 standard; DNA; 1181 BP.
DE Maize W64A CCoAOMT2 gene substitution mutant #5.
PN FR2833615-A1.
PD 20-JUN-2003.
PA (GENO-) GENOPLANTE-VALOR SAS.
Query Match 9.4%; Score 93; DB 10; Length 1181;
Best Local Similarity 59.7%; Pred. No. 1.1e-06;
RESULT 131
ID ADK69904 standard; DNA; 1181 BP.
DE Maize W64A CCoAOMT2 gene, seq id 1.
PN FR2833615-A1.
PD 20-JUN-2003.
PA (GENO-) GENOPLANTE-VALOR SAS.
Query Match 9.4%; Score 93; DB 10; Length 1181;
Best Local Similarity 59.7%; Pred. No. 1.1e-06;
RESULT 132
ID ADK69922 standard; DNA; 1181 BP.
DE Maize W64A CCoAOMT2 gene substitution mutant #4.
PN FR2833615-A1.
PD 20-JUN-2003.
PA (GENO-) GENOPLANTE-VALOR SAS.
Query Match 9.4%; Score 93; DB 10; Length 1181;
Best Local Similarity 59.7%; Pred. No. 1.1e-06;
RESULT 133
ID ADK69924 standard; DNA; 1181 BP.
DE Maize W64A CCoAOMT2 gene substitution mutant #6.
PN FR2833615-A1.
PD 20-JUN-2003.
PA (GENO-) GENOPLANTE-VALOR SAS.
Query Match 9.4%; Score 93; DB 10; Length 1181;
Best Local Similarity 59.7%; Pred. No. 1.1e-06;
RESULT 134
ID ADK69929 standard; DNA; 1181 BP.
DE Maize W64A CCoAOMT2 gene substitution mutant #8.
PN FR2833615-A1.
PD 20-JUN-2003.
PA (GENO-) GENOPLANTE-VALOR SAS.
Query Match 9.4%; Score 93; DB 10; Length 1181;
Best Local Similarity 59.7%; Pred. No. 1.1e-06;
RESULT 135
ID ADK69931 standard; DNA; 1181 BP.
DE Maize W64A CCoAOMT2 gene substitution mutant #10.
PN FR2833615-A1.
PD 20-JUN-2003.
PA (GENO-) GENOPLANTE-VALOR SAS.
Query Match 9.4%; Score 93; DB 10; Length 1181;
Best Local Similarity 59.7%; Pred. No. 1.1e-06;
RESULT 136
ID ADK69921 standard; DNA; 1181 BP.
DE Maize W64A CCoAOMT2 gene substitution mutant #3.
PN FR2833615-A1.
PD 20-JUN-2003.
PA (GENO-) GENOPLANTE-VALOR SAS.
Query Match 9.4%; Score 93; DB 10; Length 1181;
Best Local Similarity 59.7%; Pred. No. 1.1e-06;
RESULT 137
ID ADK69930 standard; DNA; 1181 BP.
DE Maize W64A CCoAOMT2 gene substitution mutant #9.
PN FR2833615-A1.
PD 20-JUN-2003.
PA (GENO-) GENOPLANTE-VALOR SAS.
Query Match 9.4%; Score 93; DB 10; Length 1181;
Best Local Similarity 59.7%; Pred. No. 1.1e-06;
RESULT 138
ID ADK69917 standard; DNA; 1186 BP.
DE Maize W64A CCoAOMT2 gene insertion mutant #1.
PN FR2833615-A1.
PD 20-JUN-2003.

PA (GENO-) GENOPLANTE-VALOR SAS.
Query Match 8.5%; Score 84; DB 12; Length 780;
Best Local Similarity 51.9%; Pred. No. 3.4e-05;
RESULT 147
ID ADN73162 standard; cDNA; 780 BP.
DE Thale cress cDNA upregulated in E2Fa/Dpa expressing plants SeqID 1057.
PN WO2004035798-A2.
PD 29-APR-2004.
PA (CROP-) CROPDESIGN NV.
Query Match 8.5%; Score 84; DB 12; Length 780;
Best Local Similarity 51.9%; Pred. No. 3.4e-05;
RESULT 148
ID AAC45547 standard; DNA; 1032 BP.
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 46896.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 8.5%; Score 84; DB 3; Length 1032;
Best Local Similarity 51.9%; Pred. No. 3.4e-05;
RESULT 149
ID AAC42559 standard; DNA; 1033 BP.
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 36009.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 8.5%; Score 84; DB 3; Length 1033;
Best Local Similarity 51.9%; Pred. No. 3.4e-05;
RESULT 150
ID ABN98364 standard; DNA; 1072 BP.
DE Arabidopsis thaliana expressed polynucleotide SEQ ID NO 132.
PN US2002023281-A1.
PD 21-FEB-2002.
PA (GORL/) GORLACH J.
PA (ANYI/) AN Y.
PA (HAMI/) HAMILTON C M.
PA (PRIC/) PRICE J L.
PA (RAIN/) RAINES T M.
PA (YUYI/) YU Y.
PA (RAME/) RAMEKA J G.
PA (PAGE/) PAGE A.
PA (MATH/) MATHAW A V.
PA (LEDF/) LEDFORD B L.
PA (WOES/) WOESSNER J P.
PA (HAAS/) HAAS W D.
PA (GARC/) GARCIA C A.
PA (KRIC/) KRICKER M.
PA (SLAT/) SLATER T.
PA (DAVI/) DAVIS K R.
PA (ALLE/) ALLEN K.
PA (HOFF/) HOFFMAN N.
PA (HURB/) HURBAN P.
Query Match 8.5%; Score 84; DB 6; Length 1072;
Best Local Similarity 51.9%; Pred. No. 3.4e-05;
RESULT 151
ID AAC44172 standard; DNA; 1180 BP.
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 41890.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 8.5%; Score 84; DB 3; Length 1180;
Best Local Similarity 51.9%; Pred. No. 3.4e-05;
RESULT 152
ID ABS63417 standard; cDNA; 980 BP.
DE DNA encoding soybean caffeoyl-CoA O-methyltransferase (CCOMT).
PN US2002081693-A1.
PD 27-JUN-2002.
PA (CAHO/) CAHOON R E.
PA (FADE/) FADER G M.
PA (RAFA/) RAFALSKI J A.
Query Match 8.0%; Score 79.2; DB 6; Length 980;
Best Local Similarity 51.2%; Pred. No. 0.00022;
RESULT 153
ID AAV23845 standard; DNA; 760 BP.
DE Plant OMT enzyme DNA sequence.
PN WO9811205-A2.
PD 19-MAR-1998.
PA (GENE-) GENESIS RES & DEV CORP LTD.

PA (GENO-) GENOPLANTE-VALOR SAS.
Query Match 9.4%; Score 93; DB 10; Length 1186;
Best Local Similarity 59.7%; Pred. No. 1.1e-06;
RESULT 139
ID ADK69925 standard; DNA; 1196 BP.
DE Maize W64A CCoAOMT2 gene insertion mutant #3.
PN FR2833615-A1.
PD 20-JUN-2003.
PA (GENO-) GENOPLANTE-VALOR SAS.
Query Match 9.4%; Score 93; DB 10; Length 1196;
Best Local Similarity 59.7%; Pred. No. 1.1e-06;
RESULT 140
ID ADK69932 standard; DNA; 1199 BP.
DE Maize W64A CCoAOMT2 gene insertion mutant #5.
PN FR2833615-A1.
PD 20-JUN-2003.
PA (GENO-) GENOPLANTE-VALOR SAS.
Query Match 9.4%; Score 93; DB 10; Length 1199;
Best Local Similarity 59.7%; Pred. No. 1.1e-06;
RESULT 141
ID ABS63415 standard; cDNA; 931 BP.
DE DNA encoding soybean caffeoyl-CoA O-methyltransferase (CCOMT).
PN US2002081693-A1.
PD 27-JUN-2002.
PA (CAHO/) CAHOON R E.
PA (FADE/) FADER G M.
PA (RAFA/) RAFALSKI J A.
Query Match 8.9%; Score 88; DB 6; Length 931;
Best Local Similarity 50.7%; Pred. No. 7.4e-06;
RESULT 142
ID ABS63430 standard; cDNA; 534 BP.
DE DNA encoding wheat caffeoyl-CoA O-methyltransferase (CCOMT).
PN US2002081693-A1.
PD 27-JUN-2002.
PA (CAHO/) CAHOON R E.
PA (FADE/) FADER G M.
PA (RAFA/) RAFALSKI J A.
Query Match 8.9%; Score 87.8; DB 6; Length 534;
Best Local Similarity 54.1%; Pred. No. 8.1e-06;
RESULT 143
ID ABS63418 standard; cDNA; 962 BP.
DE DNA encoding soybean caffeoyl-CoA O-methyltransferase (CCOMT).
PN US2002081693-A1.
PD 27-JUN-2002.
PA (CAHO/) CAHOON R E.
PA (FADE/) FADER G M.
PA (RAFA/) RAFALSKI J A.
Query Match 8.7%; Score 85.6; DB 6; Length 962;
Best Local Similarity 52.2%; Pred. No. 1.9e-05;
RESULT 144
ID ABS63419 standard; cDNA; 1023 BP.
DE DNA encoding soybean caffeoyl-CoA O-methyltransferase (CCOMT).
PN US2002081693-A1.
PD 27-JUN-2002.
PA (CAHO/) CAHOON R E.
PA (FADE/) FADER G M.
PA (RAFA/) RAFALSKI J A.
Query Match 8.7%; Score 85.6; DB 6; Length 1023;
Best Local Similarity 52.2%; Pred. No. 1.8e-05;
RESULT 145
ID AQO32259 standard; cDNA; 1258 BP.
DE Caffeoyl-CoA-3-O-methyltransferase gene (pl2-4).
PN DE411747-A.
PD 03-DEC-1992.
PA (FARB) BAYER AG.
Query Match 8.5%; Score 84.4; DB 2; Length 1258;
Best Local Similarity 49.8%; Pred. No. 2.9e-05;
RESULT 146
ID ADN74200 standard; cDNA; 780 BP.
DE Thale cress cDNA repressed in E2Fa/Dpa expressing plants SeqID 2095.
PN WO2004035798-A2.
PD 29-APR-2004.
PA (CROP-) CROPDESIGN NV.

PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.
Query Match 7.7%; Score 76.2; DB 2; Length 760;
Best Local Similarity 56.6%; Pred. No. 0.00069;
RESULT 154
ID AA206846 standard; cDNA; 760 BP.
DE Eucalyptus O-methyl transferase (OMT) partial cDNA 4.
PN US5952486-A.
PD 14-SEP-1999.
PA (GENE-) GENESIS RES & DEV CORP LTD.
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.
Query Match 7.7%; Score 76.2; DB 2; Length 760;
Best Local Similarity 56.6%; Pred. No. 0.00069;
RESULT 155
ID AA69584 standard; cDNA; 760 BP.
DE Eucalyptus grandis cinnamoyl-CoA reductase cDNA SEQ ID NO:58.
PN WO2000306081-A2.
PD 22-JUN-2000.
PA (GENE-) GENESIS RES & DEV CORP LTD.
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.
Query Match 7.7%; Score 76.2; DB 3; Length 760;
Best Local Similarity 56.6%; Pred. No. 0.00069;
RESULT 156
ID AA69732 standard; DNA; 760 BP.
DE Eucalyptus grandis OMT nucleotide sequence SEQ ID NO:25.
PN WO200022099-A1.
PD 20-APR-2000.
PA (GENE-) GENESIS RES & DEV CORP LTD.
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.
Query Match 7.7%; Score 76.2; DB 3; Length 760;
Best Local Similarity 56.6%; Pred. No. 0.00069;
RESULT 157
ID AD041682 standard; DNA; 760 BP.
DE O-methyl transferase DNA #5.
PN US2003131373-A1.
PD 10-JUL-2003.
PA (BLOK/) BLOKBERG L N.
PA (HAVU/) HAVUKALA I.
Query Match 7.7%; Score 76.2; DB 10; Length 760;
Best Local Similarity 56.6%; Pred. No. 0.00069;
RESULT 158
ID ABG63416 standard; cDNA; 929 BP.
DE DNA encoding soybean caffeoyl-CoA O-methyltransferase (CCOMT).
PN US20002081693-A1.
PD 27-JUN-2002.
PA (CAHO/) CAHOON R E.
PA (FADE/) FADER G M.
PA (RAFA/) RAFALSKI J A.
Query Match 7.5%; Score 74.4; DB 6; Length 929;
Best Local Similarity 50.5%; Pred. No. 0.0014;
RESULT 159
ID ABG54112 standard; DNA; 870 BP.
DE Tobacco caffeoyl CoA O-methyltransferase-1 (CCOAMT-1) cDNA.
PN US6441272-B1.
PD 27-AUG-2002.
PA (UTGE-) UNIV GEORGIA RES FOUND INC.
Query Match 7.4%; Score 73.2; DB 6; Length 870;
Best Local Similarity 48.4%; Pred. No. 0.0022;
RESULT 160
ID AAQ13306 standard; DNA; 1107 BP.
DE Human catechol-O-methyltransferase gene.
PN WO9111513-A.
PD 08-AUG-1991.
PA (ORIN) ORION YHTYMAE OY.
Query Match 7.2%; Score 71; DB 2; Length 1107;
Best Local Similarity 50.7%; Pred. No. 0.005;
RESULT 161
ID AAC77872 standard; cDNA; 1350 BP.
DE Human cancer associated gene sequence SEQ ID NO:266.
PN WO200055350-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 7.1%; Score 70.6; DB 3; Length 1350;
Best Local Similarity 50.4%; Pred. No. 0.0058;

RESULT 162
ID ABS44113 standard; DNA; 811 BP.
DE Tobacco caffeoyl CoA O-methyltransferase-2 (CCOAMT-2) cDNA.
PN US6441272-B1.
PD 27-AUG-2002.
PA (UTGE-) UNIV GEORGIA RES FOUND INC.
Query Match 7.1%; Score 70; DB 6; Length 811;
Best Local Similarity 47.9%; Pred. No. 0.0074;
RESULT 163
ID ADH02845 standard; cDNA; 888 BP.
DE Petunia E2O cDNA #SEQ ID 4.
PN WO2003062428-A1.
PD 31-JUL-2003.
PA (ITFL-) INT FLOWER DEV PTY LTD.
Query Match 7.0%; Score 69.6; DB 10; Length 888;
Best Local Similarity 50.3%; Pred. No. 0.0086;
RESULT 164
ID ADH02842 standard; cDNA; 969 BP.
DE Petunia diffe cDNA #SEQ ID 1.
PN WO2003062428-A1.
PD 31-JUL-2003.
PA (ITFL-) INT FLOWER DEV PTY LTD.
Query Match 7.0%; Score 69.6; DB 10; Length 969;
Best Local Similarity 50.3%; Pred. No. 0.0086;
RESULT 165
ID AB283278 standard; cDNA; 1024 BP.
DE Toxicologically relevant human nucleotide sequence #437.
PN WO2003016500-A2.
PD 27-FEB-2003.
PA (PHAS-) PHASE-1 MOLECULAR TOXICOLOGY INC.
Query Match 7.0%; Score 69.4; DB 10; Length 1024;
Best Local Similarity 50.4%; Pred. No. 0.0093;
RESULT 166
ID ADE84973 standard; DNA; 1206 BP.
DE Farnesyl transferase inhibitor modulated leukemia associated gene #192.
PN WO2003038129-A2.
PD 08-MAY-2003.
PA (ORTH) ORTHO CLINICAL DIAGNOSTICS INC.
Query Match 7.0%; Score 69.4; DB 10; Length 1206;
Best Local Similarity 50.4%; Pred. No. 0.0092;
RESULT 167
ID ABX63642 standard; cDNA; 1327 BP.
DE Human cDNA #642 differentially expressed in activated vascular tissue.
PN US2002137081-A1.
PD 26-SEP-2002.
PA (BAND/) BANDMAN O.
Query Match 7.0%; Score 69.4; DB 8; Length 1327;
Best Local Similarity 50.4%; Pred. No. 0.0092;
RESULT 168
ID ADH02882 standard; cDNA; 841 BP.
DE Fuchsia FMT (3282) cDNA #SEQ ID 41.
PN WO2003062428-A1.
PD 31-JUL-2003.
PA (ITFL-) INT FLOWER DEV PTY LTD.
Query Match 7.0%; Score 69.2; DB 10; Length 841;
Best Local Similarity 49.5%; Pred. No. 0.01;
RESULT 169
ID ADH02884 standard; cDNA; 943 BP.
DE Fuchsia FMT full (3289) cDNA #SEQ ID 43.
PN WO2003062428-A1.
PD 31-JUL-2003.
PA (ITFL-) INT FLOWER DEV PTY LTD.
Query Match 7.0%; Score 69.2; DB 10; Length 943;
Best Local Similarity 49.5%; Pred. No. 0.01;
RESULT 170
ID AAC42096 standard; DNA; 1186 BP.
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 34272.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.9%; Score 68.6; DB 3; Length 1186;
Best Local Similarity 46.7%; Pred. No. 0.013;
RESULT 171
ID ADH02852 standard; cDNA; 1006 BP.

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DE Torenia TWT5.nt cdna #SEQ ID 11.
 PN WO2003062428-A1.
 PD 31-JUL-2003.
 PA (ITFL-) INT FLOWER DEV PTY LTD.
 Query Match 6.8%; Score 67.4; DB 10; Length 1006;
 Best Local Similarity 50.1%; Pred. No. 0.02;
 RESULT 172
 ID ABA90338 standard; cDNA; 1149 BP.
 DE Human polynucleotide #13.
 PN WO200181363-A1.
 PD 01-NOV-2001.
 PA (SMIK) SMITHKLINE BEECHAM CORP.
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 Query Match 6.8%; Score 67; DB 6; Length 1149;
 Best Local Similarity 51.5%; Pred. No. 0.023;
 RESULT 173
 ID AAV23874 standard; DNA; 1074 BP.
 DE Plant OMT enzyme DNA sequence.
 PN WO9811205-A2.
 PD 19-MAR-1998.
 PA (GENE-) GENESIS RES & DEV CORP LTD.
 PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.
 Query Match 6.8%; Score 66.8; DB 2; Length 1074;
 Best Local Similarity 49.3%; Pred. No. 0.025;
 RESULT 174
 ID AAZ06877 standard; cDNA; 1074 BP.
 DE Pine O-methyl transferase (OMT) partial cDNA 3.
 PN US952486-A.
 PD 14-SEP-1999.
 PA (GENE-) GENESIS RES & DEV CORP LTD.
 PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.
 Query Match 6.8%; Score 66.8; DB 2; Length 1074;
 Best Local Similarity 49.3%; Pred. No. 0.025;
 RESULT 175
 ID AAA67961 standard; DNA; 1074 BP.
 DE Pinus radiata OMT nucleotide sequence SEQ ID NO:54.
 PN WO200022099-A1.
 PD 20-APR-2000.
 PA (GENE-) GENESIS RES & DEV CORP LTD.
 PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.
 Query Match 6.8%; Score 66.8; DB 3; Length 1074;
 Best Local Similarity 49.3%; Pred. No. 0.025;
 RESULT 176
 ID ADD41711 standard; DNA; 1074 BP.
 DE O-methyl transferase DNA #7.
 PN US2003131373-A1.
 PD 10-JUL-2003.
 PA (BLOK/) BLOKSBERG L N.
 PA (HAVU/) HAVUKKALA I.
 Query Match 6.8%; Score 66.8; DB 10; Length 1074;
 Best Local Similarity 49.3%; Pred. No. 0.025;
 RESULT 177
 ID AAV23875 standard; DNA; 1075 BP.
 DE Plant OMT enzyme DNA sequence.
 PN WO9811205-A2.
 PD 19-MAR-1998.
 PA (GENE-) GENESIS RES & DEV CORP LTD.
 PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.
 Query Match 6.8%; Score 66.8; DB 2; Length 1075;
 Best Local Similarity 49.3%; Pred. No. 0.025;
 RESULT 178
 ID AAZ06878 standard; cDNA; 1075 BP.
 DE Pine O-methyl transferase (OMT) partial cDNA 4.
 PN US952486-A.
 PD 14-SEP-1999.
 PA (GENE-) GENESIS RES & DEV CORP LTD.
 PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.
 Query Match 6.8%; Score 66.8; DB 2; Length 1075;
 Best Local Similarity 49.3%; Pred. No. 0.025;
 RESULT 179
 ID AAA67962 standard; DNA; 1075 BP.
 DE Pinus radiata OMT nucleotide sequence SEQ ID NO:55.
 PN WO200022099-A1.

PD 20-APR-2000.
 PA (GENE-) GENESIS RES & DEV CORP LTD.
 PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.
 Query Match 6.8%; Score 66.8; DB 3; Length 1075;
 Best Local Similarity 49.3%; Pred. No. 0.025;
 RESULT 180
 ID ADD41712 standard; DNA; 1075 BP.
 DE O-methyl transferase DNA #8.
 PN US2003131373-A1.
 PD 10-JUL-2003.
 PA (BLOK/) BLOKSBERG L N.
 PA (HAVU/) HAVUKKALA I.
 Query Match 6.8%; Score 66.8; DB 10; Length 1075;
 Best Local Similarity 49.3%; Pred. No. 0.025;
 RESULT 181
 ID AAX53491 standard; DNA; 114955 BP.
 DE Human adenosine A1 receptor antisense oligonucleotide fragment.
 PN WO9913886-A1.
 PD 25-MAR-1999.
 PA (UVEC-) UNIV EAST CAROLINA.
 Query Match 6.7%; Score 66.6; DB 2; Length 114955;
 Best Local Similarity 33.8%; Pred. No. 0.024;
 RESULT 182
 ID AAD19545 standard; cDNA; 744 BP.
 DE Medicago sativa caffeic acid 3-O-methyltransferase (COMT) cDNA.
 PN WO200173090-A2.
 PD 04-OCT-2001.
 PA (ROBE-) ROBERTS NOBLE FOUND INC SAMMUEL.
 Query Match 6.7%; Score 66.4; DB 4; Length 744;
 Best Local Similarity 49.3%; Pred. No. 0.03;
 RESULT 183
 ID ADI30327 standard; cDNA; 744 BP.
 DE Alfalfa harvest inducible cDNA sequence H12.
 PN WO2004002216-A2.
 PD 08-JAN-2004.
 PA (UYGU-) UNIV GUELPH.
 Query Match 6.7%; Score 66.4; DB 12; Length 744;
 Best Local Similarity 49.3%; Pred. No. 0.03;
 RESULT 184
 ID ADI30333 standard; DNA; 1906 BP.
 DE Alfalfa harvest inducible H12 gene genomic DNA sequence.
 PN WO2004002216-A2.
 PD 08-JAN-2004.
 PA (UYGU-) UNIV GUELPH.
 Query Match 6.7%; Score 66.4; DB 12; Length 1906;
 Best Local Similarity 49.3%; Pred. No. 0.029;
 RESULT 185
 ID ABS63420 standard; cDNA; 912 BP.
 DE DNA encoding soybean caffeoyl-CoA O-methyltransferase (CCOMT).
 PN US2002081693-A1.
 PD 27-JUN-2002.
 PA (CAHO/) CAHOON R E.
 PA (FADE/) FADER G M.
 PA (RAFA/) RAFALSKI J A.
 Query Match 6.7%; Score 66.2; DB 6; Length 912;
 Best Local Similarity 47.9%; Pred. No. 0.032;
 RESULT 186
 ID ABS44115 standard; DNA; 967 BP.
 DE Tobacco caffeoyl CoA O-methyltransferase-9 (CCOAMT-9) cDNA.
 PN US6441272-B1.
 PD 27-AUG-2002.
 PA (UYGE-) UNIV GEORGIA RES FOUND INC.
 Query Match 6.6%; Score 64.8; DB 6; Length 967;
 Best Local Similarity 49.0%; Pred. No. 0.054;
 RESULT 187
 ID ABO55289 standard; cDNA; 553 BP.
 DE Human ovarian antigen HCOX38 cDNA, SEQ ID NO:1169.
 PN WO200200677-A1.
 PD 03-JAN-2002.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 6.5%; Score 64.6; DB 6; Length 553;
 Best Local Similarity 49.5%; Pred. No. 0.06;
 RESULT 188

ID AAC11287 standard; cDNA; 143 BP.
DE Human secreted protein 5' EST, SEQ ID NO: 15362.
PN EPI03401-A2.
PD 06-SEP-2000.
PA (GEST) GENST.
Query Match 6.5%; Score 64.4; DB 3; Length 143;
Best Local Similarity 98.5%; Pred. No. 0.067;
RESULT 189
ID ABS63426 standard; cDNA; 600 BP.
DE DNA encoding wheat caffeoyl-CoA O-methyltransferase (CCOMT).
PN US2002081693-A1.
PD 27-JUN-2002.
PA (CAHO/) CAHOON R E.
PA (FADE/) FADER G M.
PA (RAPA/) RAPALSKI J A.
Query Match 6.5%; Score 64.2; DB 6; Length 600;
Best Local Similarity 53.4%; Pred. No. 0.069;
RESULT 190
ID ABS63411 standard; cDNA; 510 BP.
DE DNA encoding rice caffeoyl-CoA O-methyltransferase (CCOMT).
PN US2002081693-A1.
PD 27-JUN-2002.
PA (CAHO/) CAHOON R E.
PA (FADE/) FADER G M.
PA (RAPA/) RAPALSKI J A.
Query Match 6.4%; Score 63.6; DB 6; Length 510;
Best Local Similarity 45.9%; Pred. No. 0.088;
RESULT 191
ID AD019501 standard; DNA; 135005 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 2320.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 6.4%; Score 63; DB 12; Length 135005;
Best Local Similarity 47.8%; Pred. No. 0.095;
RESULT 192
ID ABX09141 standard; DNA; 75216 BP.
DE Mycobacterium tuberculosis H37Rv BAC clone BAC-RV230.
PN WO200274903-A2.
PD 26-SEP-2002.
PA (INSP) INST PASTEUR.
Query Match 6.3%; Score 62.8; DB 6; Length 75216;
Best Local Similarity 46.4%; Pred. No. 0.1;
RESULT 193
Query Match 6.3%; Score 62.8; DB 4; Length 110000;
Best Local Similarity 46.4%; Pred. No. 0.1;
RESULT 194
Query Match 6.3%; Score 62.8; DB 4; Length 110000;
Best Local Similarity 46.4%; Pred. No. 0.1;
RESULT 195
Query Match 6.3%; Score 62.4; DB 4; Length 110000;
Best Local Similarity 49.7%; Pred. No. 0.12;
RESULT 196
Query Match 6.3%; Score 62.4; DB 4; Length 110000;
Best Local Similarity 49.7%; Pred. No. 0.12;
RESULT 197
ID ABS54114 standard; DNA; 845 BP.
DE Tobacco caffeoyl CoA O-methyltransferase-3 (CCOAMT-3) cDNA.
PN US641272-B1.
PD 27-AUG-2002.
PA (UYGE-) UNIV GEORGIA RES FOUND INC.
Query Match 6.2%; Score 61.6; DB 6; Length 845;
Best Local Similarity 48.5%; Pred. No. 0.19;
RESULT 198
ID AAX53491 standard; DNA; 114955 BP.
DE Human adenosine A1 receptor antisense oligonucleotide fragment.
PN WO9913886-A1.
PD 25-MAR-1999.
PA (UYEC-) UNIV EAST CAROLINA.
Query Match 6.2%; Score 61.2; DB 2; Length 114955;
Best Local Similarity 31.2%; Pred. No. 0.19;
RESULT 199
ID AAQ61817 standard; DNA; 1578 BP.

DE Open reading frame of pseudorabies virus.
PN WO9408000-A1.
PD 14-APR-1994.
PA (ALKU) AKZO NV.
Query Match 6.1%; Score 60.8; DB 2; Length 1578;
Best Local Similarity 45.3%; Pred. No. 0.25;
RESULT 200
ID ABQ81846 standard; DNA; 349980 BP.
DE Bifidobacterium longum NCC2705 related nucleotide sequence SEQ ID:1102.
PN EPI227152-A1.
PD 31-JUL-2002.
PA (NEST) SOC PROD NESTLE SA.
Query Match 6.1%; Score 60.4; DB 6; Length 349980;
Best Local Similarity 49.0%; Pred. No. 0.25;
RESULT 201
ID AB214595 standard; DNA; 729 BP.
DE Arabidopsis thaliana stress regulated gene SEQ ID NO 2400.
PN WO200216655-A2.
PD 28-FEB-2002.
PA (SCRI) SCRIPPS RES INST.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 6.1%; Score 60; DB 6; Length 729;
Best Local Similarity 48.5%; Pred. No. 0.35;
RESULT 202
ID AAC45004 standard; DNA; 917 BP.
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 44938.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 6.1%; Score 60; DB 3; Length 917;
Best Local Similarity 48.5%; Pred. No. 0.34;
RESULT 203
ID ABS63422 standard; cDNA; 982 BP.
DE DNA encoding soybean caffeoyl-CoA O-methyltransferase (CCOMT).
PN US2002081693-A1.
PD 27-JUN-2002.
PA (CAHO/) CAHOON R E.
PA (FADE/) FADER G M.
PA (RAPA/) RAPALSKI J A.
Query Match 6.1%; Score 60; DB 6; Length 982;
Best Local Similarity 48.7%; Pred. No. 0.34;
RESULT 204
ID ADH02867 standard; cDNA; 1079 BP.
DE Petunia E33 (Corrected) cDNA #SEQ ID 26.
PN WO2003062428-A1.
PD 31-JUL-2003.
PA (ITFL-) INT FLOWER DEV PTY LTD.
Query Match 6.1%; Score 60; DB 10; Length 1079;
Best Local Similarity 48.7%; Pred. No. 0.34;
RESULT 205
ID ACA38007 standard; DNA; 1143 BP.
DE Prokaryotic essential gene #19664.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.1%; Score 60; DB 8; Length 1143;
Best Local Similarity 45.4%; Pred. No. 0.34;
RESULT 206
ID AAA68101 standard; DNA; 399 BP.
DE E. grandis caffeoyl CoA methyl transferase DNA sequence SEQ ID NO:194.
PN WO200022099-A1.
PD 20-APR-2000.
PA (GENE-) GENESIS RES & DEV CORP LTD.
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.
Query Match 6.0%; Score 59.6; DB 3; Length 399;
Best Local Similarity 55.2%; Pred. No. 0.41;
RESULT 207
ID ADD41851 standard; DNA; 399 BP.
DE Caffeoyl CoA methyl transferase DNA #2.
PN US2003131373-A1.
PD 10-JUL-2003.
PA (BLOK/) BLOKSBERG L N.
PA (HAVU/) HAVUKKALA I.
Query Match 6.0%; Score 59.6; DB 10; Length 399;

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Best Local Similarity 55.2%; Pred. No. 0.41;

RESULT 208

ID AD123934 standard; DNA; 7185 BP.
DE Streptomyces refuineus 024A locus ORF7.
PN US2003198981-A1.
PD 23-OCT-2003.

Query Match
PA (ECOP-) ECOPIA BIOSCIENCES INC.

Best Local Similarity 6.0%; Score 59.6; DB 10; Length 7185;
Pred. No. 0.38;

RESULT 209

ID AD123920 standard; DNA; 61944 BP.
DE Streptomyces refuineus 024A locus (NRRL 3143).
PN US2003198981-A1.
PD 23-OCT-2003.

Query Match
PA (ECOP-) ECOPIA BIOSCIENCES INC.

Best Local Similarity 6.0%; Score 59.6; DB 10; Length 61944;
Pred. No. 0.36;

RESULT 210

ID ADQ22939 standard; DNA; 4667 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5759.
PN WO2004048938-A2.
PD 10-JUN-2004.

Query Match
PA (PROT-) PROTEIN DESIGN LABS INC.

Best Local Similarity 6.0%; Score 59.2; DB 12; Length 4667;
Pred. No. 0.45;

RESULT 211

ID ADQ22939 standard; DNA; 4667 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5759.
PN WO2004048938-A2.
PD 10-JUN-2004.

Query Match
PA (PROT-) PROTEIN DESIGN LABS INC.

Best Local Similarity 44.6%; Score 59; DB 12; Length 4667;
Pred. No. 0.48;

RESULT 212

ID ABQ93881 standard; DNA; 10800 BP.
DE Human laminin alpha-5-like NOV1c DNA, SEQ ID NO:5.
PN WO200253742-A2.
PD 11-JUL-2002.

Query Match
PA (CURA-) CURAGEN CORP.

Best Local Similarity 46.8%; Score 59; DB 6; Length 10800;
Pred. No. 0.47;

RESULT 213

ID ADO10046 standard; cDNA; 10800 BP.
DE Novel human protein Nov1c cDNA.
PN US2004052806-A1.
PD 18-MAR-2004.

Query Match
PA (KEKU/) KEKUDA R.

PA (ALSO/) ALSOBROOK J P.

PA (TCHE/) TCHERNEV V T.

PA (LIUX/) LIU X.

PA (SPYT/) SPYTEK K A.

PA (PATT/) PATTURAJAN M.

PA (GROS/) GROSSE W M.

PA (LEPL/) LEPLY D M.

PA (BURG/) BURGESS C E.

PA (VERN/) VERNET C A M.

PA (LILL/) LI L.

PA (GORM/) GORMAN L.

PA (EDIN/) EDINGER S R.

PA (SCIO/) SCIORE P.

PA (ELLE/) ELLERMAN K.

PA (MALY/) MALYANKAR U M.

PA (ROTH/) ROTHENBERG M E.

PA (STON/) STONE D J.

PA (BOLD/) BOLDOG F L.

PA (GUOX/) GUO X.

PA (SHEN/) SHENOY S G.

PA (ANDE/) ANDERSON D W.

PA (PADI/) PADIGARU M.

PA (TAUP/) TAUPIER R J.

PA (MILL/) MILLER C E.

PA (EISE/) EISEN A.

Query Match

Best Local Similarity 6.0%; Score 59; DB 12; Length 10800;

Best Local Similarity 46.8%; Pred. No. 0.47;

RESULT 214

ID ABQ93879 standard; DNA; 10809 BP.
DE Human laminin alpha-5-like NOV1a DNA, SEQ ID NO:1.
PN WO200253742-A2.
PD 11-JUL-2002.

Query Match
PA (CURA-) CURAGEN CORP.

Best Local Similarity 6.0%; Score 59; DB 6; Length 10809;
Pred. No. 0.47;

RESULT 215

ID ADO10042 standard; cDNA; 10809 BP.
DE Novel human protein Nov1a cDNA.
PN US2004052806-A1.
PD 18-MAR-2004.

Query Match
PA (KEKU/) KEKUDA R.

PA (ALSO/) ALSOBROOK J P.

PA (TCHE/) TCHERNEV V T.

PA (LIUX/) LIU X.

PA (SPYT/) SPYTEK K A.

PA (PATT/) PATTURAJAN M.

PA (GROS/) GROSSE W M.

PA (LEPL/) LEPLY D M.

PA (BURG/) BURGESS C E.

PA (VERN/) VERNET C A M.

PA (LILL/) LI L.

PA (GORM/) GORMAN L.

PA (EDIN/) EDINGER S R.

PA (SCIO/) SCIORE P.

PA (ELLE/) ELLERMAN K.

PA (MALY/) MALYANKAR U M.

PA (ROTH/) ROTHENBERG M E.

PA (STON/) STONE D J.

PA (BOLD/) BOLDOG F L.

PA (GUOX/) GUO X.

PA (SHEN/) SHENOY S G.

PA (ANDE/) ANDERSON D W.

PA (PADI/) PADIGARU M.

PA (TAUP/) TAUPIER R J.

PA (MILL/) MILLER C E.

PA (EISE/) EISEN A.

Query Match

Best Local Similarity 6.0%; Score 59; DB 12; Length 10809;
Pred. No. 0.47;

RESULT 216

ID ADH02847 standard; cDNA; 1077 BP.
DE Petunia E33 cDNA #SEQ ID 5.
PN WO2003062428-A1.
PD 31-JUL-2003.

Query Match
PA (ITEL-) INT FLOWER DEV PTY LTD.

Best Local Similarity 5.9%; Score 58.8; DB 10; Length 1077;
Pred. No. 0.54;

RESULT 217

ID AAF25795 standard; DNA; 3849 BP.
DE S. chrysomallus acm-C DNA.
PN DE19928313-A1.
PD 21-DEC-2000.

Query Match
PA (KELL/) KELLER U.

Best Local Similarity 5.9%; Score 58.8; DB 4; Length 3849;
Pred. No. 0.52;

RESULT 218

ID AAD5726 standard; DNA; 5858 BP.
DE Nephila madagascariensis major ampullate spidroin 2 (MaSp2)-like DNA.
PN WO2003020916-A2.
PD 13-MAR-2003.

Query Match
PA (UYWY-) UNIV WYOMING.

Best Local Similarity 5.9%; Score 58.8; DB 8; Length 5858;
Pred. No. 0.52;

RESULT 219

ID ADA71279 standard; DNA; 897 BP.
DE Rice gene, SEQ ID 4602.
PN WO2003000898-A1.
PD 03-JAN-2003.

Query Match
PA (SYGN) SYNGENTA PARTICIPATIONS AG.

Best Local Similarity 5.9%; Score 58; DB 8; Length 897;
Pred. No. 0.52;

Best Local Similarity 44.9%; Pred. No. 0.74;
RESULT 220
ID AAL40781 standard; DNA; 88421 BP.
DE 88421nt genomic DNA of ramoplanin producing Actinoplanes sp.
PN WO200231155-A2.
PD 18-APR-2002.
PA (ECOP-) ECOPIA BIOSCIENCES INC.
Query Match 5.9%; Score 58; DB 6; Length 88421;
Best Local Similarity 44.5%; Pred. No. 0.65;
RESULT 221
ID ABN87109 standard; CDNA; 557 BP.
DE Lolium perenne LpCCoAMTA partial nucleotide sequence SEQ ID NO:3.
PN WO200226994-A1.
PD 04-APR-2002.
PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.
PA (AGRE-) AGRESEARCH LTD.
Query Match 5.8%; Score 57.8; DB 6; Length 557;
Best Local Similarity 49.7%; Pred. No. 0.81;
RESULT 222
ID AB222145 standard; DNA; 1029 BP.
DE Thermus thermophilus DNA repair enzyme RecF encoding DNA SEQ ID NO:5.
PN JP2002247985-A.
PD 03-SEP-2002.
PA (RIKA-) RIKAGAKU KENKYUSHO.
Query Match 5.8%; Score 57.4; DB 8; Length 1029;
Best Local Similarity 48.6%; Pred. No. 0.93;
RESULT 223
ID ADO42841 standard; DNA; 1275 BP.
DE Pseudomonas aurantiaca S-4380 levansucrase encoding sequence.
PN KR2003005996-A.
PD 23-JAN-2003.
PA (KORE-) KOREA RES INST BIOSCIENCE & BIOTECHNOLOG.
PA (REAL-) REAL BIOTECH CO LTD.
Query Match 5.8%; Score 57.4; DB 11; Length 1275;
Best Local Similarity 45.6%; Pred. No. 0.92;
RESULT 224
ID ADA48866 standard; DNA; 584 BP.
DE Banana gene conferring disease resistance in plants.
PN WO200300906-A2.
PD 03-JAN-2003.
PA (SYGN-) SYNGENTA PARTICIPATIONS AG.
Query Match 5.8%; Score 57.2; DB 9; Length 584;
Best Local Similarity 60.1%; Pred. No. 1;
RESULT 225
ID ADB74275 standard; DNA; 38494 BP.
DE Mycobacterium leprae DNA #2.
PN US6583266-B1.
PD 24-JUN-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.8%; Score 57; DB 10; Length 38494;
Best Local Similarity 50.9%; Pred. No. 0.98;
RESULT 226
ID ADB74386 standard; DNA; 38675 BP.
DE Mycobacterium leprae DNA #20.
PN US6583266-B1.
PD 24-JUN-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.8%; Score 57; DB 10; Length 38675;
Best Local Similarity 50.9%; Pred. No. 0.98;
RESULT 227
ID AAD14507 standard; DNA; 1182 BP.
DE S. clavuligerus clavulanic acid biosynthesis enzyme DNA #3.
PN US6232106-B1.
PD 15-MAY-2001.
PA (UYAL-) UNIV ALBERTA.
Query Match 5.7%; Score 56.8; DB 4; Length 1182;
Best Local Similarity 43.6%; Pred. No. 1.2;
RESULT 228
ID ADD26448 standard; DNA; 1182 BP.
DE Streptomyces clavuligerus ORF6 DNA.
PN US6589775-B1.
PD 08-JUL-2003.
PA (UYAL-) UNIV ALBERTA.

Query Match 5.7%; Score 56.8; DB 10; Length 1182;
Best Local Similarity 43.6%; Pred. No. 1.2;
RESULT 229
ID ADG47793 standard; DNA; 1182 BP.
DE Streptomyces clavuligerus 15 kb gene ORF6 DNA.
PN US2003207411-A1.
PD 06-NOV-2003.
PA (UYAL-) UNIV ALBERTA.
Query Match 5.7%; Score 56.8; DB 10; Length 1182;
Best Local Similarity 43.6%; Pred. No. 1.2;
RESULT 230
ID ACA62930 standard; DNA; 1182 BP.
DE DNA encoding clavulanic acid synthesis associated protein #6.
PN US6514735-B1.
PD 04-FEB-2003.
PA (UYAL-) UNIV ALBERTA.
Query Match 5.7%; Score 56.8; DB 10; Length 1182;
Best Local Similarity 43.6%; Pred. No. 1.2;
RESULT 231
ID ADA71938 standard; DNA; 2000 BP.
DE Rice gene, SEQ ID 5263.
PN WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN-) SYNGENTA PARTICIPATIONS AG.
Query Match 5.7%; Score 56.8; DB 8; Length 2000;
Best Local Similarity 10.5%; Pred. No. 1.1;
RESULT 232
ID AAD14501 standard; DNA; 11604 BP.
DE Streptomyces clavuligerus genomic DNA fragment.
PN US6232106-B1.
PD 15-MAY-2001.
PA (UYAL-) UNIV ALBERTA.
Query Match 5.7%; Score 56.8; DB 4; Length 11604;
Best Local Similarity 43.6%; Pred. No. 1.1;
RESULT 233
ID ADD26442 standard; DNA; 11604 BP.
DE Streptomyces clavuligerus 11.6 kb genomic fragment.
PN US6589775-B1.
PD 08-JUL-2003.
PA (UYAL-) UNIV ALBERTA.
Query Match 5.7%; Score 56.8; DB 10; Length 11604;
Best Local Similarity 43.6%; Pred. No. 1.1;
RESULT 234
ID ADG47787 standard; DNA; 11604 BP.
DE Streptomyces clavuligerus 15 kb gene fragment DNA.
PN US2003207411-A1.
PD 06-NOV-2003.
PA (UYAL-) UNIV ALBERTA.
Query Match 5.7%; Score 56.8; DB 10; Length 11604;
Best Local Similarity 43.6%; Pred. No. 1.1;
RESULT 235
ID ACA62924 standard; DNA; 11604 BP.
DE Clavulanic acid synthesis associated DNA.
PN US6514735-B1.
PD 04-FEB-2003.
PA (UYAL-) UNIV ALBERTA.
Query Match 5.7%; Score 56.8; DB 10; Length 11604;
Best Local Similarity 43.6%; Pred. No. 1.1;
RESULT 236
ID AAQ91580 standard; DNA; 15079 BP.
DE S. clavuligerus cla gene region.
PN CA2108113-A.
PD 09-APR-1995.
PA (UYAL-) UNIV ALBERTA.
Query Match 5.7%; Score 56.8; DB 2; Length 15079;
Best Local Similarity 43.6%; Pred. No. 1.1;
RESULT 237
ID AAD14499 standard; DNA; 15079 BP.
DE Streptomyces clavuligerus 15 kb genomic DNA fragment.
PN US6232106-B1.
PD 15-MAY-2001.
PA (UYAL-) UNIV ALBERTA.
Query Match 5.7%; Score 56.8; DB 4; Length 15079;

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Best Local Similarity 43.6%; Pred. No. 1.1;
RESULT 238
ID ACA62922 standard; DNA; 15079 BP.
DE Streptomyces clavuligerus 15kb genomic DNA sequence.
PN US6514735-B1.
PD 04-FEB-2003.
PA (UYAL-) UNIV ALBERTA.
Query Match 5.7%; Score 56.8; DB 10; Length 15079;
Best Local Similarity 43.6%; Pred. No. 1.1;
RESULT 239
ID ADD26455 standard; DNA; 15120 BP.
DE Streptomyces clavuligerus 15 kb genomic fragment.
PN US6589775-B1.
PD 08-JUL-2003.
PA (UYAL-) UNIV ALBERTA.
Query Match 5.7%; Score 56.8; DB 10; Length 15120;
Best Local Similarity 43.6%; Pred. No. 1.1;
RESULT 240
ID ADG47775 standard; DNA; 15120 BP.
DE Streptomyces clavuligerus 15 kb gene.
PN US2003207411-A1.
PD 06-NOV-2003.
PA (UYAL-) UNIV ALBERTA.
Query Match 5.7%; Score 56.8; DB 10; Length 15120;
Best Local Similarity 43.6%; Pred. No. 1.1;
RESULT 241
ID AAX81426 standard; DNA; 22976 BP.
DE Genomic region containing human lipolysis stimulated receptor gene.
PN WO9907737-A2.
PD 18-FEB-1999.
PA (GEST) GENSET.
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
Query Match 5.7%; Score 56.8; DB 2; Length 22976;
Best Local Similarity 45.6%; Pred. No. 1.1;
RESULT 242
ID AAD36874 standard; DNA; 29870 BP.
DE Streptomyces clavuligerus clavulanic acid biosynthesis gene cluster.
PN WO2003040372-A2.
PD 15-MAY-2003.
PA (SMIK) SMITHKLINE BEECHAM PLC.
PA (UYAL-) UNIV ALBERTA.
Query Match 5.7%; Score 56.8; DB 8; Length 29870;
Best Local Similarity 43.6%; Pred. No. 1.1;
RESULT 243
ID ABL67924 standard; DNA; 41936 BP.
DE Ovary cancer related gene sequence SEQ ID NO:6261.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AYAL-) AYALON PHARM.
Query Match 5.7%; Score 56.8; DB 6; Length 41936;
Best Local Similarity 45.6%; Pred. No. 1.1;
RESULT 244
ID ADA71360 standard; DNA; 2450 BP.
DE Rice gene. SEQ ID 4683.
PN WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 5.7%; Score 56.6; DB 8; Length 2450;
Best Local Similarity 43.1%; Pred. No. 1.2;
RESULT 245
ID ADJ11693 standard; DNA; 3414 BP.
DE Rice DNA modulated by post-transcriptional gene silencing SeqID 329.
PN US2003135888-A1.
PD 17-JUL-2003.
PA (ZHUT/) ZHU T.
PA (WANG/) WANG X.
PA (CHAM/) CHANG H.
PA (BRIG/) BRIGGS S P.
PA (COOP/) COOPER B.
PA (GLAZ/) GLAZEBROOK J.
PA (GOFF/) GOFF S A.
PA (KATA/) KATAGIRI F.
PA (KREP/) KREPS J.

PA (MOUG/) MOUGHAMER T.
PA (PROV/) PROVART N.
PA (RICK/) RICHE D.
Query Match 5.7%; Score 56.6; DB 11; Length 3414;
Best Local Similarity 43.1%; Pred. No. 1.2;
RESULT 246
ID AAD54235 standard; DNA; 25085 BP.
DE Streptomyces amphibiosporus lactimidomycin ORF5 DNA.
PN WO200288176-A2.
PD 07-NOV-2002.
PA (ECOP-) ECOPIA BIOSCIENCES INC.
Query Match 5.7%; Score 56.6; DB 10; Length 25085;
Best Local Similarity 45.1%; Pred. No. 1.2;
RESULT 247
ID AAD54230 standard; DNA; 50543 BP.
DE Streptomyces amphibiosporus lactimidomycin DNA.
PN WO200288176-A2.
PD 07-NOV-2002.
PA (ECOP-) ECOPIA BIOSCIENCES INC.
Query Match 5.7%; Score 56.6; DB 10; Length 50543;
Best Local Similarity 45.1%; Pred. No. 1.1;
RESULT 248
ID AAA09686 standard; DNA; 3957 BP.
DE HSV-2 immediate early protein ICP4 DNA sequence.
PN WO9516779-A1.
PD 22-JUN-1995.
PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
Query Match 5.7%; Score 56.4; DB 5; Length 3957;
Best Local Similarity 49.8%; Pred. No. 1.3;
RESULT 249
ID ADG75121 standard; DNA; 3957 BP.
DE Human herpesvirus 2 ICP4 ORF DNA - SEQ ID 193.
PN WO2003086308-A2.
PD 23-OCT-2003.
PA (CORI-) CORIXA CORP.
Query Match 5.7%; Score 56.4; DB 10; Length 3957;
Best Local Similarity 49.8%; Pred. No. 1.3;
RESULT 250
ID ADI23932 standard; DNA; 15738 BP.
DE Streptomyces refuineus 024A locus ORF6.
PN US2003198981-A1.
PD 23-OCT-2003.
PA (ECOP-) ECOPIA BIOSCIENCES INC.
Query Match 5.7%; Score 56.4; DB 10; Length 15738;
Best Local Similarity 51.7%; Pred. No. 1.3;
RESULT 251
ID AAD25519 standard; DNA; 154746 BP.
DE Human herpesvirus 2 complete DNA genome.
PN WO200176643-A1.
PD 18-OCT-2001.
PA (BAYU) BAYLOR COLLEGE MEDICINE.
Query Match 5.7%; Score 56.4; DB 6; Length 154746;
Best Local Similarity 49.8%; Pred. No. 1.2;
RESULT 252
ID AAD25519 standard; DNA; 154746 BP.
DE Human herpesvirus 2 complete DNA genome.
PN WO200176643-A1.
PD 18-OCT-2001.
PA (BAYU) BAYLOR COLLEGE MEDICINE.
Query Match 5.7%; Score 56.4; DB 6; Length 154746;
Best Local Similarity 49.8%; Pred. No. 1.2;
RESULT 253
ID ABZ66780 standard; DNA; 1143 BP.
DE Orthomyxovirus biosynthetic polynucleotide SEQ ID NO 222.
PN WO200279505-A2.
PD 10-OCT-2002.
PA (ECOP-) ECOPIA BIOSCIENCES INC.
Query Match 5.7%; Score 56.2; DB 10; Length 1143;
Best Local Similarity 45.6%; Pred. No. 1.5;
RESULT 254
ID AAQ98470 standard; cDNA; 2744 BP.
DE MSPI-containing plasmid pMiss1.
PN WO9525165-A1.

PD 21-SEP-1995.
PA (UYNY-) UNIV WYOMING.
Query Match 5.7%; Score 56.2; DB 2; Length 2744;
Best Local Similarity 48.0%; Pred. No. 1.4;
RESULT 255
ID ABL50559 standard; DNA; 14186 BP.
DE Micromonospora carbonacea evernimycin locus nucleotide contig 5.
PN WO200155180-A2.
PD 02-AUG-2001.
PA (ECOP-) ECOPIA BIOSCIENCES INC.
PA (FARN/) FARNET C.
Query Match 5.7%; Score 56.2; DB 4; Length 14186;
Best Local Similarity 45.6%; Pred. No. 1.4;
RESULT 256
ID ABZ66811 standard; DNA; 48221 BP.
DE Orthosmycin biosynthetic gene cluster SEQ ID NO 280.
PN WO200279505-A2.
PD 10-OCT-2002.
PA (ECOP-) ECOPIA BIOSCIENCES INC.
Query Match 5.7%; Score 56.2; DB 10; Length 48221;
Best Local Similarity 45.6%; Pred. No. 1.3;
RESULT 257
ID ACH44935 standard; cDNA; 494 BP.
DE Human foetal brain cDNA #5660.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRNA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Query Match 5.7%; Score 56; DB 9; Length 494;
Best Local Similarity 51.2%; Pred. No. 1.6;
RESULT 258
ID ABD15803 standard; DNA; 1098 BP.
DE Pseudomonas aeruginosa polynucleotide #14407.
PN US5551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.7%; Score 56; DB 11; Length 1098;
Best Local Similarity 49.7%; Pred. No. 1.6;
RESULT 259
ID ACA42208 standard; DNA; 1473 BP.
DE Prokaryotic essential gene #23865.
PN WO20027183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.7%; Score 56; DB 8; Length 1473;
Best Local Similarity 49.7%; Pred. No. 1.6;
RESULT 260
ID ABD15660 standard; DNA; 1566 BP.
DE Pseudomonas aeruginosa polynucleotide #14264.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.7%; Score 56; DB 11; Length 1566;
Best Local Similarity 49.7%; Pred. No. 1.6;
RESULT 261
ID ABD15749 standard; DNA; 1908 BP.
DE Pseudomonas aeruginosa polynucleotide #14353.
PN US5551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.7%; Score 56; DB 11; Length 1908;
Best Local Similarity 49.7%; Pred. No. 1.6;
RESULT 262
ID AAZ07194 standard; cDNA; 2109 BP.
DE Human lung tumour protein SAL-50 5' cDNA sequence.
PN WO9938973-A2.
PD 05-AUG-1999.
PA (CORI-) CORIXA CORP.
Query Match 5.7%; Score 56; DB 2; Length 2109;
Best Local Similarity 49.3%; Pred. No. 1.6;

RESULT 263
ID AAC79147 standard; cDNA; 2109 BP.
DE Human lung tumour-specific cDNA #100.
PN WO200060077-A2.
PD 12-OCT-2000.
PA (CORI-) CORIXA CORP.
Query Match 5.7%; Score 56; DB 3; Length 2109;
Best Local Similarity 49.3%; Pred. No. 1.6;
RESULT 264
ID AAD23222 standard; cDNA; 2109 BP.
DE Human lung tumour-specific protein SAL-50 cDNA.
PN WO200172295-A2.
PD 04-OCT-2001.
PA (CORI-) CORIXA CORP.
Query Match 5.7%; Score 56; DB 4; Length 2109;
Best Local Similarity 49.3%; Pred. No. 1.6;
RESULT 265
ID AD066461 standard; cDNA; 2109 BP.
DE Human lung tumour-specific related cDNA, SEQ ID NO 153.
PN WO200292001-A2.
PD 21-NOV-2002.
PA (CORI-) CORIXA CORP.
Query Match 5.7%; Score 56; DB 10; Length 2109;
Best Local Similarity 49.3%; Pred. No. 1.6;
RESULT 266
ID ADE87715 standard; cDNA; 2109 BP.
DE Human lung tumour antigen cDNA #100.
PN US2003118599-A1.
PD 26-JUN-2003.
PA (CORI-) CORIXA CORP.
Query Match 5.7%; Score 56; DB 10; Length 2109;
Best Local Similarity 49.3%; Pred. No. 1.6;
RESULT 267
ID AAH15254 standard; cDNA; 2142 BP.
DE Human cDNA sequence SEQ ID NO:11376.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 5.7%; Score 56; DB 4; Length 2142;
Best Local Similarity 51.2%; Pred. No. 1.6;
RESULT 268
ID AAH14344 standard; cDNA; 2198 BP.
DE Human cDNA sequence SEQ ID NO:11730.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 5.7%; Score 56; DB 4; Length 2198;
Best Local Similarity 51.2%; Pred. No. 1.6;
RESULT 269
ID AAX61221 standard; DNA; 2392 BP.
DE Mouse DNA demethylase, dmtase2, coding sequence.
PN WO9924583-A1.
PD 20-MAY-1999.
PA (UYMC-) UNIV MCGILL.
Query Match 5.7%; Score 56; DB 2; Length 2392;
Best Local Similarity 51.2%; Pred. No. 1.6;
RESULT 270
ID ADD14651 standard; cDNA; 2392 BP.
DE Human src biomarker polynucleotide SEQ ID NO:45.
PN WO2003062395-A2.
PD 31-JUL-2003.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match 5.7%; Score 56; DB 10; Length 2392;
Best Local Similarity 51.2%; Pred. No. 1.6;
RESULT 271
ID AAV68520 standard; DNA; 4257 BP.
DE The nucleotide sequence of the Herpes simplex virus ICP4.
PN WO9846637-A2.
PD 22-OCT-1998.
PA (ARCH-) ARCH DEV CORP.
Query Match 5.7%; Score 56; DB 2; Length 4257;
Best Local Similarity 45.6%; Pred. No. 1.5;
RESULT 272

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DE AAV10362 standard; cDNA; 4257 BP.
DE Infected cell protein number 4 alpha-4 gene.
PN WO9804709-A2.
PD 05-FEB-1998.
PA (ARCH-) ARCH DEV CORP.
Query Match
Best Local Similarity 45.6%; Score 56; DB 2; Length 4257;
Best Local Similarity 45.6%; Pred. No. 1.5;
RESULT 273
ID ADCS9464 standard; DNA; 4943 BP.
DE DNA sequence encoding novel human tyrosine kinase protein.
PN JP2003024075-A.
PD 28-JAN-2003.
PA (KAZU-) ZH KAZUSA DNA KENKYUSHO.
Query Match
Best Local Similarity 49.3%; Score 56; DB 10; Length 4943;
Best Local Similarity 49.3%; Pred. No. 1.5;
RESULT 274
ID AAD34321 standard; cDNA; 4988 BP.
DE Human PKIN-24 cDNA.
PN WO200218557-A2.
PD 07-MAR-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match
Best Local Similarity 49.3%; Score 56; DB 6; Length 4988;
Best Local Similarity 49.3%; Pred. No. 1.5;
RESULT 275
ID AAQ76213 standard; DNA; 12001 BP.
DE HSV 1/ST region.
PN WO9428156-A1.
PD 08-DEC-1994.
PA (DAND) DANA FARBER CANCER INST INC.
Query Match
Best Local Similarity 45.6%; Score 56; DB 2; Length 12001;
Best Local Similarity 45.6%; Pred. No. 1.5;
RESULT 276
ID AAL02789 standard; DNA; 13862 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 5477.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 49.3%; Score 56; DB 4; Length 13862;
Best Local Similarity 49.3%; Pred. No. 1.5;
RESULT 277
ID AAL07516 standard; DNA; 13862 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 10204.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 49.3%; Score 56; DB 4; Length 13862;
Best Local Similarity 49.3%; Pred. No. 1.5;
RESULT 278
ID ABA08208 standard; DNA; 13862 BP.
DE Human ovarian and breast cancer associated polynucleotide SEQ ID NO 1003.
PN WO200155325-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 49.3%; Score 56; DB 4; Length 13862;
Best Local Similarity 49.3%; Pred. No. 1.5;
RESULT 279
ID ABL64982 standard; DNA; 43058 BP.
DE Lung cancer related gene sequence SEQ ID NO:3319.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Query Match
Best Local Similarity 45.5%; Score 56; DB 6; Length 43058;
Best Local Similarity 45.5%; Pred. No. 1.4;
RESULT 280
ID ABL65219 standard; DNA; 43058 BP.
DE Lung cancer related gene sequence SEQ ID NO:3556.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Query Match
Best Local Similarity 45.5%; Score 56; DB 6; Length 43058;
Best Local Similarity 45.5%; Pred. No. 1.4;
RESULT 281
ID ABN97455 standard; DNA; 43058 BP.
DE Gene #3953 used to diagnose liver cancer.
PN WO200229103-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Query Match
Best Local Similarity 45.5%; Score 56; DB 6; Length 43058;
Best Local Similarity 45.5%; Pred. No. 1.4;
RESULT 282
ID ADH02862 standard; cDNA; 780 BP.
DE Fuchsella FMT cDNA #SEQ ID 21.
PN WO2003062428-A1.
PD 31-JUL-2003.
PA (ITFL-) INT FLOWER DEV PTY LTD.
Query Match
Best Local Similarity 49.1%; Score 55.8; DB 10; Length 780;
Best Local Similarity 49.1%; Pred. No. 1.7;
RESULT 283
ID ADA70053 standard; DNA; 1152 BP.
DE Rice gene, SEQ ID 3376.
PN WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match
Best Local Similarity 45.5%; Score 55.8; DB 8; Length 1152;
Best Local Similarity 45.5%; Pred. No. 1.7;
RESULT 284
ID ADJ11565 standard; DNA; 1152 BP.
DE Rice DNA modulated by post-transcriptional gene silencing SeqID 201.
PN U2003135888-A1.
PD 17-JUL-2003.
PA (ZHUT/) ZHU T.
PA (WANG/) WANG X.
PA (CHAN/) CHANG H.
PA (BRIG/) BRIGGS S P.
PA (COOP/) COOPER B.
PA (GLAZ/) GLAZEBROOK J.
PA (GOFF/) GOFF S A.
PA (KATA/) KATAGIRI F.
PA (KREP/) KEEPS J.
PA (MOUG/) MOUGHAMER T.
PA (PROV/) PROVART N.
PA (RICK/) RICK D.
Query Match
Best Local Similarity 45.5%; Score 55.8; DB 11; Length 1152;
Best Local Similarity 45.5%; Pred. No. 1.7;
RESULT 285
ID AA50254 standard; DNA; 1926 BP.
DE Epstein Barr virus nuclear antigen 1 protein (EBNA1) DNA.
PN WO200047778-A1.
PD 17-AUG-2000.
PA (PHAR-) PHARMACOEPIA INC.
Query Match
Best Local Similarity 46.7%; Score 55.8; DB 3; Length 1926;
Best Local Similarity 46.7%; Pred. No. 1.7;
RESULT 286
ID AAF82902 standard; DNA; 1926 BP.
DE EBV tethering protein EBNA1 encoding DNA.
PN WO200125484-A2.
PD 12-APR-2001.
PA (UNMI) UNIV MICHIGAN.
Query Match
Best Local Similarity 46.7%; Score 55.8; DB 4; Length 1926;
Best Local Similarity 46.7%; Pred. No. 1.7;
RESULT 287
ID ADK65580 standard; DNA; 1926 BP.
DE Human herpesvirus 4 nuclear antigen-1 coding sequence.
PN DE10207135-A1.
PD 11-SEP-2003.
PA (EURO-) EUROIMMUN GMBH.
Query Match
Best Local Similarity 46.7%; Score 55.8; DB 10; Length 1926;
Best Local Similarity 46.7%; Pred. No. 1.7;
RESULT 288
ID AAA75454 standard; DNA; 2580 BP.
DE Nucleotide sequence of the Epstein Barr nuclear antigen.
PN US6114111-A.
PD 05-SEP-2000.
PA (RIGE-) RIGEL PHARM INC.
Query Match
Best Local Similarity 46.7%; Score 55.8; DB 3; Length 2580;
Best Local Similarity 46.7%; Pred. No. 1.7;

RESULT 289
ID AAI64275 standard; DNA; 2580 BP.
DE Epstein-Barr virus nuclear antigen coding sequence.
PN US6316223-B1.
PD 13-NOV-2001.
PA (RIGI-) RIGEL PHARM INC.
Query Match 5.6%; Score 55.8; DB 6; Length 2580;
Best Local Similarity 46.7%; Pred. No. 1.7;
RESULT 290
ID AAX90923 standard; DNA; 5452 BP.
DE Anti-sense strand of pCMVEBNA plasmid.
PN WO9947647-A1.
PD 23-SEP-1999.
PA (PHAR-) PHARMACOEPIA INC.
Query Match 5.6%; Score 55.8; DB 2; Length 5452;
Best Local Similarity 46.7%; Pred. No. 1.6;
RESULT 291
ID AAZ23778 standard; DNA; 8705 BP.
DE Vector pShuttle DNA.
PN WO9950457-A1.
PD 07-OCT-1999.
PA (UTAH) UNIV UTAH RES FOUND.
Query Match 5.6%; Score 55.8; DB 2; Length 8705;
Best Local Similarity 46.7%; Pred. No. 1.6;
RESULT 292
ID ADM10659 standard; DNA; 8705 BP.
DE Expression vector pShuttle.
PN US2004077082-A1.
PD 22-APR-2004.
PA (KOEH/) KOEHN R K.
PA (RUFF/) RUFFNER D E.
PA (PRAK/) FRANKSH R K.
Query Match 5.6%; Score 55.8; DB 12; Length 8705;
Best Local Similarity 46.7%; Pred. No. 1.6;
RESULT 293
ID ADP64415 standard; DNA; 9482 BP.
DE Vector pCEFPu nucleotide sequence SEQ ID NO:1.
PN WO2004053137-A2.
PD 24-JUN-2004.
PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
Query Match 5.6%; Score 55.8; DB 12; Length 9482;
Best Local Similarity 46.7%; Pred. No. 1.6;
RESULT 294
ID AAZ22301 standard; cDNA; 9551 BP.
DE cDNA encoding a human trichohyalin (TRHY) protein.
PN US5958752-A.
PD 28-SEP-1999.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
Query Match 5.6%; Score 55.8; DB 2; Length 9551;
Best Local Similarity 49.9%; Pred. No. 1.6;
RESULT 295
ID AAV21683 standard; DNA; 9600 BP.
DE Vector plasmid pCMVknITR-EPI.
PN WO9806437-A2.
PD 19-FEB-1998.
PA (CHIR) CHIRON CORP.
Query Match 5.6%; Score 55.8; DB 2; Length 9600;
Best Local Similarity 46.7%; Pred. No. 1.6;
RESULT 296
ID ABS71027 standard; DNA; 10285 BP.
DE pCEP-Xa-Fc construct DNA sequence.
PN WO200256905-A2.
PD 25-JUL-2002.
PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
Query Match 5.6%; Score 55.8; DB 6; Length 10285;
Best Local Similarity 46.7%; Pred. No. 1.6;
RESULT 297
ID ABS66453 standard; DNA; 10285 BP.
DE Plasmid pCEP-Xa-Fc* expressing human IgG/protease cleavage site.
PN WO200256907-A2.
PD 25-JUL-2002.
PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
PA (NOVS) NOVARTIS PHARMA AG.

PA (MAUR/) MAURER P.
PA (LECH/) LECHNER F.
PA (ORTM/) ORTMANN R.
PA (LUEO/) LUEOEND R.
PA (STAU/) STAUFENBIEL M.
PA (FREY/) FREY P.
Query Match 5.6%; Score 55.8; DB 6; Length 10285;
Best Local Similarity 46.7%; Pred. No. 1.6;
RESULT 298
ID ADL67154 standard; DNA; 10330 BP.
DE Plasmid pCEP-mB7-H6(ECD)-comp-FL-C nucleotide sequence SEQ ID NO:24.
PN WO2004022594-A2.
PD 18-MAR-2004.
PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
Query Match 5.6%; Score 55.8; DB 12; Length 10330;
Best Local Similarity 46.7%; Pred. No. 1.6;
RESULT 299
ID AAZ22248 standard; DNA; 10380 BP.
DE Nucleotide sequence of pCEP4 vector.
PN WO9947921-A1.
PD 23-SEP-1999.
PA (PHAR-) PHARMACOEPIA INC.
Query Match 5.6%; Score 55.8; DB 2; Length 10380;
Best Local Similarity 46.7%; Pred. No. 1.6;
RESULT 300
ID ADL67152 standard; DNA; 10477 BP.
DE Plasmid pCEP-mB7-H5(ECD)-comp-FL-C nucleotide sequence SEQ ID NO:22.
PN WO2004022594-A2.
PD 18-MAR-2004.
PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
Query Match 5.6%; Score 55.8; DB 12; Length 10477;
Best Local Similarity 46.7%; Pred. No. 1.6;
RESULT 301
ID ADL67150 standard; DNA; 10516 BP.
DE Plasmid pCEP-hsB7-H5(ECD)-comp-FL-C nucleotide sequence SEQ ID NO:20.
PN WO2004022594-A2.
PD 18-MAR-2004.
PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
Query Match 5.6%; Score 55.8; DB 12; Length 10516;
Best Local Similarity 46.7%; Pred. No. 1.6;
RESULT 302
ID ADL67148 standard; DNA; 10561 BP.
DE Plasmid pCEP-hsB7-H4(ECD)-comp-FL-C nucleotide sequence SEQ ID NO:18.
PN WO2004022594-A2.
PD 18-MAR-2004.
PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
Query Match 5.6%; Score 55.8; DB 12; Length 10561;
Best Local Similarity 46.7%; Pred. No. 1.6;
RESULT 303
ID AAQ51731 standard; DNA; 10596 BP.
DE Plasmid pCiEBON for subcloning huHGF variants.
PN WO9323541-A1.
PD 25-NOV-1993.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 55.8; DB 2; Length 10596;
Best Local Similarity 46.7%; Pred. No. 1.6;
RESULT 304
ID AAX15650 standard; DNA; 10596 BP.
DE Nucleotide sequence of plasmid pCiS.EBON.
PN US8679910-A.
PD 09-MAR-1999.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 55.8; DB 2; Length 10596;
Best Local Similarity 46.7%; Pred. No. 1.6;
RESULT 305
ID AAY40348 standard; DNA; 10596 BP.
DE Plasmid pCiEBON for expression of hepatocyte growth factor.
PN US5547856-A.
PD 20-AUG-1996.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 55.8; DB 2; Length 10596;
Best Local Similarity 46.7%; Pred. No. 1.6;
RESULT 306

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ADL67175 standard; DNA; 10615 BP.
ID Plasmid pCEP-hsb7-H6-COMP-FLAG nucleotide sequence SEQ ID NO:45.
DE WO2004022594-A2.
PN 18-MAR-2004.
PD (CYTO-) CYTOS BIOTECHNOLOGY AG.
PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
Query Match 5.6%; Score 55.8; DB 12; Length 10615;
Best Local Similarity 46.7%; Pred. No. 1.6;
RESULT 307
ID ADL67153 standard; DNA; 10774 BP.
DE Plasmid pCEP-mb7-H6(ECD)-FC nucleotide sequence SEQ ID NO:23.
PN WO2004022594-A2.
PD 18-MAR-2004.
PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
Query Match 5.6%; Score 55.8; DB 12; Length 10774;
Best Local Similarity 46.7%; Pred. No. 1.6;
RESULT 308
ID ADL67151 standard; DNA; 10921 BP.
DE Plasmid pCEP-mb7-H5(ECD)-FC nucleotide sequence SEQ ID NO:21.
PN WO2004022594-A2.
PD 18-MAR-2004.
PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
Query Match 5.6%; Score 55.8; DB 12; Length 10921;
Best Local Similarity 46.7%; Pred. No. 1.6;
RESULT 309
ID ADL67149 standard; DNA; 10961 BP.
DE Plasmid pCEP-hsb7-H5(ECD)-FC nucleotide sequence SEQ ID NO:19.
PN WO2004022594-A2.
PD 18-MAR-2004.
PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
Query Match 5.6%; Score 55.8; DB 12; Length 10961;
Best Local Similarity 46.7%; Pred. No. 1.6;
RESULT 310
ID ADL67147 standard; DNA; 11006 BP.
DE Plasmid pCEP-hsb7-H4(ECD)-FC nucleotide sequence SEQ ID NO:17.
PN WO2004022594-A2.
PD 18-MAR-2004.
PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
Query Match 5.6%; Score 55.8; DB 12; Length 11006;
Best Local Similarity 46.7%; Pred. No. 1.6;
RESULT 311
ID ADL67176 standard; DNA; 11059 BP.
DE Plasmid pCEP-hsb7-H6-Xa1-FC nucleotide sequence SEQ ID NO:46.
PN WO2004022594-A2.
PD 18-MAR-2004.
PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
Query Match 5.6%; Score 55.8; DB 12; Length 11059;
Best Local Similarity 46.7%; Pred. No. 1.6;
RESULT 312
ID AD007395 standard; DNA; 11924 BP.
DE Modified human hepsin plasmid pCEP4W/hep36.
PN WO2004033630-A2.
PD 22-APR-2004.
PA (SCHD) SCHERING AG.
Query Match 5.6%; Score 55.8; DB 12; Length 11924;
Best Local Similarity 46.7%; Pred. No. 1.6;
RESULT 313
ID AD007394 standard; DNA; 12242 BP.
DE Modified human hepsin plasmid pCEP4W/hepEK.
PN WO2004033630-A2.
PD 22-APR-2004.
PA (SCHD) SCHERING AG.
Query Match 5.6%; Score 55.8; DB 12; Length 12242;
Best Local Similarity 46.7%; Pred. No. 1.6;
RESULT 314
ID AAA59553 standard; DNA; 16080 BP.
DE DNA clone pCEK Cl.127 encoding a human beta-secretase enzyme.
PN WO200047618-A2.
PD 17-AUG-2000.
PA (ELAN-) ELAN PHARM INC.
Query Match 5.6%; Score 55.8; DB 3; Length 16080;
Best Local Similarity 46.7%; Pred. No. 1.6;
RESULT 315
ID ADL71910 standard; cDNA; 17753 BP.
DE Expression vector pCytts-OPE.
PN WO2004018506-A2.
PD 04-MAR-2004.
PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
Query Match 5.6%; Score 55.8; DB 12; Length 17753;
Best Local Similarity 46.7%; Pred. No. 1.6;
RESULT 316
ID ADN12161 standard; DNA; 17281 BP.
DE Epstein-Barr virus genome B95-8.
PN WO2004027036-A2.
PD 01-APR-2004.
PA (UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
Query Match 5.6%; Score 55.8; DB 12; Length 17281;
Best Local Similarity 46.7%; Pred. No. 1.5;
RESULT 317
ID AAH03407 standard; cDNA; 726 BP.
DE Human cDNA clone (5'-primer) SEQ ID NO:242.
PN EPI074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 5.6%; Score 55.6; DB 4; Length 726;
Best Local Similarity 53.5%; Pred. No. 1.9;
RESULT 318
ID AAL61200 standard; DNA; 1026 BP.
DE Actinosynnema pretiosum glucose 1-dehydrogenase gene.
PN WO2003045312-A2.
PD 05-JUN-2003.
PA (UNIW) UNIV WASHINGTON.
Query Match 5.6%; Score 55.6; DB 8; Length 1026;
Best Local Similarity 46.2%; Pred. No. 1.9;
RESULT 319
ID ABD11061 standard; DNA; 774 BP.
DE Pseudomonas aeruginosa polynucleotide #9665.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.6%; Score 55.4; DB 11; Length 774;
Best Local Similarity 45.2%; Pred. No. 2;
RESULT 320
ID ABX56066 standard; DNA; 3033 BP.
DE M. echinospira calicheamicin biosynthesis gene orfVI.
PN WO200279465-A2.
PD 10-OCT-2002.
PA (SLOK) SLOAN KETTERING INST CANCER RES.
Query Match 5.6%; Score 55.4; DB 8; Length 3033;
Best Local Similarity 44.4%; Pred. No. 1.9;
RESULT 321
ID AAQ46806 standard; DNA; 29879 BP.
DE eryA region of S. erythraea chromosome.
PN WO9313663-A1.
PD 22-JUL-1993.
PA (ABBO) ABBOTT LAB.
Query Match 5.6%; Score 55.4; DB 2; Length 29879;
Best Local Similarity 49.3%; Pred. No. 1.8;
RESULT 322
ID ADM45913 standard; DNA; 84428 BP.
DE Streptomyces mycarofaciens midcamycin polyketide synthetase DNA.
PN JP2004049100-A.
PD 19-FEB-2004.
PA (MEIJ) MEIJI SEIKA KAISHA LTD.
Query Match 5.6%; Score 55.4; DB 12; Length 84428;
Best Local Similarity 48.3%; Pred. No. 1.8;
RESULT 323
ID ABZ78139 standard; cDNA; 1679 BP.
DE Human cancer-related coding sequence, 187p3f2.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 5.6%; Score 55.2; DB 8; Length 1679;
Best Local Similarity 46.9%; Pred. No. 2.1;
RESULT 324
ID ACC00700 standard; cDNA; 1885 BP.
DE Oryza sativa oil trait related cDNA sequence SEQ ID NO:149.

PN WO2003002751-A2.
PD 09-JAN-2003.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
PA (PION-) PIONEER HI-BRED INT INC.
Query Match 5.6%; Score 55.2; DB 8; Length 1885;
Best Local Similarity 47.8%; Pred. No. 2.1;
RESULT 325
ID ACA38134 standard; DNA; 1887 BP.
DE Prokaryotic essential gene #19791.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.6%; Score 55.2; DB 8; Length 1887;
Best Local Similarity 45.0%; Pred. No. 2.1;
RESULT 326
ID AAAG3350 standard; DNA; 21185 BP.
DE Streptomyces globisporus C-1027 gene cluster ORF 25-42.
PN WO200040596-A1.
PD 13-JUL-2000.
PA (REGC) UNIV CALIFORNIA.
Query Match 5.6%; Score 55.2; DB 3; Length 21185;
Best Local Similarity 50.3%; Pred. No. 2;
RESULT 327
ID AAAG3348 standard; DNA; 63164 BP.
DE Streptomyces globisporus C-1027 gene cluster.
PN WO200040596-A1.
PD 13-JUL-2000.
PA (REGC) UNIV CALIFORNIA.
Query Match 5.6%; Score 55.2; DB 3; Length 63164;
Best Local Similarity 50.3%; Pred. No. 1.9;
RESULT 328
ID ADK13938 standard; DNA; 2559 BP.
DE Human methyl-CpG-binding protein DNA #11.
PN US6709817-B1.
PD 23-MAR-2004.
PA (BAYU) BAYLOR COLLEGE MEDICINE.
Query Match 5.6%; Score 55; DB 12; Length 2559;
Best Local Similarity 53.5%; Pred. No. 2.3;
RESULT 329
ID ADQ19517 standard; DNA; 2559 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 2336.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 5.6%; Score 55; DB 12; Length 2559;
Best Local Similarity 53.5%; Pred. No. 2.3;
RESULT 330
ID ADM80034 standard; DNA; 30943 BP.
DE Spiramycin biosynthesis related DNA, SEQ ID 1.
PN FR2845394-A1.
PD 09-APR-2004.
PA (AVET) AVENTIS PHARMA SA.
Query Match 5.6%; Score 55; DB 12; Length 30943;
Best Local Similarity 44.9%; Pred. No. 2.1;
RESULT 331
ID ADN97550 standard; DNA; 30943 BP.
DE S ambotfaciens spiramycin biosynthetic enzyme genomic region.
PN WO2004033689-A2.
PD 22-APR-2004.
PA (AVET) AVENTIS PHARMA SA.
Query Match 5.6%; Score 55; DB 12; Length 30943;
Best Local Similarity 44.9%; Pred. No. 2.1;
RESULT 332
ID AA21187 standard; DNA; 53789 BP.
DE Amycolatopsis mediterranei rifamycin synthesis gene cluster fragment.
PN WO9807868-A1.
PD 26-FEB-1998.
PA (NOVS) NOVARTIS AG.
Query Match 5.6%; Score 55; DB 2; Length 53789;
Best Local Similarity 47.9%; Pred. No. 2.1;
RESULT 333
ID AAA68012 standard; DNA; 594 BP.
DE Eucalyptus grandis OMT nucleotide sequence SEQ ID NO:105.
PN WO200022099-A1.
PD 20-APR-2000.
PA (GENE-) GENESIS RES & DEV CORP LTD.
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.
Query Match 5.5%; Score 54.8; DB 3; Length 594;
Best Local Similarity 57.6%; Pred. No. 2.6;
RESULT 334
ID ADD41762 standard; DNA; 594 BP.
DE O-methyl transferase DNA #11.
PN US2003131373-A1.
PD 10-JUL-2003.
PA (BLOK/) BLOKSBERG L N.
PA (HAVU/) HAVUKKALA I.
Query Match 5.5%; Score 54.8; DB 10; Length 594;
Best Local Similarity 57.6%; Pred. No. 2.6;
RESULT 335
ID AAV23843 standard; DNA; 607 BP.
DE Plant OMT enzyme DNA sequence.
PN WO9811205-A2.
PD 19-MAR-1998.
PA (GENE-) GENESIS RES & DEV CORP LTD.
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.
Query Match 5.5%; Score 54.8; DB 2; Length 607;
Best Local Similarity 57.6%; Pred. No. 2.6;
RESULT 336
ID AA206844 standard; cDNA; 607 BP.
DE Eucalyptus O-methyl transferase (OMT) partial cDNA 2.
PN US9592486-A.
PD 14-SEP-1999.
PA (GENE-) GENESIS RES & DEV CORP LTD.
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.
Query Match 5.5%; Score 54.8; DB 2; Length 607;
Best Local Similarity 57.6%; Pred. No. 2.6;
RESULT 337
ID AA69594 standard; cDNA; 607 BP.
DE Eucalyptus grandis O-methyltransferase cDNA SEQ ID NO:68.
PN WO200036081-A2.
PD 22-JUN-2000.
PA (GENE-) GENESIS RES & DEV CORP LTD.
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.
Query Match 5.5%; Score 54.8; DB 3; Length 607;
Best Local Similarity 57.6%; Pred. No. 2.6;
RESULT 338
ID AA67930 standard; DNA; 607 BP.
DE Eucalyptus grandis OMT nucleotide sequence SEQ ID NO:23.
PN WO200022099-A1.
PD 20-APR-2000.
PA (GENE-) GENESIS RES & DEV CORP LTD.
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.
Query Match 5.5%; Score 54.8; DB 3; Length 607;
Best Local Similarity 57.6%; Pred. No. 2.6;
RESULT 339
ID ADD41680 standard; DNA; 607 BP.
DE O-methyl transferase DNA #3.
PN US2003131373-A1.
PD 10-JUL-2003.
PA (BLOK/) BLOKSBERG L N.
PA (HAVU/) HAVUKKALA I.
Query Match 5.5%; Score 54.8; DB 10; Length 607;
Best Local Similarity 57.6%; Pred. No. 2.6;
RESULT 340
ID AB277318 standard; cDNA; 2684 BP.
DE Nucleotide sequence of a murine ADCK3 polypeptide.
PN WO2003008557-A2.
PD 30-JAN-2003.
PA (UVFL) UNIV FLORIDA.
Query Match 5.5%; Score 54.8; DB 8; Length 2684;
Best Local Similarity 50.6%; Pred. No. 2.5;
RESULT 341
ID ADA69536 standard; DNA; 980 BP.
DE Rice gene, SEQ ID 2859.

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PN WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN ) SYNGENTA PARTICIPATIONS AG.
Query Match 5.5%; Score 54.6; DB 8; Length 980;
Best Local Similarity 48.5%; Pred. No. 2.7;
RESULT 342
ID AAV19115 standard; DNA; 1308 BP.
DE Human secreted apoptosis-related protein hSARP2 DNA.
PN WO9813493-A2.
PD 02-APR-1998.
PA (LXRB-) LXR BIOTECHNOLOGY INC.
Query Match 5.5%; Score 54.6; DB 2; Length 1308;
Best Local Similarity 45.5%; Pred. No. 2.7;
RESULT 343
ID ADF31997 standard; DNA; 39949 BP.
DE Full length cosmid 2A7.
PN WO2003099993-A2.
PD 04-DEC-2003.
PA (AVET ) AVENTIS PHARM INC.
Query Match 5.5%; Score 54.2; DB 12; Length 39949;
Best Local Similarity 45.6%; Pred. No. 2.9;
RESULT 344
ID ADF31998 standard; DNA; 48200 BP.
DE Cosmid 2A7.
PN WO2003099993-A2.
PD 04-DEC-2003.
PA (AVET ) AVENTIS PHARM INC.
Query Match 5.5%; Score 54.2; DB 12; Length 48200;
Best Local Similarity 45.6%; Pred. No. 2.9;
RESULT 345
ID AAD17184 standard; DNA; 65140 BP.
DE Streptomyces noursei nysl DNA of nystatin PKS gene cluster.
PN WO200159126-A2.
PD 16-AUG-2001.
PA (UVNO-) UNIV NORGES TEKNISK NATURVITENSKAPELIGE.
PA (SNTF ) SINTEF STIFTELSEN IND TEK FORSK.
PA (ALPH-) ALPHARMA AS.
PA (SINV-) SINVENT AS.
PA (DZIE/) DZIEGLEWSKA H.
PA (ZOTC/) ZOTCHEV S B.
PA (SEKU/) SEKUROVA O N.
PA (EJAE/) EJAERVIK E.
PA (BRAU/) BRAUTASET T.
PA (STRO/) STROM A R.
PA (VALL/) VALLA S.
Query Match 5.5%; Score 54.2; DB 4; Length 65140;
Best Local Similarity 51.9%; Pred. No. 2.8;
RESULT 346
ID AAD17186 standard; DNA; 125401 BP.
DE Streptomyces noursei nystatin PKS gene cluster DNA.
PN WO200159126-A2.
PD 16-AUG-2001.
PA (UVNO-) UNIV NORGES TEKNISK NATURVITENSKAPELIGE.
PA (SNTF ) SINTEF STIFTELSEN IND TEK FORSK.
PA (ALPH-) ALPHARMA AS.
PA (SINV-) SINVENT AS.
PA (DZIE/) DZIEGLEWSKA H.
PA (ZOTC/) ZOTCHEV S B.
PA (SEKU/) SEKUROVA O N.
PA (FJAE/) FJAERVIK E.
PA (BRAU/) BRAUTASET T.
PA (STRO/) STROM A R.
PA (VALL/) VALLA S.
Query Match 5.5%; Score 54.2; DB 4; Length 125401;
Best Local Similarity 51.9%; Pred. No. 2.8;
RESULT 347
ID ACA23654 standard; DNA; 897 BP.
DE Prokaryotic essential gene #5311.
PN WO20027183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.5%; Score 54; DB 8; Length 897;
Best Local Similarity 44.4%; Pred. No. 3.4;

RESULT 348
ID ACC00684 standard; cDNA; 1118 BP.
DE Oryza sativa oil trait related cDNA sequence SEQ ID NO:117.
PN WO2003002751-A2.
PD 09-JAN-2003.
PA (DUPO ) DU PONT DE NEMOURS & CO E I.
PA (PION-) PIONEER HI-BRED INT INC.
Query Match 5.5%; Score 54; DB 8; Length 1118;
Best Local Similarity 46.2%; Pred. No. 3.4;
RESULT 349
ID ADC23596 standard; cDNA; 1118 BP.
DE cDNA encodes protein used to alter plant oil phenotype (SeqID 101).
PN WO2003001902-A2.
PD 09-JAN-2003.
PA (DUPO ) DU PONT DE NEMOURS & CO E I.
PA (PION-) PIONEER HI-BRED INT INC.
Query Match 5.5%; Score 54; DB 10; Length 1118;
Best Local Similarity 46.2%; Pred. No. 3.4;
RESULT 350
ID ABK12029 standard; DNA; 1217 BP.
DE DNA encoding aminoglycoside multidrug resistance protein.
PN KX90074514-A.
PD 05-OCT-1999.
PA (DONG-) DONGWHA PHARM IND CO LTD.
PA (SUHJ/) SUH J W.
Query Match 5.5%; Score 54; DB 3; Length 1217;
Best Local Similarity 46.3%; Pred. No. 3.4;
RESULT 351
ID AAV67187 standard; DNA; 1380 BP.
DE M. luteus salt-resistant glutaminase encoding DNA.
PN JPI0243787-A.
PD 14-SEP-1998.
PA (FUND-) FUNDOKIN SHOYU KK.
Query Match 5.5%; Score 54; DB 2; Length 1380;
Best Local Similarity 47.1%; Pred. No. 3.4;
RESULT 352
ID AAS85408 standard; cDNA; 4056 BP.
DE DNA encoding novel human diagnostic protein #21212.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 5.5%; Score 54; DB 5; Length 4056;
Best Local Similarity 52.2%; Pred. No. 3.3;
RESULT 353
ID ABZ11999 standard; cDNA; 4530 BP.
DE Human polynucleotide SEQ ID NO 881.
PN WO200270539-A2.
PD 12-SEP-2002.
PA (HYSE-) HYSEQ INC.
Query Match 5.5%; Score 54; DB 6; Length 4530;
Best Local Similarity 52.2%; Pred. No. 3.3;
RESULT 354
ID ADM44517 standard; cDNA; 4530 BP.
DE Novel human arginine-rich protein cDNA #881.
PN US2004053250-A1.
PD 18-MAR-2004.
PA (TANG/) TANG Y T.
PA (XUEA/) XUE A.
PA (DRMA/) DRMANAC R T.
Query Match 5.5%; Score 54; DB 12; Length 4530;
Best Local Similarity 52.2%; Pred. No. 3.3;
RESULT 355
ID AAA31496 standard; DNA; 451 BP.
DE Plant microsatellite marker #457.
PN WO9967421-A1.
PD 29-DEC-1999.
PA (GENE-) GENESIS RES & DEV CORP LTD.
PA (FLET-) FLETCHER CHALLENGE FOREST LTD.
Query Match 5.4%; Score 53.8; DB 3; Length 451;
Best Local Similarity 57.1%; Pred. No. 3.8;
RESULT 356
ID ADM80038 standard; DNA; 1272 BP.
DE Spiramycin biosynthesis orf2*c, SEQ ID 5.

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PN FR2845394-A1.
 PD 09-APR-2004.
 PA (AVET) AVENTIS PHARMA SA.
 PA (CNRS) CNRS CENT NAT RECH SCI.
 Query Match 5.4%; Score 53.8; DB 12; Length 1272;
 Best Local Similarity 48.0%; Pred. No. 3.7;
 RESULT 357
 ID ADN97554 standard; DNA; 1272 BP.
 DE S ambofaciens spiramycin biosynthetic gene ORF2*c.
 PN WO2004033689-A2.
 PD 22-APR-2004.
 PA (AVET) AVENTIS PHARMA SA.
 PA (CNRS) CNRS.
 Query Match 5.4%; Score 53.8; DB 12; Length 1272;
 Best Local Similarity 48.0%; Pred. No. 3.7;
 RESULT 358
 ID ABA95453 standard; DNA; 2082 BP.
 DE Thermus thermophilus uvrD coding sequence.
 PN WO200173052-A2.
 PD 04-OCT-2001.
 PA (MCHE/) MCHENRY C S.
 Query Match 5.4%; Score 53.8; DB 4; Length 2082;
 Best Local Similarity 48.1%; Pred. No. 3.6;
 RESULT 359
 ID ADM80035 standard; DNA; 11171 BP.
 DE Spiramycin biosynthesis related DNA, SEQ ID 2.
 PN FR2845394-A1.
 PD 09-APR-2004.
 PA (AVET) AVENTIS PHARMA SA.
 PA (CNRS) CNRS CENT NAT RECH SCI.
 Query Match 5.4%; Score 53.8; DB 12; Length 11171;
 Best Local Similarity 48.0%; Pred. No. 3.5;
 RESULT 360
 ID ADN97551 standard; DNA; 11171 BP.
 DE S ambofaciens spiramycin biosynthetic enzyme genomic region #2.
 PN WO2004033689-A2.
 PD 22-APR-2004.
 PA (AVET) AVENTIS PHARMA SA.
 PA (CNRS) CNRS.
 Query Match 5.4%; Score 53.8; DB 12; Length 11171;
 Best Local Similarity 48.0%; Pred. No. 3.5;
 RESULT 361
 ID AAR80414 standard; DNA; 44377 BP.
 DE Platenolide synthase gene cluster.
 PN EP791655-A2.
 PD 27-AUG-1997.
 PA (ELIL) LILLY & CO ELI.
 Query Match 5.4%; Score 53.8; DB 2; Length 44377;
 Best Local Similarity 48.0%; Pred. No. 3.3;
 RESULT 362
 ID AAT78508 standard; DNA; 44377 BP.
 DE Platenolide synthase gene cluster.
 PN EP791656-A2.
 PD 27-AUG-1997.
 PA (ELIL) LILLY & CO ELI.
 Query Match 5.4%; Score 53.8; DB 2; Length 44377;
 Best Local Similarity 48.0%; Pred. No. 3.3;
 RESULT 363
 ID ADK16023 standard; DNA; 64492 BP.
 DE Streptomyces halstedii vincenistatin gene cluster seq id 1.
 PN US2004053274-A1.
 PD 18-MAR-2004.
 PA (TOKD) TOKYO INST TECHNOLOGY.
 Query Match 5.4%; Score 53.8; DB 12; Length 64492;
 Best Local Similarity 50.6%; Pred. No. 3.3;
 RESULT 364
 ID AAD08215 standard; DNA; 114793 BP.
 DE Human genome from BAC clone, hbml168.
 PN WO200142434-A1.
 PD 14-JUN-2001.
 PA (MERI) MERCK & CO INC.
 Query Match 5.4%; Score 53.8; DB 4; Length 114793;
 Best Local Similarity 47.2%; Pred. No. 3.2;

RESULT 365
 ID AAZ32020 standard; DNA; 38734 BP.
 DE Human METH1 related EST AL021529.
 PN WO9937660-A1.
 PD 29-JUL-1999.
 PA (IRUE/) IRUELA-ARISPE L.
 PA (HAST/) HASTINGS G A.
 PA (RUBE/) RUBEN S M.
 Query Match 5.4%; Score 53.6; DB 2; Length 38734;
 Best Local Similarity 44.9%; Pred. No. 3.6;
 RESULT 366
 ID AAC90077 standard; DNA; 38734 BP.
 DE AL021529 cDNA clone.
 PN WO200071577-A1.
 PD 30-NOV-2000.
 PA (HUMA-) HUMAN GENOME SCI INC.
 PA (SMIK) SMITHKLINE BEECHAM CORP.
 PA (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
 PA (IRUE/) IRUELA-ARISPE L.
 PA (HAST/) HASTINGS G A.
 PA (RUBE/) RUBEN S M.
 PA (JONA/) JONAK Z L.
 PA (TRUL/) TRULLI S H.
 PA (FORN/) FORNWALD J A.
 PA (TERR/) TERRETT J A.
 Query Match 5.4%; Score 53.6; DB 5; Length 38734;
 Best Local Similarity 44.9%; Pred. No. 3.6;
 RESULT 367
 ID AAL61221 standard; DNA; 1554 BP.
 DE Actinosynnema pretiosum transcriptional activator gene #2.
 PN WO2003045312-A2.
 PD 05-JUN-2003.
 PA (UNIW) UNIV WASHINGTON.
 Query Match 5.4%; Score 53.4; DB 8; Length 1554;
 Best Local Similarity 48.5%; Pred. No. 4.3;
 RESULT 368
 ID AAZ50651 standard; cDNA; 2248 BP.
 DE Corn starch synthase SSB DNA fragment inserted in pSPB47.
 PN WO200006755-A2.
 PD 10-FEB-2000.
 PA (DUPO) DU PONT DE NEMOURS & CO E I.
 Query Match 5.4%; Score 53.4; DB 3; Length 2248;
 Best Local Similarity 50.2%; Pred. No. 4.2;
 RESULT 369
 ID AAQ14183 standard; cDNA; 2338 BP.
 DE N-clavipes dragline silk protein coding sequence.
 PN EP452925-A.
 PD 23-OCT-1991.
 PA (UYWY-) UNIV OF WYOMING.
 Query Match 5.4%; Score 53.4; DB 2; Length 2338;
 Best Local Similarity 45.5%; Pred. No. 4.2;
 RESULT 370
 ID AAV23249 standard; cDNA; 2338 BP.
 DE Nephila clavipes spider silk protein encoding cDNA.
 PN US5728810-A.
 PD 17-MAR-1998.
 PA (UYWY-) UNIV WYOMING.
 Query Match 5.4%; Score 53.4; DB 2; Length 2338;
 Best Local Similarity 45.5%; Pred. No. 4.2;
 RESULT 371
 ID AAZ38195 standard; cDNA; 2338 BP.
 DE N. clavipes spider silk protein 1 encoding cDNA.
 PN US5989894-A.
 PD 23-NOV-1999.
 PA (UYWY-) UNIV WYOMING.
 Query Match 5.4%; Score 53.4; DB 3; Length 2338;
 Best Local Similarity 45.5%; Pred. No. 4.2;
 RESULT 372
 ID AAI57831 standard; cDNA; 4176 BP.
 DE Human polynucleotide SEQ ID NO 34.
 PN WO200153312-A1.
 PD 26-JUL-2001.
 PA (HYSE-) HYSEQ INC.

Query Match	5.4%;	Score 53.4;	DB 4;	Length 4176;
Best Local Similarity	48.9%;	Pred. No. 4.1;		
RESULT 373				
ID AAL61225 standard; DNA; 11905 BP.				
DE Actinosynnema pretiosum aneasmitocin biosynthetic gene cluster II.				
PN WO2003045312-A2.				
PD 05-JUN-2003.				
PA (UNIW) UNIV WASHINGTON.				
Query Match	5.4%;	Score 53.4;	DB 8;	Length 11905;
Best Local Similarity	48.5%;	Pred. No. 4;		
RESULT 374				
Query Match	5.4%;	Score 53.4;	DB 11;	Length 110000;
Best Local Similarity	45.7%;	Pred. No. 3.8;		
RESULT 375				
ID ACA26842 standard; DNA; 900 BP.				
DE Prokaryotic essential gene #8499.				
PN WO200277183-A2.				
PD 03-OCT-2002.				
PA (ELIT-) ELITRA PHARM INC.				
Query Match	5.4%;	Score 53.2;	DB 8;	Length 900;
Best Local Similarity	49.6%;	Pred. No. 4.7;		
RESULT 376				
ID AEX34289 standard; DNA; 135638 BP.				
DE S. atroolivaceus leinamycin biosynthesis gene cluster.				
PN WO200277179-A2.				
PD 03-OCT-2002.				
PA (REGC) UNIV CALIFORNIA.				
PA (KYOW) KYOWA HAKKO KOGYO KK.				
Query Match	5.4%;	Score 53.2;	DB 10;	Length 135638;
Best Local Similarity	47.9%;	Pred. No. 4.1;		
RESULT 377				
ID ADU27274 standard; cDNA; 1929 BP.				
DE Mouse HSP70.1 coding sequence.				
PN WO2003061684-A2.				
PD 31-JUL-2003.				
PA (VLA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.				
Query Match	5.4%;	Score 53;	DB 11;	Length 1929;
Best Local Similarity	44.3%;	Pred. No. 4.9;		
RESULT 378				
ID AAT45060 standard; cDNA; 1236 BP.				
DE Maize Tst2 cDNA nucleotide sequence.				
PN WO9505732-A1.				
PD 02-MAR-1995.				
PA (UYVA) UNIV YALE.				
Query Match	5.3%;	Score 52.8;	DB 2;	Length 1236;
Best Local Similarity	47.3%;	Pred. No. 5.4;		
RESULT 379				
ID ACA38386 standard; DNA; 2712 BP.				
DE Prokaryotic essential gene #20043.				
PN WO200277183-A2.				
PD 03-OCT-2002.				
PA (ELIT-) ELITRA PHARM INC.				
Query Match	5.3%;	Score 52.8;	DB 8;	Length 2712;
Best Local Similarity	46.8%;	Pred. No. 5.3;		
RESULT 380				
ID ACA40526 standard; DNA; 2715 BP.				
DE Prokaryotic essential gene #22183.				
PN WO200277183-A2.				
PD 03-OCT-2002.				
PA (ELIT-) ELITRA PHARM INC.				
Query Match	5.3%;	Score 52.8;	DB 8;	Length 2715;
Best Local Similarity	46.8%;	Pred. No. 5.3;		
RESULT 381				
ID ADP90617 standard; DNA; 34719 BP.				
DE Micromonospora echinospora gentamycin biosynthesis gene SeqID 1.				
PN JP2004180638-A.				
PD 02-JUL-2004.				
PA (MEIJ) MEIJI SEIKA KAISHA LTD.				
Query Match	5.3%;	Score 52.8;	DB 12;	Length 34719;
Best Local Similarity	50.4%;	Pred. No. 4.9;		
RESULT 382				
Query Match	5.3%;	Score 52.8;	DB 4;	Length 110000;
Best Local Similarity	46.8%;	Pred. No. 4.8;		

PN WO2003004620-A2.
PD 16-JAN-2003.
PA (CHIR) CHIRON CORP.
Query Match 5.3%; Score 52.6; DB 10; Length 3624;
Best Local Similarity 43.1%; Pred. No. 5.7;
RESULT 392
ID ADG73810 standard; cDNA; 3705 BP.
DE Human subtilase-like serine protease polynucleotide.
PN WO2003106667-A2.
PD 24-DEC-2003.
PA (FARB) BAYER HEALTHCARE AG.
Query Match 5.3%; Score 52.6; DB 12; Length 3705;
Best Local Similarity 45.8%; Pred. No. 5.7;
RESULT 393
ID ADOS8090 standard; DNA; 4199 BP.
DE Thermus thermophilus V1 ATPase gene operon.
PN WO2004046350-A1.
PD 03-JUN-2004.
PA (NISC-) JAPAN SCI & TECHNOLOGY AGENCY.
Query Match 5.3%; Score 52.6; DB 12; Length 4199;
Best Local Similarity 55.1%; Pred. No. 5.6;
RESULT 394
Query Match 5.3%; Score 52.6; DB 4; Length 110000;
Best Local Similarity 52.0%; Pred. No. 5.1;
RESULT 395
Query Match 5.3%; Score 52.6; DB 4; Length 110000;
Best Local Similarity 52.0%; Pred. No. 5.1;
RESULT 396
ID ABU61294 standard; DNA; 1227 BP.
DE N. uniformis p-hydroxymandelate oxidase DNA.
PN WO200234921-A2.
PD 02-MAY-2002.
PA (STAM) DSM NV.
PA (STAM) DSM BIOTECH GMBH.
PA (UJO) UNIV JOHNS HOPKINS.
Query Match 5.3%; Score 52.4; DB 6; Length 1227;
Best Local Similarity 45.0%; Pred. No. 6.3;
RESULT 397
ID ABU69280 standard; DNA; 1891 BP.
DE Prostate cancer related gene sequence SEQ ID NO:7617.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Query Match 5.3%; Score 52.4; DB 6; Length 1891;
Best Local Similarity 45.9%; Pred. No. 6.2;
RESULT 398
ID ABV94243 standard; cDNA; 1891 BP.
DE Breast carcinoma related nucleotide sequence SEQ ID NO:234.
PN WO200246467-A2.
PD 13-JUN-2002.
PA (IPSO-) IPSOGEN.
Query Match 5.3%; Score 52.4; DB 6; Length 1891;
Best Local Similarity 45.9%; Pred. No. 6.2;
RESULT 399
ID ABK84580 standard; cDNA; 1891 BP.
DE Human cDNA differentially expressed in granulocytic cells #1151.
PN WO200228999-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 5.3%; Score 52.4; DB 6; Length 1891;
Best Local Similarity 45.9%; Pred. No. 6.2;
RESULT 400
ID AA53918 standard; cDNA; 3978 BP.
DE Adenyllyl cyclase type I-C1 C1 alpha domain coding sequence.
PN US6107076-A.
PD 22-AUG-2000.
PA (TEXA) UNIV TEXAS SYSTEM.
Query Match 5.3%; Score 52.4; DB 3; Length 3978;
Best Local Similarity 47.8%; Pred. No. 6.1;
RESULT 401
ID ADL15099 standard; DNA; 5117 BP.
DE Human male brain KIAA0533 protein DNA for cancer treatment.

PN WO2003068268-A2.
PD 21-AUG-2003.
PA (BIOI-) BIOINVENT INT AB.
Query Match 5.3%; Score 52.4; DB 10; Length 5117;
Best Local Similarity 50.0%; Pred. No. 6.1;
RESULT 402
ID ADN95659 standard; DNA; 5117 BP.
DE Human BEC/LBC-related gene sequence SeqID583.
PN WO2003080640-A1.
PD 02-OCT-2003.
PA (LUDW-) LUDWIG INST CANCER RES.
PA (LICN) LICENTIA LTD.
Query Match 5.3%; Score 52.4; DB 11; Length 5117;
Best Local Similarity 50.0%; Pred. No. 6.1;
RESULT 403
ID ABQ93882 standard; DNA; 5204 BP.
DE Human laminin alpha-5-like NOVIid DNA, SEQ ID NO:7.
PN WO200253742-A2.
PD 11-JUL-2002.
PA (CURA-) CURAGEN CORP.
Query Match 5.3%; Score 52.4; DB 6; Length 5204;
Best Local Similarity 50.0%; Pred. No. 6.1;
RESULT 404
ID ADM87490 standard; cDNA; 5403 BP.
DE Human EST derived nucleotide sequence. SEQ ID NO:583.
PN WO2004009834-A2.
PD 29-JAN-2004.
PA (NUVE-) NUVELO INC.
Query Match 5.3%; Score 52.4; DB 12; Length 5403;
Best Local Similarity 50.0%; Pred. No. 6;
RESULT 405
ID AA158165 standard; cDNA; 5640 BP.
DE Human polynucleotide SEQ ID NO 368.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 5.3%; Score 52.4; DB 4; Length 5640;
Best Local Similarity 50.0%; Pred. No. 6;
RESULT 406
ID ADQ98371 standard; cDNA; 5640 BP.
DE DNA encoding human GPCR-like protein seqid 41.
PN US6569662-B1.
PD 27-MAY-2003.
PA (HYSE-) HYSEQ INC.
Query Match 5.3%; Score 52.4; DB 5; Length 5640;
Best Local Similarity 50.0%; Pred. No. 6;
RESULT 407
ID AD848131 standard; cDNA; 5640 BP.
DE Novel human cDNA SEQ ID NO 41.
PN US2003104529-A1.
PD 05-JUN-2003.
PA (ZHOU/) ZHOU P.
PA (TANG/) TANG Y T.
PA (LIUC/) LIU C.
PA (ASUN/) ASUNDI V.
PA (DRMA/) DRMANAC R T.
Query Match 5.3%; Score 52.4; DB 9; Length 5640;
Best Local Similarity 50.0%; Pred. No. 6;
RESULT 408
ID ABQ72930 standard; cDNA; 8296 BP.
DE Human laminin alpha 5 2743 N-terminal amino acids cDNA SEQ ID NO:35.
PN WO200250111-A2.
PD 27-JUN-2002.
PA (BIOS-) BIOSTRATUM INC.
Query Match 5.3%; Score 52.4; DB 6; Length 8296;
Best Local Similarity 50.0%; Pred. No. 6;
RESULT 409
ID AAD27805 standard; DNA; 11091 BP.
DE Human laminin alpha gene, sbg417005LAMININ_ALPHA #2.
PN WO200198342-A1.
PD 27-DEC-2001.
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.

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PA (GLAX) GLAXO GROUP LTD.
 Query Match 5.3%; Score 52.4; DB 6; Length 11091;
 Best Local Similarity 50.0%; Pred. No. 5.9;
 RESULT 410
 ID AAD27804 standard; DNA; 11118 BP.
 DE Human laminin alpha gene, sbg417005LAMININ_ALPHA #1.
 PN WO200198342-A1.
 PD 27-DEC-2001.
 PA (SMIK) SMITHKLINE BEECHAM CORP.
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 PA (GLAX) GLAXO GROUP LTD.
 Query Match 5.3%; Score 52.4; DB 6; Length 11118;
 Best Local Similarity 50.0%; Pred. No. 5.9;
 RESULT 411
 ID AAD55817 standard; DNA; 11238 BP.
 DE Micromonospora carbonacea polyketide synthase (PKS) type I gene #7.
 PN CA2391131-A1.
 PD 19-NOV-2002.
 PA (ECOP-) ECOPIA BIOSCIENCES INC.
 Query Match 5.3%; Score 52.4; DB 10; Length 11238;
 Best Local Similarity 45.6%; Pred. No. 5.9;
 RESULT 412
 ID ABQ72906 standard; cDNA; 11350 BP.
 DE Human laminin alpha 5 encoding cDNA SEQ ID NO:1.
 PN WO200250111-A2.
 PD 27-JUN-2002.
 PA (BIOS-) BIOSTRATUM INC.
 Query Match 5.3%; Score 52.4; DB 6; Length 11350;
 Best Local Similarity 50.0%; Pred. No. 5.9;
 RESULT 413
 ID ADI28066 standard; cDNA; 11367 BP.
 DE ECMCAD gene clone 638272CBL.
 PN WO200202634-A2.
 PD 10-JAN-2002.
 PA (INCY-) INCYTE GENOMICS INC.
 Query Match 5.3%; Score 52.4; DB 6; Length 11367;
 Best Local Similarity 50.0%; Pred. No. 5.9;
 RESULT 414
 ID ADN04477 standard; cDNA; 11426 BP.
 DE Antiporiatric cDNA sequence #440.
 PN WO2004028479-A2.
 PD 08-APR-2004.
 PA (GETH) GENENTECH INC.
 Query Match 5.3%; Score 52.4; DB 12; Length 11426;
 Best Local Similarity 50.0%; Pred. No. 5.9;
 RESULT 415
 ID ADM87010 standard; cDNA; 11640 BP.
 DE Human protein encoding cDNA SEQ ID NO:103.
 PN WO2004009834-A2.
 PD 29-JAN-2004.
 PA (NUVE-) NUVELO INC.
 Query Match 5.3%; Score 52.4; DB 12; Length 11640;
 Best Local Similarity 50.0%; Pred. No. 5.9;
 RESULT 416
 ID AAD55810 standard; DNA; 60196 BP.
 DE Micromonospora carbonacea polyketide synthase (PKS) type I gene cluster.
 PN CA2391131-A1.
 PD 19-NOV-2002.
 PA (ECOP-) ECOPIA BIOSCIENCES INC.
 Query Match 5.3%; Score 52.4; DB 10; Length 60196;
 Best Local Similarity 45.6%; Pred. No. 5.7;
 RESULT 417
 ID AAC47161 standard; DNA; 738 BP.
 DE Arabidopsis thaliana DNA fragment SEQ ID NO: 52786.
 PN EP1033405-A2.
 PD 06-SEP-2000.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Query Match 5.3%; Score 52.2; DB 3; Length 738;
 Best Local Similarity 47.8%; Pred. No. 6.9;
 RESULT 418
 ID AAC47930 standard; DNA; 833 BP.
 DE Arabidopsis thaliana DNA fragment SEQ ID NO: 55635.
 PN EP1033405-A2.
 PD 06-SEP-2000.
 PA (GENO-) GENOME THERAPEUTICS CORP.

Query Match 5.3%; Score 52.2; DB 3; Length 833;
 Best Local Similarity 47.8%; Pred. No. 6.9;
 RESULT 419
 ID AAT85356 standard; DNA; 2004 BP.
 DE Nephila clavipes spider silk protein 2 Kb DNA sequence.
 PN WO9708315-A1.
 PD 06-MAR-1997.
 PA (BASE/) BASEL R M.
 PA (ELIO/) ELION G R.
 Query Match 5.3%; Score 52.2; DB 2; Length 2004;
 Best Local Similarity 47.2%; Pred. No. 6.7;
 RESULT 420
 ID ACA38157 standard; DNA; 2757 BP.
 DE Prokaryotic essential gene #19814.
 PN WO200277183-A2.
 PD 03-OCT-2002.
 PA (ELIT-) ELITRA PHARM INC.
 Query Match 5.3%; Score 52.2; DB 8; Length 2757;
 Best Local Similarity 46.7%; Pred. No. 6.7;
 RESULT 421
 ID ADC30607 standard; cDNA; 4542 BP.
 DE Human novel cDNA sequence, SEQ ID NO:689.
 PN WO2003029271-A2.
 PD 10-APR-2003.
 PA (HYSE-) HYSEQ INC.
 Query Match 5.3%; Score 52.2; DB 10; Length 4542;
 Best Local Similarity 47.6%; Pred. No. 6.6;
 RESULT 422
 ID AAD54236 standard; DNA; 6297 BP.
 DE Streptomyces amphibiosporus lactimidomycin ORF6 DNA.
 PN WO200288176-A2.
 PD 07-NOV-2002.
 PA (ECOP-) ECOPIA BIOSCIENCES INC.
 Query Match 5.3%; Score 52.2; DB 10; Length 6297;
 Best Local Similarity 47.2%; Pred. No. 6.5;
 RESULT 423
 ID ABQ77491 standard; DNA; 67459 BP.
 DE S. aurantiaca DNA containing sti gene cluster.
 PN DE10128661-A1.
 PD 19-DEC-2002.
 PA (GBFB) GES BIOTECHNOLOGISCHE FORSCHUNG MBH.
 Query Match 5.3%; Score 52.2; DB 8; Length 67459;
 Best Local Similarity 43.5%; Pred. No. 6.1;
 RESULT 424
 ID AD059147 standard; DNA; 70782 BP.
 DE Angiococcus disciformis tubulysin biosynthesis cluster DNA.
 PN DE10241152-A1.
 PD 18-MAR-2004.
 PA (GBFB) GES BIOTECHNOLOGISCHE FORSCHUNG MBH.
 Query Match 5.3%; Score 52.2; DB 12; Length 70782;
 Best Local Similarity 44.2%; Pred. No. 6.1;
 RESULT 425
 ID ACF06127 standard; DNA; 1218 BP.
 DE Bacterial P450 enzyme encoding DNA SEQ ID NO:37.
 PN WO2003052050-A2.
 PD 26-JUN-2003.
 PA (DIVE-) DIVERSA CORP.
 Query Match 5.3%; Score 52; DB 9; Length 1218;
 Best Local Similarity 50.6%; Pred. No. 7.3;
 RESULT 426
 ID ABD03077 standard; DNA; 1248 BP.
 DE Pseudomonas aeruginosa polynucleotide #1681.
 PN US6551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Query Match 5.3%; Score 52; DB 11; Length 1248;
 Best Local Similarity 50.4%; Pred. No. 7.3;
 RESULT 427
 ID ASD02833 standard; DNA; 1302 BP.
 DE Pseudomonas aeruginosa polynucleotide #1437.
 PN US6551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.

Query Match 5.3%; Score 52; DB 11; Length 1302;
Best Local Similarity 50.4%; Pred. No. 7.3;
RESULT 428
ID ABL40020 standard; DNA; 1491 BP.
DE Synthetic Gag polynucleotide sequence SEQ ID NO:99.
PN WO200204493-A2.
PD 17-JAN-2002.
PA (CHIR) CHIRON CORP.
PA (UYST-) UNIV STELLENBOSCH.
Query Match 5.3%; Score 52; DB 6; Length 1491;
Best Local Similarity 46.4%; Pred. No. 7.3;
RESULT 429
ID ADM73833 standard; DNA; 1491 BP.
DE HIV-1 polynucleotide #68.
PN US2003233961-A1.
PD 04-DEC-2003.
PA (MEGE/) MEGEDE J Z.
PA (BARN/) BARNETT S W.
PA (ENGE/) ENGELBRECHT S.
PA (RENS/) RENSBERG E J V.
Query Match 5.3%; Score 52; DB 12; Length 1491;
Best Local Similarity 46.4%; Pred. No. 7.3;
RESULT 430
ID ABD02890 standard; DNA; 1956 BP.
DE Pseudomonas aeruginosa polynucleotide #1494.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.3%; Score 52; DB 11; Length 1956;
Best Local Similarity 50.4%; Pred. No. 7.3;
RESULT 431
ID ADP69917 standard; DNA; 3078 BP.
DE Mammalian codon optimised E. coli LacZ gene.
PN WO2004050872-A1.
PD 17-JUN-2004.
PA (WOME-) WOMEN'S & CHILDREN'S HOSPITAL.
Query Match 5.3%; Score 52; DB 12; Length 3078;
Best Local Similarity 45.4%; Pred. No. 7.2;
RESULT 432
ID ABD11785 standard; DNA; 498 BP.
DE Pseudomonas aeruginosa polynucleotide #10389.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.2%; Score 51.8; DB 11; Length 498;
Best Local Similarity 46.5%; Pred. No. 8.1;
RESULT 433
ID ABD11976 standard; DNA; 561 BP.
DE Pseudomonas aeruginosa polynucleotide #10580.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.2%; Score 51.8; DB 11; Length 561;
Best Local Similarity 46.5%; Pred. No. 8.1;
RESULT 434
ID ABD12080 standard; DNA; 1053 BP.
DE Pseudomonas aeruginosa polynucleotide #10684.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.2%; Score 51.8; DB 8; Length 1227;
Best Local Similarity 46.9%; Pred. No. 7.9;
RESULT 435
ID ACA27206 standard; DNA; 1227 BP.
DE Prokaryotic essential gene #8863.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.2%; Score 51.8; DB 12; Length 2075;
Best Local Similarity 45.0%; Pred. No. 7.8;
RESULT 436
ID ABD04500 standard; DNA; 1233 BP.
DE Pseudomonas aeruginosa polynucleotide #3104.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.2%; Score 51.8; DB 11; Length 1233;
Best Local Similarity 48.2%; Pred. No. 7.9;
RESULT 437
ID ABD04263 standard; DNA; 1386 BP.
DE Pseudomonas aeruginosa polynucleotide #2867.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.2%; Score 51.8; DB 11; Length 1386;
Best Local Similarity 48.2%; Pred. No. 7.9;
RESULT 438
ID ABZ81830 standard; DNA; 2072 BP.
DE Receptor FZD10 nucleic acid sequence.
PN WO2003012082-A2.
PD 13-FEB-2003.
PA (AXOR-) AXORDIA LTD.
Query Match 5.2%; Score 51.8; DB 8; Length 2072;
Best Local Similarity 45.0%; Pred. No. 7.8;
RESULT 439
ID AAD17401 standard; DNA; 2075 BP.
DE Human secreted Frizzled-related protein (sFRP) gene.
PN WO200164717-A1.
PD 07-SEP-2001.
PA (UYCO) UNIV COLUMBIA NEW YORK.
Query Match 5.2%; Score 51.8; DB 4; Length 2075;
Best Local Similarity 45.0%; Pred. No. 7.8;
RESULT 440
ID ABV73022 standard; cDNA; 2075 BP.
DE Human secreted Frizzled-related protein (sFRP)-1 encoding cDNA.
PN WO200255547-A2.
PD 18-JUL-2002.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA (SVIN) ST VINCENTS INST MEDICAL RES.
Query Match 5.2%; Score 51.8; DB 6; Length 2075;
Best Local Similarity 45.0%; Pred. No. 7.8;
RESULT 441
ID ABX75330 standard; cDNA; 2075 BP.
DE Human cDNA encoding Frizzled-8.
PN WO200277204-A2.
PD 03-OCT-2002.
PA (AXOR-) AXORDIA LTD.
Query Match 5.2%; Score 51.8; DB 8; Length 2075;
Best Local Similarity 45.0%; Pred. No. 7.8;
RESULT 442
ID AAD52558 standard; DNA; 2075 BP.
DE FRP DNA.
PN WO200290992-A2.
PD 14-NOV-2002.
PA (AXOR-) AXORDIA LTD.
Query Match 5.2%; Score 51.8; DB 8; Length 2075;
Best Local Similarity 45.0%; Pred. No. 7.8;
RESULT 443
ID ADC71197 standard; cDNA; 2075 BP.
DE Human secreted frizzled related protein (sFRP) cDNA.
PN US6600018-B1.
PD 29-JUL-2003.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
Query Match 5.2%; Score 51.8; DB 10; Length 2075;
Best Local Similarity 45.0%; Pred. No. 7.8;
RESULT 444
ID ADH43319 standard; cDNA; 2075 BP.
DE Human secreted frizzled related protein 1 (sFRP-1) cDNA.
PN US2003187223-A1.
PD 02-OCT-2003.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA (UYMA-) UNIV MASSACHUSETTS.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
Query Match 5.2%; Score 51.8; DB 12; Length 2075;
Best Local Similarity 45.0%; Pred. No. 7.8;
RESULT 445

DE Gene encoding a subunit of cellulose synthase.
 PN JP2000050568-A.
 PD 29-FEB-2000.
 PA (MIZU/) MIZUNO K.
 PA (OJIP) OJI PAPER CO.
 Query Match 5.2%; Score 51.8; DB 3; Length 10732;
 Best Local Similarity 13.2%; Pred. No. 7.5;
 RESULT 455
 ID AAL61170 standard; DNA; 14055 BP.
 DE Actinosynnema pretiosum polyketide synthase (PKS) gene #1.
 PN WO2003045312-A2.
 PD 05-JUN-2003.
 PA (UNIW) UNIV WASHINGTON.
 Query Match 5.2%; Score 51.8; DB 8; Length 14055;
 Best Local Similarity 44.1%; Pred. No. 7.4;
 RESULT 456
 ID AAD54645 standard; DNA; 113193 BP.
 DE Streptomyces nodosus amphotericin (amph) biosynthetic gene cluster.
 PN WO200297082-A2.
 PD 05-DEC-2002.
 PA (UYDU-) UNIV COLLEGE DUBLIN.
 Query Match 5.2%; Score 51.8; DB 8; Length 113193;
 Best Local Similarity 46.9%; Pred. No. 7;
 RESULT 457
 ID ACC0687 standard; cDNA; 893 BP.
 DE Oryza sativa oil trait related cDNA sequence SEQ ID NO:123.
 PN WO2003002751-A2.
 PD 09-JAN-2003.
 PA (DUPO) DU PONT DE NEMOURS & CO E I.
 PA (PION-) PIONEER HI-BRED INT INC.
 Query Match 5.2%; Score 51.6; DB 8; Length 893;
 Best Local Similarity 46.7%; Pred. No. 8.6;
 RESULT 458
 ID ADC23602 standard; cDNA; 893 BP.
 DE cDNA encodes protein used to alter plant oil phenotype (SeqID 107).
 PN WO2003001902-A2.
 PD 09-JAN-2003.
 PA (DUPO) DU PONT DE NEMOURS & CO E I.
 PA (PION-) PIONEER HI-BRED INT INC.
 Query Match 5.2%; Score 51.6; DB 10; Length 893;
 Best Local Similarity 46.7%; Pred. No. 8.6;
 RESULT 459
 ID ACA38013 standard; DNA; 1242 BP.
 DE Prokaryotic essential gene #19670.
 PN WO200277183-A2.
 PD 03-OCT-2002.
 PA (ELIT-) ELITRA PHARM INC.
 Query Match 5.2%; Score 51.6; DB 8; Length 1242;
 Best Local Similarity 44.5%; Pred. No. 8.6;
 RESULT 460
 ID ABD15461 standard; DNA; 1311 BP.
 DE Pseudomonas aeruginosa polynucleotide #14065.
 PN US6551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Query Match 5.2%; Score 51.6; DB 11; Length 1311;
 Best Local Similarity 43.9%; Pred. No. 8.5;
 RESULT 461
 ID ABD15601 standard; DNA; 2850 BP.
 DE Pseudomonas aeruginosa polynucleotide #14205.
 PN US6551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Query Match 5.2%; Score 51.6; DB 11; Length 2850;
 Best Local Similarity 43.9%; Pred. No. 8.4;
 RESULT 462
 ID ACA26098 standard; DNA; 2853 BP.
 DE Prokaryotic essential gene #7755.
 PN WO200277183-A2.
 PD 03-OCT-2002.
 PA (ELIT-) ELITRA PHARM INC.
 Query Match 5.2%; Score 51.6; DB 8; Length 2853;
 Best Local Similarity 45.4%; Pred. No. 8.4;
 ID ACa43985 standard; DNA; 2145 BP.
 DE Prokaryotic essential gene #25642.
 PN WO200277183-A2.
 PD 03-OCT-2002.
 PA (ELIT-) ELITRA PHARM INC.
 Query Match 5.2%; Score 51.8; DB 8; Length 2145;
 Best Local Similarity 44.4%; Pred. No. 7.8;
 RESULT 446
 ID AAK94307 standard; cDNA; 2525 BP.
 DE Human full-length cDNA, SEQ ID NO: 2971.
 PN EP1130094-A2.
 PD 05-SEP-2001.
 PA (HELI-) HELIX RES INST.
 Query Match 5.2%; Score 51.8; DB 4; Length 2525;
 Best Local Similarity 43.0%; Pred. No. 7.8;
 RESULT 447
 ID ADL30938 standard; cDNA; 2525 BP.
 DE Full length human cDNA clone SeqID 2971.
 PN EP1396543-A2.
 PD 10-MAR-2004.
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.
 Query Match 5.2%; Score 51.8; DB 12; Length 2525;
 Best Local Similarity 43.0%; Pred. No. 7.8;
 RESULT 448
 ID ABS78645 standard; cDNA; 2597 BP.
 DE Human cDNA encoding CGDD3, INCYTE 3089944CB1.
 PN WO200272830-A2.
 PD 19-SEP-2002.
 PA (INCY-) INCYTE GENOMICS INC.
 Query Match 5.2%; Score 51.8; DB 6; Length 2597;
 Best Local Similarity 43.0%; Pred. No. 7.8;
 RESULT 449
 ID ABX77526 standard; cDNA; 4462 BP.
 DE Differentially expressed breast cancer associated cDNA #21.
 PN US2002156263-A1.
 PD 24-OCT-2002.
 PA (CHEN/) CHEN H.
 Query Match 5.2%; Score 51.8; DB 8; Length 4462;
 Best Local Similarity 45.0%; Pred. No. 7.7;
 RESULT 450
 ID AAS12954 standard; cDNA; 4469 BP.
 DE Human Frizzles Related Protein (FRP-1) cDNA.
 PN WO200164949-A2.
 PD 07-SEP-2001.
 PA (ALCO-) ALCON LAB INC.
 Query Match 5.2%; Score 51.8; DB 4; Length 4469;
 Best Local Similarity 45.0%; Pred. No. 7.7;
 RESULT 451
 ID ABT10165 standard; cDNA; 4469 BP.
 DE Human breast cancer associated coding sequence SEQ ID NO: 299.
 PN WO200259271-A2.
 PD 01-AUG-2002.
 PA (GENE-) GENE LOGIC INC.
 Query Match 5.2%; Score 51.8; DB 6; Length 4469;
 Best Local Similarity 45.0%; Pred. No. 7.7;
 RESULT 452
 ID ABZ34845 standard; cDNA; 4469 BP.
 DE Coding sequence SEQ ID 203, differentially expressed in osteogenesis.
 PN WO200281745-A2.
 PD 17-OCT-2002.
 PA (AVET) AVENTIS PHARMA SA.
 Query Match 5.2%; Score 51.8; DB 8; Length 4469;
 Best Local Similarity 45.0%; Pred. No. 7.7;
 RESULT 453
 ID ADP21417 standard; DNA; 4469 BP.
 DE Gene SFRP1 for screening for cardiac therapeutic preparation.
 PN WO2004050894-A2.
 PD 17-JUN-2004.
 PA (ARTE-) ARTESIAN THERAPEUTICS INC.
 Query Match 5.2%; Score 51.8; DB 12; Length 4469;
 Best Local Similarity 45.0%; Pred. No. 7.7;
 RESULT 454
 ID AAA10594 standard; DNA; 10732 BP.

RESULT 463
ID ABX09933 standard; DNA; 2865 BP.
DE DNA encoding maize Starch synthase Iia.
PN WO200279410-A2.
PD 10-OCT-2002.
PA (BADI) BASF PLANT SCI GMBH.
Query Match 5.2%; Score 51.6; DB 8; Length 2865;
Best Local Similarity 49.6%; Pred. No. 8.4;
RESULT 464
ID ADG75175 standard; DNA; 9369 BP.
DE Human herpesvirus 2 strain HG52 UL36 DNA - SEQ ID 247.
PN WO2003086308-A2.
PD 23-OCT-2003.
PA (CORI-) CORIXA CORP.
Query Match 5.2%; Score 51.6; DB 10; Length 9369;
Best Local Similarity 44.9%; Pred. No. 8.1;
RESULT 465
ID ADG75118 standard; DNA; 9369 BP.
DE Human herpesvirus 2 UL36 ORF DNA - SEQ ID 190.
PN WO2003086308-A2.
PD 23-OCT-2003.
PA (CORI-) CORIXA CORP.
Query Match 5.2%; Score 51.6; DB 10; Length 9369;
Best Local Similarity 44.9%; Pred. No. 8.1;
RESULT 466
ID AAV62154 standard; DNA; 21034 BP.
DE HSV-2 strain SB5 Contig ID 10 DNA sequence.
PN WO9820016-A1.
PD 14-MAY-1998.
PA (SMIK) SMITHKLINE BEECHAM CORP.
Query Match 5.2%; Score 51.6; DB 2; Length 21034;
Best Local Similarity 44.9%; Pred. No. 7.9;
RESULT 467
ID AAV62134 standard; DNA; 26338 BP.
DE HSV-2 strain SB5 Contig ID 104 DNA sequence.
PN WO9820016-A1.
PD 14-MAY-1998.
PA (SMIK) SMITHKLINE BEECHAM CORP.
Query Match 5.2%; Score 51.6; DB 2; Length 26338;
Best Local Similarity 44.9%; Pred. No. 7.9;
RESULT 468
ID ADP64454 standard; DNA; 76994 BP.
DE Sorangium cellulosum disorazole polyketide synthase gene cluster DNA.
PN WO2004053065-A2.
PD 24-JUN-2004.
PA (KOSA-) KOSAN BIOSCIENCES INC.
Query Match 5.2%; Score 51.6; DB 12; Length 76994;
Best Local Similarity 44.5%; Pred. No. 7.6;
RESULT 469
ID AAD54645 standard; DNA; 113193 BP.
DE Streptomyces nodosus amphotericin (amph) biosynthetic gene cluster.
PN WO200297082-A2.
PD 05-DEC-2002.
PA (UYDU-) UNIV COLLEGE DUBLIN.
Query Match 5.2%; Score 51.6; DB 8; Length 113193;
Best Local Similarity 44.0%; Pred. No. 7.6;
RESULT 470
ID AAV62176 standard; DNA; 117213 BP.
DE HSV-2 strain SB5 Contig ID 15 DNA sequence.
PN WO200297082-A2.
PD 05-DEC-2002.
PA (UYDU-) UNIV COLLEGE DUBLIN.
Query Match 5.2%; Score 51.6; DB 2; Length 117213;
Best Local Similarity 44.9%; Pred. No. 7.5;
RESULT 471
ID ABA99457 standard; DNA; 813 BP.
DE Actinoplanes sp DNA encoding acarbose synthase ACBOASP.
PN DE10021667-A1.
PD 08-NOV-2001.
PA (FARB) BAYER AG.
Query Match 5.2%; Score 51.4; DB 6; Length 813;
Best Local Similarity 44.7%; Pred. No. 9.4;
RESULT 472
ID AAZ29167 standard; cDNA; 1106 BP.
DE Rice 4-hydroxyphenylpyruvate dioxygenase partial cDNA.
PN WO200032757-A2.

PD 08-JUN-2000.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 5.2%; Score 51.4; DB 3; Length 1106;
Best Local Similarity 45.0%; Pred. No. 9.3;
RESULT 473
ID ADG36364 standard; DNA; 1197 BP.
DE Weed controller metabolism associated gene SEQ ID NO:232.
PN WO2003040370-A1.
PD 15-MAY-2003.
PA (SUMO) SUMITOMO CHEM CO LTD.
Query Match 5.2%; Score 51.4; DB 10; Length 1197;
Best Local Similarity 43.9%; Pred. No. 9.3;
RESULT 474
ID ADC36374 standard; DNA; 1411 BP.
DE Weed controller metabolism associated gene SEQ ID NO:242.
PN WO2003040370-A1.
PD 15-MAY-2003.
PA (SUMO) SUMITOMO CHEM CO LTD.
Query Match 5.2%; Score 51.4; DB 10; Length 1411;
Best Local Similarity 43.9%; Pred. No. 9.2;
RESULT 475
ID ADJ27276 standard; cDNA; 1926 BP.
DE Mouse HSP70.3 coding sequence.
PN WO2003061684-A2.
PD 31-JUL-2003.
PA (VLA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.
Query Match 5.2%; Score 51.4; DB 11; Length 1926;
Best Local Similarity 44.1%; Pred. No. 9.1;
RESULT 476
ID AAS10678 standard; cDNA; 1929 BP.
DE Murine hsp70 cDNA sequence.
PN WO200151081-A1.
PD 19-JUL-2001.
PA (WHED) WHITEHEAD INST BIOMEDICAL RES.
Query Match 5.2%; Score 51.4; DB 4; Length 1929;
Best Local Similarity 44.1%; Pred. No. 9.1;
RESULT 477
ID ACA23299 standard; DNA; 2307 BP.
DE Prokaryotic essential gene #4956.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.2%; Score 51.4; DB 8; Length 2307;
Best Local Similarity 49.8%; Pred. No. 9.1;
RESULT 478
ID ADQ18001 standard; DNA; 2526 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 818.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 5.2%; Score 51.4; DB 12; Length 2526;
Best Local Similarity 44.1%; Pred. No. 9.1;
RESULT 479
ID ADQ22602 standard; DNA; 2652 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5422.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 5.2%; Score 51.4; DB 12; Length 2652;
Best Local Similarity 44.1%; Pred. No. 9.1;
RESULT 480
ID AAD55818 standard; DNA; 4725 BP.
DE Micronospora carbonacea polyketide synthase (PKS) type I gene #8.
PN CA2391131-A1.
PD 19-NOV-2002.
PA (ECOP-) ECOPIA BIOSCIENCES INC.
Query Match 5.2%; Score 51.4; DB 10; Length 4725;
Best Local Similarity 50.6%; Pred. No. 8.9;
RESULT 481
ID ABZ11709 standard; cDNA; 7847 BP.
DE Human polynucleotide SEQ ID NO 591.
PN WO200270539-A2.

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PD 12-SEP-2002.
PA (HYSE-) HYSE INC.
Query Match 5.2%; Score 51.4; DB 6; Length 7847;
Best Local Similarity 50.2%; Pred. No. 8.8;
RESULT 482
ID ADM44227 standard; cDNA; 7847 BP.
DE Novel human arginine-rich protein cDNA #591.
PN US2004053250-A1.
PD 18-MAR-2004.
PA (TANG/) TANG Y T.
PA (XUEA/) XUE A.
PA (DRNA/) DRMANAC R T.
Query Match 5.2%; Score 51.4; DB 12; Length 7847;
Best Local Similarity 50.2%; Pred. No. 8.8;
RESULT 483
ID ADP90617 standard; DNA; 34719 BP.
DE Micromonospora echinospora gentamycin biosynthesis gene SeqID 1.
PN JP2004180638-A.
PD 02-JUL-2004.
PA (MEIJ) MEIJI SEIKA KAISHA LTD.
Query Match 5.2%; Score 51.4; DB 12; Length 34719;
Best Local Similarity 47.1%; Pred. No. 8.4;
RESULT 484
ID ABA99469 standard; DNA; 38064 BP.
DE Actinoplanes sp SE 50/110 (CBS614.71) DNA encoding acarbose operon.
PN DE10021667-A1.
PD 08-NOV-2001.
PA (PARB) BAYER AG.
Query Match 5.2%; Score 51.4; DB 6; Length 38064;
Best Local Similarity 44.7%; Pred. No. 8.4;
RESULT 485
ID ABX04971 standard; DNA; 103599 BP.
DE S. cinamonensis monensin type I polyketide synthase gene cluster.
PN WO200168867-A1.
PD 20-SEP-2001.
PA (BIOT-) BIOTICA TECHNOLOGY LTD.
Query Match 5.2%; Score 51.4; DB 4; Length 103599;
Best Local Similarity 44.8%; Pred. No. 8.2;
RESULT 486
ID ADP95323 standard; cDNA; 447 BP.
DE Cotton expressed sequence tag, EST, #4334.
PN US2004123338-A1.
PD 24-JUN-2004.
PA (FINC/) FINCHER K L.
Query Match 5.2%; Score 51.2; DB 12; Length 447;
Best Local Similarity 50.8%; Pred. No. 10;
RESULT 487
ID ABZ13934 standard; DNA; 699 BP.
DE Arabidopsis thaliana stress regulated gene SEQ ID NO 1739.
PN WO200216655-A2.
PD 28-FEB-2002.
PA (SCRI) SCRIPPS RES INST.
Query Match 5.2%; Score 51.2; DB 6; Length 699;
Best Local Similarity 47.5%; Pred. No. 10;
RESULT 488
ID ADG87603 standard; cDNA; 699 BP.
DE A. thaliana RPP7/RPP8-upregulated pathogen infection-related gene #45.
PN WO200222675-A2.
PD 21-MAR-2002.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
PA (UYNC-) UNIV NORTH CAROLINA.
PA (GLAZ/) GLAZEBROOK J.
PA (WANG/) WANG X.
PA (DANG/) DANG J L.
PA (EULG/) EULGEM T.
PA (ZHUT/) ZHU T.
Query Match 5.2%; Score 51.2; DB 6; Length 699;
Best Local Similarity 47.5%; Pred. No. 10;
RESULT 489
ID ADG87604 standard; cDNA; 699 BP.
DE A. thaliana RPP7/RPP8-upregulated pathogen infection-related gene #46.
PN WO200222675-A2.
PD 15-JAN-1998.
PD 21-MAR-2002.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
PA (UYNC-) UNIV NORTH CAROLINA.
PA (GLAZ/) GLAZEBROOK J.
PA (WANG/) WANG X.
PA (DANG/) DANG J L.
PA (EULG/) EULGEM T.
PA (ZHUT/) ZHU T.
Query Match 5.2%; Score 51.2; DB 6; Length 699;
Best Local Similarity 47.5%; Pred. No. 10;
RESULT 490
ID ADA67907 standard; DNA; 699 BP.
DE Arabidopsis thaliana gene, SEQ ID 151.
PN WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 5.2%; Score 51.2; DB 8; Length 699;
Best Local Similarity 47.5%; Pred. No. 10;
RESULT 491
ID ABN9073 standard; DNA; 792 BP.
DE Arabidopsis thaliana expressed polynucleotide SEQ ID NO 841.
PN US2002023281-A1.
PD 21-FEB-2002.
PA (GORL/) GORLACH J.
PA (ANYI/) AN Y.
PA (HAMI/) HAMILTON C M.
PA (PRIC/) PRICE J L.
PA (RAIN/) RAINES T M.
PA (YUYI/) YU Y.
PA (RAME/) RAMEKA J G.
PA (PAGE/) PAGE A.
PA (MATH/) MATHAW A V.
PA (LEDF/) LEDFORD B L.
PA (WOES/) WOESSNER J P.
PA (HAAS/) HAAS W D.
PA (GARC/) GARCIA C A.
PA (KRIC/) KRICKER M.
PA (SLAT/) SLATER T.
PA (DAVI/) DAVIS K R.
PA (ALLE/) ALLEN K.
PA (HOFF/) HOFFMAN N.
PA (HURB/) HURBAN P.
Query Match 5.2%; Score 51.2; DB 6; Length 792;
Best Local Similarity 47.5%; Pred. No. 10;
RESULT 492
ID ACA26840 standard; DNA; 1107 BP.
DE Prokaryotic essential gene #8497.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.2%; Score 51.2; DB 8; Length 1107;
Best Local Similarity 45.2%; Pred. No. 10;
RESULT 493
ID AAD55811 standard; DNA; 1683 BP.
DE Micromonospora carbonacea polyketide synthase (PKS) type I gene #1.
PN CA2391131-A1.
PD 19-NOV-2002.
PA (ECOP-) ECOPIA BIOSCIENCES INC.
Query Match 5.2%; Score 51.2; DB 10; Length 1683;
Best Local Similarity 48.3%; Pred. No. 9.9;
RESULT 494
ID AAS54365 standard; DNA; 2034 BP.
DE Pseudomonas aeruginosa DNA for cellular proliferation protein #496.
PN WO200170955-A2.
PD 27-SEP-2001.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.2%; Score 51.2; DB 4; Length 2034;
Best Local Similarity 46.0%; Pred. No. 9.8;
RESULT 495
ID AAV13836 standard; cDNA; 2277 BP.
DE Homo sapiens mammalian codon-optimized telomerase protein p105 gene.
PN WO9801543-A1.
PD 15-JAN-1998.

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PA (TULA-) TULARIK INC.
 Query Match 5.2%; Score 51.2; DB 2; Length 2277;
 Best Local Similarity 46.4%; Pred. No. 9.8;
 RESULT 496
 ID AAV05372 standard; RNA; 2277 BP.
 DE Human telomerase p105 subunit mammalian optimised synthetic RNA.
 PN WO9801542-A1.
 PD 15-JAN-1998.
 PA (REGC) UNIV CALIFORNIA.
 Query Match 5.2%; Score 51.2; DB 2; Length 2277;
 Best Local Similarity 46.4%; Pred. No. 9.8;
 RESULT 497
 ID AAR07385 standard; DNA; 4467 BP.
 DE Heterosigma akashiwo Nat-Atrase gene.
 PN JP2000050874-A.
 PD 22-FEB-2000.
 PA (NORQ) NORINSUISANGSHO KOKUSAI NORIN SUITSANGYO.
 Query Match 5.2%; Score 51.2; DB 3; Length 4467;
 Best Local Similarity 44.1%; Pred. No. 9.6;
 RESULT 498
 ID AAA58471 standard; DNA; 58857 BP.
 DE Nucleotide sequence of the bleomycin (BLM) gene cluster ORFs 8-30.
 PN WO200040704-A1.
 PD 13-JUL-2000.
 PA (REGC) UNIV CALIFORNIA.
 Query Match 5.2%; Score 51.2; DB 3; Length 58857;
 Best Local Similarity 45.2%; Pred. No. 9;
 RESULT 499
 ID ADP03244 standard; DNA; 473 BP.
 DE S. fradiae IF012773 L-glutamine DOI aminotransferase partial DNA.
 PN JP2004089151-A.
 PD 25-MAR-2004.
 PA (TOKD) TOKYO INST TECHNOLOGY.
 Query Match 5.2%; Score 51; DB 12; Length 473;
 Best Local Similarity 44.4%; Pred. No. 11;
 RESULT 500
 ID ABD13343 standard; DNA; 501 BP.
 DE Pseudomonas aeruginosa polynucleotide #11947.
 PN US6551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Query Match 5.2%; Score 51; DB 11; Length 501;
 Best Local Similarity 48.5%; Pred. No. 11;
 RESULT 501
 ID AAV55831 standard; DNA; 799 BP.
 DE Nucleotide sequence of the stabilising sequence-encoding insert.
 PN WO9822577-A1.
 PD 28-MAY-1998.
 PA (MASU/) MASUCCI M G.
 Query Match 5.2%; Score 51; DB 2; Length 799;
 Best Local Similarity 46.1%; Pred. No. 11;
 RESULT 502
 ID ACA37639 standard; DNA; 1497 BP.
 DE Prokaryotic essential gene #1296.
 PN WO20027183-A2.
 PD 03-OCT-2002.
 PA (ELIT-) ELITRA PHARM INC.
 Query Match 5.2%; Score 51; DB 8; Length 1497;
 Best Local Similarity 48.0%; Pred. No. 11;
 RESULT 503
 ID ABD13303 standard; DNA; 1500 BP.
 DE Pseudomonas aeruginosa polynucleotide #11907.
 PN US6551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Query Match 5.2%; Score 51; DB 11; Length 1500;
 Best Local Similarity 48.5%; Pred. No. 11;
 RESULT 504
 ID ADJ40244 standard; cDNA; 1503 BP.
 DE Plant cDNA #1244.
 PN US2004016025-A1.
 PD 22-JAN-2004.
 PA (BUDW/) BUDWORTH P.

PA (MOUG/) MOUGHAMER T.
 PA (BRIG/) BRIGGS S P.
 PA (COOP/) COOPER B.
 PA (GLAZ/) GLAZEBROOK J.
 PA (GOFF/) GOFF S A.
 PA (KATA/) KATAGIRI F.
 PA (KREP/) KREPS J.
 PA (PROV/) PROVART N.
 PA (RICK/) RICHE D.
 PA (ZHUT/) ZHU T.
 Query Match 5.2%; Score 51; DB 12; Length 1503;
 Best Local Similarity 47.6%; Pred. No. 11;
 RESULT 505
 ID AAL44275 standard; DNA; 1632 BP.
 DE Micrococcus luteus crtI gene sequence.
 PN WO200241833-A2.
 PD 30-MAY-2002.
 PA (CRGI) CARGILL INC.
 Query Match 5.2%; Score 51; DB 6; Length 1632;
 Best Local Similarity 42.9%; Pred. No. 11;
 RESULT 506
 ID ADG93408 standard; DNA; 1632 BP.
 DE Maize lipoxxygenase (LOX) DNA #20.
 PN US2003166855-A1.
 PD 04-SEP-2003.
 PA (PION-) PIONEER HI-BRED INT INC.
 Query Match 5.2%; Score 51; DB 10; Length 1632;
 Best Local Similarity 45.9%; Pred. No. 11;
 RESULT 507
 ID AAL61149 standard; DNA; 1713 BP.
 DE Human mutant ARX gene #2.
 PN WO2003045989-A1.
 PD 05-JUN-2003.
 PA (WOME-) WOMEN'S & CHILDREN'S HOSPITAL.
 Query Match 5.2%; Score 51; DB 9; Length 1713;
 Best Local Similarity 46.2%; Pred. No. 11;
 RESULT 508
 ID ADG93406 standard; DNA; 1803 BP.
 DE Maize lipoxxygenase (LOX) DNA #19.
 PN US2003166855-A1.
 PD 04-SEP-2003.
 PA (PION-) PIONEER HI-BRED INT INC.
 Query Match 5.2%; Score 51; DB 10; Length 1803;
 Best Local Similarity 45.9%; Pred. No. 11;
 RESULT 509
 ID AAH26500 standard; cDNA; 2561 BP.
 DE Rabbit low density lipoprotein binding protein 2 (LBP-2) cDNA.
 PN WO200164874-A2.
 PD 07-SEP-2001.
 PA (BOST-) BOSTON HEART FOUND INC.
 Query Match 5.2%; Score 51; DB 5; Length 2561;
 Best Local Similarity 47.3%; Pred. No. 11;
 RESULT 510
 ID ABN85324 standard; cDNA; 2710 BP.
 DE Human cytoskeleton-associated protein, CSAP-15, coding sequence.
 PN WO200253719-A2.
 PD 11-JUL-2002.
 PA (INCY-) INCYTE GENOMICS INC.
 Query Match 5.2%; Score 51; DB 6; Length 2710;
 Best Local Similarity 45.7%; Pred. No. 11;
 RESULT 511
 ID AAL44298 standard; DNA; 6941 BP.
 DE Micrococcus luteus C50 carotenoid producing operon.
 PN WO200241833-A2.
 PD 30-MAY-2002.
 PA (CRGI) CARGILL INC.
 Query Match 5.2%; Score 51; DB 6; Length 6941;
 Best Local Similarity 42.9%; Pred. No. 10;
 RESULT 512
 ID AAQ73500 standard; DNA; 8438 BP.
 DE DNA encoding Pseudorabies virus large latency transcript.
 PN US5352596-A.
 PD 04-OCT-1994.

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PA (USDA) US SEC OF AGRIC.
Query Match 5.1%; Score 50.8; DB 8; Length 1173;
Best Local Similarity 43.9%; Pred. No. 12;
RESULT 522
ID ADJ39706 standard; cDNA; 1173 BP.
DE Plant cDNA #706.
PN US2004016025-A1.
PD 22-JAN-2004.
PA (BUDW/) BUDWORTH P.
PA (MOUG/) MOUGHAMER T.
PA (BRIG/) BRIGGS S P.
PA (COOP/) COOPER B.
PA (GLAZ/) GLAZEBROOK J.
PA (GOFF/) GOFF S A.
PA (KATA/) KATAGIRI F.
PA (KREP/) KREPS J.
PA (PROV/) PROVART N.
PA (RICK/) RICK D.
PA (ZHUT/) ZHU T.
Query Match 5.1%; Score 50.8; DB 12; Length 1173;
Best Local Similarity 43.9%; Pred. No. 12;
RESULT 523
ID AAS51566 standard; DNA; 1317 BP.
DE Pseudomonas aeruginosa DNA for cellular proliferation protein #151.
PN WO200170955-A2.
PD 27-SEP-2001.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.1%; Score 50.8; DB 4; Length 1317;
Best Local Similarity 51.0%; Pred. No. 12;
RESULT 524
ID ACAL9467 standard; DNA; 1317 BP.
DE Prokaryotic essential gene #1124.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.1%; Score 50.8; DB 8; Length 1317;
Best Local Similarity 51.0%; Pred. No. 12;
RESULT 525
ID ADA71150 standard; DNA; 1479 BP.
DE Rice gene, SEQ ID 4473.
PN WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 5.1%; Score 50.8; DB 8; Length 1479;
Best Local Similarity 46.7%; Pred. No. 12;
RESULT 526
ID AAL51696 standard; cDNA; 1682 BP.
DE Argiope trifasciata spider silk protein coding sequence #1.
PN WO200299082-A2.
PD 12-DEC-2002.
PA (UYWV-) UNIV WYOMING.
Query Match 5.1%; Score 50.8; DB 8; Length 1682;
Best Local Similarity 45.8%; Pred. No. 12;
RESULT 527
ID ABS78661 standard; DNA; 5760 BP.
DE M. echinospora DNA encoding PKSE protein.
PN CA2387401-A1.
PD 04-SEP-2002.
PA (ECOP-) ECOPIA BIOSCIENCES INC.
Query Match 5.1%; Score 50.8; DB 6; Length 5760;
Best Local Similarity 45.0%; Pred. No. 11;
RESULT 528
ID ABS63414 standard; cDNA; 508 BP.
DE DNA encoding rice caffeoyl-CoA O-methyltransferase (CCOWT).
PN US2002081693-A1.
PD 27-JUN-2002.
PA (CAHO/) CAHOON R E.
PA (FADE/) FADER G M.
PA (RAFA/) RAFALSKI J A.
Query Match 5.1%; Score 50.6; DB 6; Length 508;
Best Local Similarity 54.6%; Pred. No. 13;
RESULT 529
ID AAF74867 standard; DNA; 1313 BP.
DE Leishmania major PPG nucleotide sequence.

PA (USDA) US SEC OF AGRIC.
Query Match 5.2%; Score 51; DB 2; Length 8438;
Best Local Similarity 44.6%; Pred. No. 10;
RESULT 513
ID ABX56062 standard; DNA; 741 BP.
DE M. echinospora calicheamicin biosynthesis gene orfII.
PN WO200279465-A2.
PD 10-OCT-2002.
PA (SLOK) SLOAN KETERING INST CANCER RES.
Query Match 5.1%; Score 50.8; DB 8; Length 741;
Best Local Similarity 45.8%; Pred. No. 12;
RESULT 514
ID ACA43508 standard; DNA; 1125 BP.
DE Prokaryotic essential gene #25165.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.1%; Score 50.8; DB 8; Length 1125;
Best Local Similarity 50.0%; Pred. No. 12;
RESULT 515
ID AAT91453 standard; DNA; 1155 BP.
DE Mycobacterium tuberculosis antigen Tbra28 encoding DNA.
PN WO9709429-A2.
PD 13-MAR-1997.
PA (CORI-) CORIXA CORP.
Query Match 5.1%; Score 50.8; DB 2; Length 1155;
Best Local Similarity 49.3%; Pred. No. 12;
RESULT 516
ID AAT91517 standard; DNA; 1155 BP.
DE Mycobacterium tuberculosis antigen Tbra28 encoding DNA.
PN WO9709428-A2.
PD 13-MAR-1997.
PA (CORI-) CORIXA CORP.
Query Match 5.1%; Score 50.8; DB 2; Length 1155;
Best Local Similarity 49.3%; Pred. No. 12;
RESULT 517
ID AAV44350 standard; DNA; 1155 BP.
DE Mycobacterium tuberculosis antigen Tbra28 DNA.
PN WO9816645-A2.
PD 23-APR-1998.
PA (CORI-) CORIXA CORP.
Query Match 5.1%; Score 50.8; DB 2; Length 1155;
Best Local Similarity 49.3%; Pred. No. 12;
RESULT 518
ID AAV64458 standard; DNA; 1155 BP.
DE M. tuberculosis immunogenic polypeptide Tbra28 DNA.
PN WO9816646-A2.
PD 23-APR-1998.
PA (CORI-) CORIXA CORP.
Query Match 5.1%; Score 50.8; DB 2; Length 1155;
Best Local Similarity 49.3%; Pred. No. 12;
RESULT 519
ID AAZ19048 standard; DNA; 1155 BP.
DE M. tuberculosis recombinant antigen DNA encoding Tbra28.
PN WO9942118-A2.
PD 26-AUG-1999.
PA (CORI-) CORIXA CORP.
Query Match 5.1%; Score 50.8; DB 2; Length 1155;
Best Local Similarity 49.3%; Pred. No. 12;
RESULT 520
ID AAZ19260 standard; DNA; 1155 BP.
DE M. tuberculosis antigen Tbra28 DNA sequence.
PN WO9942076-A2.
PD 26-AUG-1999.
PA (CORI-) CORIXA CORP.
Query Match 5.1%; Score 50.8; DB 2; Length 1155;
Best Local Similarity 49.3%; Pred. No. 12;
RESULT 521
ID ADA70376 standard; DNA; 1173 BP.
DE Rice gene, SEQ ID 3699.
PN WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.

PN CN1272542-A.
PD 08-NOV-2000.
PA (NANF-) NANFANG RES CENT STATE HUMAN GENE GROUP.
Query Match 5.1%; Score 50.6; DB 4; Length 1313;
Best Local Similarity 47.1%; Pred. No. 13;
RESULT 530
ID ACA37566 standard; DNA; 1371 BP.
DE Prokaryotic essential gene #19223.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.1%; Score 50.6; DB 8; Length 1371;
Best Local Similarity 43.7%; Pred. No. 13;
RESULT 531
ID AA192870 standard; cDNA; 2564 BP.
DE Human polynucleotide SEQ ID NO 12930.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 5.1%; Score 50.6; DB 4; Length 2564;
Best Local Similarity 48.6%; Pred. No. 12;
RESULT 532
ID ADQ21323 standard; DNA; 4233 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 4143.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 5.1%; Score 50.6; DB 12; Length 4233;
Best Local Similarity 47.3%; Pred. No. 12;
RESULT 533
ID ADQ25196 standard; DNA; 4244 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 8016.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 5.1%; Score 50.6; DB 12; Length 4244;
Best Local Similarity 47.3%; Pred. No. 12;
RESULT 534
ID ADJ39239 standard; cDNA; 549 BP.
DE Plant cDNA #239.
PN US2004016025-A1.
PD 22-JAN-2004.
PA (BUDW-) BUDWORTH P.
PA (MOUG-) MOUGHAMER T.
PA (BRIG-) BRIGGS S P.
PA (COOP-) COOPER B.
PA (GLAZ-) GLAZEBROOK J.
PA (GOFF-) GOFF S A.
PA (KATA-) KATAGIRI F.
PA (KREP-) KREPS J.
PA (PROV-) PROVART N.
PA (RICK-) RICHE D.
PA (ZHUT-) ZHU T.
Query Match 5.1%; Score 50.4; DB 12; Length 549;
Best Local Similarity 47.6%; Pred. No. 14;
RESULT 535
ID ABZ66752 standard; DNA; 669 BP.
DE Orthosomycin biosynthetic polynucleotide SEQ ID NO 166.
PN WO200279505-A2.
PD 10-OCT-2002.
PA (ECOP-) ECOPIA BIOSCIENCES INC.
Query Match 5.1%; Score 50.4; DB 10; Length 669;
Best Local Similarity 44.7%; Pred. No. 14;
RESULT 536
ID AAV62138 standard; DNA; 980 BP.
DE HSV-2 strain SB5 Contig ID 53 DNA sequence.
PN WO9820016-A1.
PD 14-MAY-1998.
PA (SMIK-) SMITHKLINE BEECHAM CORP.
Query Match 5.1%; Score 50.4; DB 2; Length 980;
Best Local Similarity 49.0%; Pred. No. 14;
RESULT 537
ID ADI42416 standard; DNA; 1159 BP.
DE Plant transcription factor polynucleotide #544.
PN US2004019927-A1.
PD 29-JAN-2004.
PA (SHER-) SHERMAN B K.
PA (RIEC-) RIECHMANN J L.
PA (JIAN-) JIANG C.
PA (HEAR-) HEARD J B.
PA (HAAK-) HAAKE V.
PA (CREE-) CREELMAN R A.
PA (RATC-) RATCLIFFE O.
PA (ADAM-) ADAM L J.
PA (REUB-) REUBER T L.
PA (KEDD-) KEDDIE J.
PA (BROU-) BROUN P E.
PA (PILG-) PILGRIM M L.
PA (DUBE-) DUBELL A N.
PA (PINE-) PINEDA O.
PA (YUGG-) YU G.
Query Match 5.1%; Score 50.4; DB 12; Length 1159;
Best Local Similarity 47.0%; Pred. No. 14;
RESULT 538
ID ADC36273 standard; DNA; 1209 BP.
DE Weed controller metabolism associated gene SEQ ID NO:141.
PN WO2003040370-A1.
PD 15-MAY-2003.
PA (SUMO-) SUMITOMO CHEM CO LTD.
Query Match 5.1%; Score 50.4; DB 10; Length 1209;
Best Local Similarity 47.0%; Pred. No. 14;
RESULT 539
ID ADC36278 standard; DNA; 1473 BP.
DE Weed controller metabolism associated gene SEQ ID NO:146.
PN WO2003040370-A1.
PD 15-MAY-2003.
PA (SUMO-) SUMITOMO CHEM CO LTD.
Query Match 5.1%; Score 50.4; DB 10; Length 1473;
Best Local Similarity 47.0%; Pred. No. 14;
RESULT 540
ID AAL61177 standard; DNA; 2247 BP.
DE Actinosynnema pretiosum ABC transporter gene.
PN WO2003045312-A2.
PD 05-JUN-2003.
PA (UNIW-) UNIV WASHINGTON.
Query Match 5.1%; Score 50.4; DB 8; Length 2247;
Best Local Similarity 43.7%; Pred. No. 13;
RESULT 541
ID AAF81370 standard; DNA; 6390 BP.
DE Quorum sensing controlled gene qsc107 ORF.
PN WO200118248-A2.
PD 15-MAR-2001.
PA (IOWA-) UNIV IOWA RES FOUND.
PA (QUOR-) QUORUM SCI INC.
Query Match 5.1%; Score 50.4; DB 4; Length 6390;
Best Local Similarity 50.7%; Pred. No. 13;
RESULT 542
ID ABZ75344 standard; DNA; 23673 BP.
DE Human R1128 gene cluster.
PN US6340774-B1.
PD 22-JAN-2002.
PA (STRD-) UNIV LELAND STANFORD JUNIOR.
Query Match 5.1%; Score 50.4; DB 6; Length 23673;
Best Local Similarity 47.7%; Pred. No. 13;
RESULT 543
ID ABZ66808 standard; DNA; 45055 BP.
DE Orthosomycin biosynthetic gene cluster SEQ ID NO 277.
PN WO200279505-A2.
PD 10-OCT-2002.
PA (ECOP-) ECOPIA BIOSCIENCES INC.
Query Match 5.1%; Score 50.4; DB 10; Length 45055;
Best Local Similarity 44.7%; Pred. No. 12;
RESULT 544
Query Match 5.1%; Score 50.4; DB 4; Length 110000;
Best Local Similarity 45.1%; Pred. No. 12;
RESULT 545

ADJ42262 standard; cDNA; 595 BP.
 DE Plant cDNA #3262.
 PN US2004016025-A1.
 PD 22-JAN-2004.
 PA (BUDW/) BUDWORTH P.
 PA (MOUG/) MOUGHAWER T.
 PA (BRIG/) BRIGGS S P.
 PA (COOP/) COOPER B.
 PA (GLAZ/) GLAZEBROOK J.
 PA (GOFF/) GOFF S A.
 PA (KATA/) KATAGIRI F.
 PA (KREP/) KREPS J.
 PA (PROV/) PROVART N.
 PA (RICK/) RIQUE D.
 PA (ZHU/) ZHU T.
 Query Match 5.1%; Score 50.2; DB 12; Length 595;
 Best Local Similarity 50.5%; Pred. No. 15;
 RESULT 546
 ID ACA26748 standard; DNA; 841 BP.
 DE Prokaryotic essential gene #8405.
 PN WO200277183-A2.
 PD 03-OCT-2002.
 PA (ELIT-) ELITRA PHARM INC.
 Query Match 5.1%; Score 50.2; DB 8; Length 841;
 Best Local Similarity 46.7%; Pred. No. 15;
 RESULT 547
 ID ABD12328 standard; DNA; 864 BP.
 DE Pseudomonas aeruginosa polynucleotide #10932.
 PN US6551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Query Match 5.1%; Score 50.2; DB 11; Length 864;
 Best Local Similarity 47.1%; Pred. No. 15;
 RESULT 548
 ID AAF61096 standard; DNA; 1545 BP.
 DE P. putida KT2440-associated DNA ORE11200.
 PN D619335088-A1.
 PD 01-FEB-2001.
 PA (TIGR-) TIGR INST GENOMIC RES.
 PA (QUIA-) QUIAGEN GMBH.
 PA (GBFB) GES BIOTECHNOLOGISCHE FORSCHUNG MBH.
 PA (DKF2-) DKFZ DEUT KREBSFORSCHUNGSZENTRUM.
 PA (MEDI-) MEDIZINISCHE HOCHSCHULE HANNOVER.
 Query Match 5.1%; Score 50.2; DB 4; Length 1545;
 Best Local Similarity 44.2%; Pred. No. 15;
 RESULT 549
 ID ABD12652 standard; DNA; 2211 BP.
 DE Pseudomonas aeruginosa polynucleotide #11256.
 PN US6551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Query Match 5.1%; Score 50.2; DB 11; Length 2211;
 Best Local Similarity 47.1%; Pred. No. 14;
 RESULT 550
 ID ABD12391 standard; DNA; 2289 BP.
 DE Pseudomonas aeruginosa polynucleotide #10995.
 PN US6551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Query Match 5.1%; Score 50.2; DB 11; Length 2289;
 Best Local Similarity 47.1%; Pred. No. 14;
 RESULT 551
 ID AAH14472 standard; cDNA; 3269 BP.
 DE Human cDNA sequence SEQ ID NO:11967.
 PN EP1074617-A2.
 PD 07-FEB-2001.
 PA (HELI-) HELIX RES INST.
 Query Match 5.1%; Score 50.2; DB 4; Length 3269;
 Best Local Similarity 47.6%; Pred. No. 14;
 RESULT 552
 ID AAL61173 standard; DNA; 9975 BP.
 DE Actinosynnema pretiosum polyketide synthase (PKS) gene #4.
 PN WO2003045312-A2.

05-JUN-2003.
 PA (UNIW) UNIV WASHINGTON.
 Query Match 5.1%; Score 50.2; DB 8; Length 9975;
 Best Local Similarity 46.0%; Pred. No. 14;
 RESULT 553
 ID AEX48858 standard; cDNA; 390 BP.
 DE Bovine EST associated with lactation/muscle/fat deposition #14023.
 PN US2002137139-A1.
 PD 26-SEP-2002.
 PA (BYAT/) BYATT J C.
 PA (MATH/) MATHIALAGAN N.
 PA (TAON/) TAO N.
 PA (WARR/) WARREN W C.
 Query Match 5.1%; Score 50; DB 8; Length 390;
 Best Local Similarity 52.2%; Pred. No. 16;
 RESULT 554
 ID AAZ52552 standard; cDNA; 888 BP.
 DE Human secreted protein clone yd61_1 nucleotide sequence SEQ ID NO:155.
 PN WO9958642-A2.
 PD 18-NOV-1999.
 PA (GEMY) GENETICS INST INC.
 Query Match 5.1%; Score 50; DB 3; Length 888;
 Best Local Similarity 49.4%; Pred. No. 16;
 RESULT 555
 ID ADO00480 standard; cDNA; 1149 BP.
 DE Novel human cDNA sequence #1295.
 PN WO2004038003-A2.
 PD 06-MAY-2004.
 PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
 Query Match 5.1%; Score 50; DB 12; Length 1149;
 Best Local Similarity 47.8%; Pred. No. 16;
 RESULT 556
 ID ADN98911 standard; cDNA; 1149 BP.
 DE Novel human cDNA sequence #511.
 PN WO2004038003-A2.
 PD 06-MAY-2004.
 PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
 Query Match 5.1%; Score 50; DB 12; Length 1149;
 Best Local Similarity 47.8%; Pred. No. 16;
 RESULT 557
 ID ACA25880 standard; DNA; 1365 BP.
 DE Prokaryotic essential gene #7537.
 PN WO200277183-A2.
 PD 03-OCT-2002.
 PA (ELIT-) ELITRA PHARM INC.
 Query Match 5.1%; Score 50; DB 8; Length 1365;
 Best Local Similarity 45.4%; Pred. No. 16;
 RESULT 558
 ID ADP28824 standard; DNA; 1470 BP.
 DE Human secreted protein encoding sequence SEQ ID #822.
 PN WO2004035732-A2.
 PD 29-APR-2004.
 PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
 Query Match 5.1%; Score 50; DB 12; Length 1470;
 Best Local Similarity 47.8%; Pred. No. 16;
 RESULT 559
 ID ADI23924 standard; DNA; 1806 BP.
 DE Streptomyces refuineus 024A locus ORF2.
 PN US2003198981-A1.
 PD 23-OCT-2003.
 PA (ECOP-) ECOPIA BIOSCIENCES INC.
 Query Match 5.1%; Score 50; DB 10; Length 1806;
 Best Local Similarity 46.3%; Pred. No. 16;
 RESULT 560
 ID ADG98257 standard; DNA; 1806 BP.
 DE Acyl-specific C-domain DNA #13.
 PN US2003211567-A1.
 PD 13-NOV-2003.
 PA (ECOP-) ECOPIA BIOSCIENCES INC.
 Query Match 5.1%; Score 50; DB 12; Length 1806;
 Best Local Similarity 46.3%; Pred. No. 16;
 RESULT 561
 ID AAZ87297 standard; DNA; 13842 BP.

DE S. venezuelae macrolide biosynthetic gene pikA1, SEQ ID NO:30.
 PN WO20000620-A2.
 PA (MINU) UNIV MINNESOTA.
 Query Match 5.1%; Score 50; DB 3; Length 13842;
 Best Local Similarity 44.7%; Pred. No. 15;
 RESULT 562
 ID ADL1915 standard; DNA; 13842 BP.
 DE Streptomyces macrolide biosynthetic protein (pikR2) coding sequence.
 PN US2003194784-A1.
 PA (SHER/) SHERMAN D H.
 PA (LIUH/) LIU H.
 PA (XUEY/) XUE Y.
 PA (ZHAO/) ZHAO L.
 Query Match 5.1%; Score 50; DB 12; Length 13842;
 Best Local Similarity 44.7%; Pred. No. 15;
 RESULT 563
 ID ADI23898 standard; DNA; 15738 BP.
 DE Streptomyces fradiae A541 locus ORF5.
 PN US2003198981-A1.
 PA (ECOP-) ECOPIA BIOSCIENCES INC.
 Query Match 5.1%; Score 50; DB 10; Length 15738;
 Best Local Similarity 43.1%; Pred. No. 15;
 RESULT 564
 ID ADOS1695 standard; DNA; 32329 BP.
 DE Streptomyces cattleya NRRL 8057 thienamycin biosynthetic gene cluster.
 PN US2004038250-A1.
 PD 26-FEB-2004.
 PA (ASTU-) ASTUR-PHARMA SA.
 PA (UYOV-) UNIV OVIEDO.
 Query Match 5.1%; Score 50; DB 12; Length 32329;
 Best Local Similarity 48.5%; Pred. No. 14;
 RESULT 565
 ID AA287318 standard; DNA; 36778 BP.
 DE S. venezuelae pik (macrolide biosynthesis) gene cluster.
 PN WO20000620-A2.
 PD 06-JAN-2000.
 PA (MINU) UNIV MINNESOTA.
 Query Match 5.1%; Score 50; DB 3; Length 36778;
 Best Local Similarity 44.7%; Pred. No. 14;
 RESULT 566
 ID ADL1933 standard; DNA; 36778 BP.
 DE Streptomyces venezuelae pik gene cluster coding sequence.
 PN US2003194784-A1.
 PD 16-OCT-2003.
 PA (SHER/) SHERMAN D H.
 PA (LIUH/) LIU H.
 PA (XUEY/) XUE Y.
 PA (ZHAO/) ZHAO L.
 Query Match 5.1%; Score 50; DB 12; Length 36778;
 Best Local Similarity 44.7%; Pred. No. 14;
 RESULT 567
 ID ADI23892 standard; DNA; 37360 BP.
 DE Streptomyces fradiae A541 locus contig 2.
 PN US2003198981-A1.
 PD 23-OCT-2003.
 PA (ECOP-) ECOPIA BIOSCIENCES INC.
 Query Match 5.1%; Score 50; DB 10; Length 37360;
 Best Local Similarity 43.1%; Pred. No. 14;
 RESULT 568
 ID AA287285 standard; DNA; 37948 BP.
 DE S. venezuelae pik (macrolide biosynthesis) gene cluster, SEQ ID NO:5.
 PN WO20000620-A2.
 PD 06-JAN-2000.
 PA (MINU) UNIV MINNESOTA.
 Query Match 5.1%; Score 50; DB 3; Length 37948;
 Best Local Similarity 44.7%; Pred. No. 14;
 RESULT 569
 ID AAT75633 standard; DNA; 38506 BP.
 DE Nucleotide sequence of the insert DNA in cosmid pKOS023-27.
 PN US6117659-A.

PD 12-SEP-2000.
 PA (KOSA-) KOSAN BIOSCIENCES INC.
 Query Match 5.1%; Score 50; DB 3; Length 38506;
 Best Local Similarity 44.7%; Pred. No. 14;
 RESULT 570
 ID AA256001 standard; DNA; 38506 BP.
 DE Recombinant cosmid pKOS023-27 containing S. venezuelae PKS genes.
 PN WO9961599-A2.
 PD 02-DEC-1999.
 PA (KOSA-) KOSAN BIOSCIENCES INC.
 Query Match 5.1%; Score 50; DB 3; Length 38506;
 Best Local Similarity 44.7%; Pred. No. 14;
 RESULT 571
 ID ADA09418 standard; DNA; 38506 BP.
 DE Cosmid pKOS023-27 containing S. venezuelae PKS gene cluster.
 PN US6509455-B1.
 PD 21-JAN-2003.
 PA (KOSA-) KOSAN BIOSCIENCES INC.
 Query Match 5.1%; Score 50; DB 8; Length 38506;
 Best Local Similarity 44.7%; Pred. No. 14;
 RESULT 572
 ID ADH53462 standard; DNA; 38506 BP.
 DE S. venezuelae pKOS023-27 cosmid DNA.
 PN US2003162862-A1.
 PD 28-AUG-2003.
 PA (ASHL/) ASHLEY G.
 PA (BETL/) BETLACH M C.
 PA (BETL/) BETLACH M.
 PA (MCDA/) MCDANIEL R.
 PA (TANG/) TANG L.
 Query Match 5.1%; Score 50; DB 10; Length 38506;
 Best Local Similarity 44.7%; Pred. No. 14;
 RESULT 573
 ID ABS56090 standard; DNA; 38506 BP.
 DE S. venezuelae DNA inserted into cosmid pKOS023-27.
 PN WO200297082-A2.
 PD 05-DEC-2002.
 PA (KOSA-) KOSAN BIOSCIENCES INC.
 Query Match 5.1%; Score 50; DB 10; Length 38506;
 Best Local Similarity 44.7%; Pred. No. 14;
 RESULT 574
 ID ABQ74179 standard; DNA; 229354 BP.
 DE Human cytomegalovirus strain AD169 genomic sequence SEQ ID NO:64.
 PN WO200257437-A2.
 PD 25-JUL-2002.
 PA (SCRI) SCRIPPS RES INST.
 Query Match 5.1%; Score 50; DB 6; Length 229354;
 Best Local Similarity 46.1%; Pred. No. 14;
 RESULT 575
 ID ABQ90211 standard; DNA; 825 BP.
 DE M. capsulatus gene #196 for DNA array.
 PN WO200255655-A2.
 PD 18-JUL-2002.
 PA (UNIF-) UNIFOB STIFTELSEN UNIV BERGEN.
 PA (TIGR-) TIGR.
 Query Match 5.0%; Score 49.8; DB 6; Length 825;
 Best Local Similarity 49.2%; Pred. No. 17;
 RESULT 576
 ID ABK34330 standard; cDNA; 856 BP.
 DE Human CDNA for novel secreted protein, SEQ ID 99.
 PN WO200177290-A2.
 PD 18-OCT-2001.
 PA (GEMY) GENETICS INST INC.
 Query Match 5.0%; Score 49.8; DB 6; Length 856;
 Best Local Similarity 50.5%; Pred. No. 17;
 RESULT 577
 ID AB266685 standard; DNA; 1272 BP.
 DE Orthomycin biosynthetic polynucleotide SEQ ID NO 32.
 PN WO200279505-A2.
 PD 10-OCT-2002.
 PA (ECOP-) ECOPIA BIOSCIENCES INC.
 Query Match 5.0%; Score 49.8; DB 10; Length 1272;
 Best Local Similarity 45.5%; Pred. No. 17;

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RESULT 578
ID AAD53025 standard; DNA; 1293 BP.
DE Streptomyces platensis ema9 gene.
PN WO200292801-A2.
PD 21-NOV-2002.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 5.0%; Score 49.8; DB 8; Length 1293;
Best Local Similarity 48.7%; Pred. No. 17;
RESULT 579
ID ACA26585 standard; DNA; 1374 BP.
DE Prokaryotic essential gene #8242.
PN WO20027183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.0%; Score 49.8; DB 8; Length 1374;
Best Local Similarity 51.1%; Pred. No. 17;
RESULT 580
ID ADA70992 standard; DNA; 1458 BP.
DE Rice gene, SEQ ID 4315.
PN WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 5.0%; Score 49.8; DB 8; Length 1458;
Best Local Similarity 48.1%; Pred. No. 17;
RESULT 581
ID ADI27212 standard; DNA; 1581 BP.
DE Rabbit LRP binding family protein DNA #1.
PN WO2003106657-A2.
PD 24-DEC-2003.
PA (STOW-) STOWERS INST MEDICAL RES.
Query Match 5.0%; Score 49.8; DB 12; Length 1581;
Best Local Similarity 46.2%; Pred. No. 17;
RESULT 582
ID ABV94776 standard; cDNA; 1814 BP.
DE Human pancreatic cancer expressed cDNA SEQ ID NO 182.
PN WO200260317-A2.
PD 08-AUG-2002.
PA (CORI-) CORIXA CORP.
Query Match 5.0%; Score 49.8; DB 6; Length 1814;
Best Local Similarity 47.5%; Pred. No. 17;
RESULT 583
ID ADP10373 standard; DNA; 1837 BP.
DE Reference mRNA sequences for marker probe #50.
PN WO2004042346-A2.
PD 21-MAY-2004.
PA (EXPR-) EXPRESSION DIAGNOSTICS INC.
Query Match 5.0%; Score 49.8; DB 12; Length 1837;
Best Local Similarity 47.5%; Pred. No. 17;
RESULT 584
ID AAF26295 standard; DNA; 2048 BP.
DE Pseudomonas sp Type II (xcp) secretion system DNA ORF04962a.
PN WO200107622-A2.
PD 01-FEB-2001.
PA (TIGR-) TIGR INST GENOMIC RES.
PA (QUIA-) QUIAGEN GMBH.
PA (GEFB) GES BIOTECHNOLOGISCHE FORSCHUNG MBH.
PA (DKFZ) DKFZ DEUT KREBSFORSCHUNGSZENTRUM.
PA (MEDI-) MEDIZINISCHE HOCHSCHULE HANNOVER.
Query Match 5.0%; Score 49.8; DB 4; Length 2048;
Best Local Similarity 43.1%; Pred. No. 17;
RESULT 585
ID ADA71072 standard; DNA; 2136 BP.
DE Rice gene, SEQ ID 4395.
PN WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 5.0%; Score 49.8; DB 8; Length 2136;
Best Local Similarity 47.8%; Pred. No. 17;
RESULT 586
ID AB161822 standard; DNA; 2520 BP.
DE Colon adenocarcinoma related gene sequence SEQ ID NO:159.
PN WO200194629-A2.
PD 13-DEC-2001.

PA (AVAL-) AVALON PHARM.
Query Match 5.0%; Score 49.8; DB 6; Length 2520;
Best Local Similarity 48.7%; Pred. No. 17;
RESULT 587
ID ABK84011 standard; cDNA; 2520 BP.
DE Human cDNA differentially expressed in granulocytic cells #582.
PN WO200228999-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 5.0%; Score 49.8; DB 6; Length 2520;
Best Local Similarity 48.7%; Pred. No. 17;
RESULT 588
ID ABD16186 standard; DNA; 3003 BP.
DE Pseudomonas aeruginosa polynucleotide #14790.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.0%; Score 49.8; DB 11; Length 3003;
Best Local Similarity 49.1%; Pred. No. 17;
RESULT 589
ID AAD28566 standard; DNA; 3113 BP.
DE Herpes simplex virus type 2 UL46fragF11F5 DNA.
PN WO200202131-A2.
PD 10-JAN-2002.
PA (CORI-) CORIXA CORP.
Query Match 5.0%; Score 49.8; DB 6; Length 3113;
Best Local Similarity 43.8%; Pred. No. 17;
RESULT 590
ID ADG74980 standard; DNA; 3113 BP.
DE Human herpesvirus 2 isolated clone insert DNA - SEQ ID 52.
PN WO2003086308-A2.
PD 23-OCT-2003.
PA (CORI-) CORIXA CORP.
Query Match 5.0%; Score 49.8; DB 10; Length 3113;
Best Local Similarity 43.8%; Pred. No. 17;
RESULT 591
ID ABD15936 standard; DNA; 3132 BP.
DE Pseudomonas aeruginosa polynucleotide #14540.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.0%; Score 49.8; DB 11; Length 3132;
Best Local Similarity 49.1%; Pred. No. 17;
RESULT 592
ID AAT86704 standard; DNA; 3147 BP.
DE DNA encoding thermostable esterase Tspa E101.
PN WO9725058-A1.
PD 17-JUL-1997.
PA (THER-) THERMOGEN INC.
Query Match 5.0%; Score 49.8; DB 2; Length 3147;
Best Local Similarity 46.4%; Pred. No. 17;
RESULT 593
ID AAS03399 standard; DNA; 3147 BP.
DE Thermus DNA encoding a thermostable esterase, Tspa/E101.
PN US6218163-B1.
PD 17-APR-2003.
PA (THER-) THERMOGEN INC.
Query Match 5.0%; Score 49.8; DB 4; Length 3147;
Best Local Similarity 46.4%; Pred. No. 17;
RESULT 594
ID RAD28565 standard; DNA; 3345 BP.
DE Herpes simplex virus type 2 full length HSV-2 UL37 gene.
PN WO200202131-A2.
PD 10-JAN-2002.
PA (CORI-) CORIXA CORP.
Query Match 5.0%; Score 49.8; DB 6; Length 3345;
Best Local Similarity 43.8%; Pred. No. 17;
RESULT 595
ID ADG75117 standard; DNA; 3345 BP.
DE Human herpesvirus 2 UL37 ORF DNA - SEQ ID 189.
PN WO2003086308-A2.
PD 23-OCT-2003.
PA (CORI-) CORIXA CORP.

Query Match 5.0%; Score 49.8; DB 10; Length 3345;
Best Local Similarity 43.8%; Pred. No. 17;
RESULT 596
ID ADG74977 standard; DNA; 3345 BP.
DE Human herpesvirus 2 UL37 DNA - SEQ ID 49.
PN WO2003086308-A2.
PD 23-OCT-2003.
PA (CORI-) CORIXA CORP.
Query Match 5.0%; Score 49.8; DB 10; Length 3345;
Best Local Similarity 43.8%; Pred. No. 17;
RESULT 597
ID ABD16219 standard; DNA; 3411 BP.
DE Pseudomonas aeruginosa polynucleotide #14823.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.0%; Score 49.8; DB 11; Length 3411;
Best Local Similarity 49.1%; Pred. No. 17;
RESULT 598
ID AD085407 standard; DNA; 3540 BP.
DE Streptomyces Phox/Phor operon containing DNA fragment, seq id 1.
PN FR2848567-A1.
PD 18-JUN-2004.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 5.0%; Score 49.8; DB 12; Length 3540;
Best Local Similarity 44.5%; Pred. No. 17;
RESULT 599
ID AAV62148 standard; DNA; 3663 BP.
DE HSV-2 strain SB5 Contig ID 94 DNA sequence.
PN WO9820016-A1.
PD 14-MAY-1998.
PA (SMIK) SMITHKLINE BEECHAM CORP.
Query Match 5.0%; Score 49.8; DB 2; Length 3663;
Best Local Similarity 43.8%; Pred. No. 17;
RESULT 600
ID AC38707 standard; DNA; 4323 BP.
DE Prokaryotic essential gene #20364.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.0%; Score 49.8; DB 8; Length 4323;
Best Local Similarity 43.3%; Pred. No. 17;
RESULT 601
ID AD085409 standard; DNA; 4440 BP.
DE Streptomyces phor:omegaac mutant, seq id 4.
PN FR2848567-A1.
PD 18-JUN-2004.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 5.0%; Score 49.8; DB 12; Length 4440;
Best Local Similarity 44.5%; Pred. No. 16;
RESULT 602
ID ABZ66810 standard; DNA; 37116 BP.
DE Orthosomycin biosynthetic gene cluster SEQ ID NO 279.
PN WO200279505-A2.
PD 10-OCT-2002.
PA (ECOP-) ECOPIA BIOSCIENCES INC.
Query Match 5.0%; Score 49.8; DB 10; Length 37116;
Best Local Similarity 45.5%; Pred. No. 16;
RESULT 603
ID AAD17184 standard; DNA; 65140 BP.
DE Streptomyces noursei nys1 DNA of nystatin PKS gene cluster.
PN WO200159126-A2.
PD 16-AUG-2001.
PA (UVNO-) UNIV NORGES TEKNISK NATURVITENSKAPELIGE.
PA (SNTF) SINTEF STIFTELSEN IND TEK FORSK.
PA (ALPH-) ALPHARMA AS.
PA (SINV-) SINVENT AS.
PA (DZIE/) DZIEGLEWSKA H.
PA (ZOTC/) ZOTCHEV S B.
PA (SEKU/) SEKUROVA O N.
PA (FJAE/) FJAEVRIK E.
PA (BRAU/) BRAUTASET T.
PA (STRO/) STROM A R.

PA (VALL/) VALLA S.
Query Match 5.0%; Score 49.8; DB 4; Length 65140;
Best Local Similarity 46.4%; Pred. No. 15;
RESULT 604
ID AAD17186 standard; DNA; 125401 BP.
DE Streptomyces noursei nystatin PKS gene cluster DNA.
PN WO200159126-A2.
PD 16-AUG-2001.
PA (UVNO-) UNIV NORGES TEKNISK NATURVITENSKAPELIGE.
PA (SNTF) SINTEF STIFTELSEN IND TEK FORSK.
PA (ALPH-) ALPHARMA AS.
PA (SINV-) SINVENT AS.
PA (DZIE/) DZIEGLEWSKA H.
PA (ZOTC/) ZOTCHEV S B.
PA (SEKU/) SEKUROVA O N.
PA (FJAE/) FJAEVRIK E.
PA (BRAU/) BRAUTASET T.
PA (STRO/) STROM A R.
PA (VALL/) VALLA S.
Query Match 5.0%; Score 49.8; DB 4; Length 125401;
Best Local Similarity 46.4%; Pred. No. 15;
RESULT 605
ID ABO03617 standard; DNA; 678 BP.
DE Pseudomonas aeruginosa polynucleotide #2221.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.0%; Score 49.6; DB 11; Length 678;
Best Local Similarity 44.8%; Pred. No. 19;
RESULT 606
ID ABO03778 standard; DNA; 753 BP.
DE Pseudomonas aeruginosa polynucleotide #2382.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.0%; Score 49.6; DB 11; Length 753;
Best Local Similarity 44.8%; Pred. No. 19;
RESULT 607
ID ACA45724 standard; DNA; 1362 BP.
DE Prokaryotic essential gene #27381.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.0%; Score 49.6; DB 8; Length 1362;
Best Local Similarity 48.3%; Pred. No. 18;
RESULT 608
ID ADB58045 standard; DNA; 1531 BP.
DE Toxicity-related gene, SEQ ID 3071.
PN WO2003064624-A2.
PD 07-AUG-2003.
PA (GENE-) GENE LOGIC INC.
Query Match 5.0%; Score 49.6; DB 10; Length 1531;
Best Local Similarity 47.2%; Pred. No. 18;
RESULT 609
ID ADB52519 standard; DNA; 1531 BP.
DE Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:3061.
PN WO2003065993-A2.
PD 14-AUG-2003.
PA (GENE-) GENE LOGIC INC.
Query Match 5.0%; Score 49.6; DB 10; Length 1531;
Best Local Similarity 47.2%; Pred. No. 18;
RESULT 610
ID AAQ13305 standard; DNA; 1591 BP.
DE Rat catechol-O-methyltransferase gene.
PN WO9111513-A.
PD 08-AUG-1991.
PA (ORIN) ORION YHTYMAE OY.
Query Match 5.0%; Score 49.6; DB 2; Length 1591;
Best Local Similarity 47.2%; Pred. No. 18;
RESULT 611
ID ADG75153 standard; DNA; 1765 BP.
DE Human herpesvirus 2 isolated clone insert DNA - SEQ ID 225.
PN WO2003086308-A2.

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PD 23-OCT-2003.
PA (CORI-) CORIXA CORP. 5.0%; Score 49.6; DB 10; Length 1765;
Query Match 45.6%; Pred. No. 18;
Best Local Similarity 44.7%; Pred. No. 18;
RESULT 612
ID AAS51445 standard; DNA; 2040 BP.
DE Pseudomonas aeruginosa DNA for cellular proliferation protein #30.
PN WO200170955-A2.
PD 27-SEP-2001.
PA (ELIT-) ELITRA PHARM INC. 5.0%; Score 49.6; DB 4; Length 2040;
Query Match 44.6%; Pred. No. 18;
Best Local Similarity 44.6%; Pred. No. 18;
RESULT 613
ID ACA19446 standard; DNA; 2040 BP.
DE Prokaryotic essential gene #1103.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC. 5.0%; Score 49.6; DB 8; Length 2040;
Query Match 44.6%; Pred. No. 18;
Best Local Similarity 44.6%; Pred. No. 18;
RESULT 614
ID ADM03489 standard; cDNA; 2218 BP.
DE Human cDNA of the invention SEQ ID NO:2174.
PN EP1347046-A1.
PD 24-SEP-2003.
PA (REAS-) RES ASSOC BIOTECHNOLOGY. 5.0%; Score 49.6; DB 11; Length 2218;
Query Match 43.5%; Pred. No. 18;
Best Local Similarity 43.5%; Pred. No. 18;
RESULT 615
ID ABZ35021 standard; cDNA; 2271 BP.
DE Human gene expression profile polynucleotide SEQ ID NO 133.
PN WO200274979-A2.
PD 26-SEP-2002.
PA (ORTH) ORTHO CLINICAL DIAGNOSTICS INC. 5.0%; Score 49.6; DB 6; Length 2271;
Query Match 47.2%; Pred. No. 18;
Best Local Similarity 47.2%; Pred. No. 18;
RESULT 616
ID ADR75311 standard; cDNA; 2487 BP.
DE Prostate cancer marker cDNA.
PN WO2003009814-A2.
PD 06-FEB-2003.
PA (MILL-) MILLENNIUM PHARM INC. 5.0%; Score 49.6; DB 10; Length 2487;
Query Match 47.2%; Pred. No. 18;
Best Local Similarity 47.2%; Pred. No. 18;
RESULT 617
ID AAS51581 standard; DNA; 2742 BP.
DE Pseudomonas aeruginosa DNA for cellular proliferation protein #166.
PN WO200170955-A2.
PD 27-SEP-2001.
PA (ELIT-) ELITRA PHARM INC. 5.0%; Score 49.6; DB 4; Length 2742;
Query Match 44.8%; Pred. No. 18;
Best Local Similarity 44.8%; Pred. No. 18;
RESULT 618
ID ACA19538 standard; DNA; 2742 BP.
DE Prokaryotic essential gene #1195.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC. 5.0%; Score 49.6; DB 8; Length 2742;
Query Match 44.8%; Pred. No. 18;
Best Local Similarity 44.8%; Pred. No. 18;
RESULT 619
ID ABD03933 standard; DNA; 2814 BP.
DE Pseudomonas aeruginosa polynucleotide #2537.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP. 5.0%; Score 49.6; DB 11; Length 2814;
Query Match 44.8%; Pred. No. 18;
Best Local Similarity 44.8%; Pred. No. 18;
RESULT 620
ID ADJ67856 standard; DNA; 3729 BP.
DE T. thermophilus dnaE gene.
PN US2004038289-A1.
PD 26-FEB-2004.

PA (ODON/) O'DONNELL M E. 5.0%; Score 49.6; DB 12; Length 3729;
PA (YUZH/) YUZHAKOV A. 44.7%; Pred. No. 18;
PA (YURI/) YURIEVA O. 5.0%; Score 49.6; DB 12; Length 3729;
PA (JERU/) JERUZALMI D. 44.7%; Pred. No. 18;
PA (BRUC/) BRUCK I. 5.0%; Score 49.6; DB 12; Length 3729;
PA (KURI/) KURIYAN J. 44.7%; Pred. No. 18;
Query Match 44.7%; Pred. No. 18;
Best Local Similarity 44.7%; Pred. No. 18;
RESULT 621
ID ADJ68068 standard; DNA; 3729 BP.
DE T. thermophilus dnaE gene.
PN US2004038290-A1.
PD 26-FEB-2004.
PA (ODON/) O'DONNELL M E. 5.0%; Score 49.6; DB 12; Length 3729;
PA (YUZH/) YUZHAKOV A. 44.7%; Pred. No. 18;
PA (YURI/) YURIEVA O. 5.0%; Score 49.6; DB 12; Length 3729;
PA (JERU/) JERUZALMI D. 44.7%; Pred. No. 18;
PA (BRUC/) BRUCK I. 5.0%; Score 49.6; DB 12; Length 3729;
PA (KURI/) KURIYAN J. 44.7%; Pred. No. 18;
Query Match 44.7%; Pred. No. 18;
Best Local Similarity 44.7%; Pred. No. 18;
RESULT 622
ID ADK01146 standard; DNA; 3729 BP.
DE DNA polymerase III-type enzyme subunit DNA #6.
PN US2004043415-A1.
PD 04-MAR-2004.
PA (ODON/) O'DONNELL M E. 5.0%; Score 49.6; DB 12; Length 3729;
PA (YUZH/) YUZHAKOV A. 44.7%; Pred. No. 18;
PA (YURI/) YURIEVA O. 5.0%; Score 49.6; DB 12; Length 3729;
PA (JERU/) JERUZALMI D. 44.7%; Pred. No. 18;
PA (BRUC/) BRUCK I. 5.0%; Score 49.6; DB 12; Length 3729;
PA (KURI/) KURIYAN J. 44.7%; Pred. No. 18;
Query Match 44.7%; Pred. No. 18;
Best Local Similarity 44.7%; Pred. No. 18;
RESULT 623
ID ADJ79365 standard; DNA; 3729 BP.
DE T. thermophilus dnaE gene.
PN US2004043414-A1.
PD 04-MAR-2004.
PA (ODON/) O'DONNELL M E. 5.0%; Score 49.6; DB 12; Length 3729;
PA (YUZH/) YUZHAKOV A. 44.7%; Pred. No. 18;
PA (YURI/) YURIEVA O. 5.0%; Score 49.6; DB 12; Length 3729;
PA (JERU/) JERUZALMI D. 44.7%; Pred. No. 18;
PA (BRUC/) BRUCK I. 5.0%; Score 49.6; DB 12; Length 3729;
PA (KURI/) KURIYAN J. 44.7%; Pred. No. 18;
Query Match 44.7%; Pred. No. 18;
Best Local Similarity 44.7%; Pred. No. 18;
RESULT 624
ID ADJ84805 standard; DNA; 3729 BP.
DE T. thermophilus DNA polymerase III alpha subunit gene.
PN US2004048309-A1.
PD 11-MAR-2004.
PA (ODON/) O'DONNELL M E. 5.0%; Score 49.6; DB 12; Length 3729;
PA (YUZH/) YUZHAKOV A. 44.7%; Pred. No. 18;
PA (YURI/) YURIEVA O. 5.0%; Score 49.6; DB 12; Length 3729;
PA (JERU/) JERUZALMI D. 44.7%; Pred. No. 18;
PA (BRUC/) BRUCK I. 5.0%; Score 49.6; DB 12; Length 3729;
PA (KURI/) KURIYAN J. 44.7%; Pred. No. 18;
Query Match 44.7%; Pred. No. 18;
Best Local Similarity 44.7%; Pred. No. 18;
RESULT 625
ID ADM77593 standard; DNA; 3729 BP.
DE DNA polymerase III-type enzyme related polynucleotide #4.
PN US2004077012-A1.
PD 22-APR-2004.
PA (ODON/) O'DONNELL M E. 5.0%; Score 49.6; DB 12; Length 3729;
PA (YUZH/) YUZHAKOV A. 44.7%; Pred. No. 18;
PA (YURI/) YURIEVA O. 5.0%; Score 49.6; DB 12; Length 3729;
PA (JERU/) JERUZALMI D. 44.7%; Pred. No. 18;
PA (BRUC/) BRUCK I. 5.0%; Score 49.6; DB 12; Length 3729;
PA (KURI/) KURIYAN J. 44.7%; Pred. No. 18;
Query Match 44.7%; Pred. No. 18;
Best Local Similarity 44.7%; Pred. No. 18;

RESULT 626
 ID ADM66260 standard; DNA; 3729 BP.
 DE T. thermophilus dnaE gene.
 PN US2004081995-A1.
 PD 29-APR-2004.
 PA (ODON/) O'DONNELL M E.
 PA (YUZH/) YUZHAKOV A.
 PA (YURI/) YURIEVA O.
 PA (JERU/) JERUZALMI D.
 PA (BRUC/) BRUCK I.
 PA (KURI/) KURIYAN J.
 Query Match 5.0%; Score 49.6; DB 12; Length 3729;
 Best Local Similarity 44.7%; Pred. No. 18;
 RESULT 627
 ID ADO04313 standard; DNA; 3729 BP.
 DE T. thermophilus DNA polymerase III dnaE gene.
 PN US2004106137-A1.
 PD 03-JUN-2004.
 PA (ODON/) O'DONNELL M E.
 PA (YUZH/) YUZHAKOV A.
 PA (YURI/) YURIEVA O.
 PA (JERU/) JERUZALMI D.
 PA (BRUC/) BRUCK I.
 PA (KURI/) KURIYAN J.
 Query Match 5.0%; Score 49.6; DB 12; Length 3729;
 Best Local Similarity 44.7%; Pred. No. 18;
 RESULT 628
 ID ADP82390 standard; DNA; 3729 BP.
 DE Thermus thermophilus dnaE gene.
 PN US2004110210-A1.
 PD 10-JUN-2004.
 PA (ODON/) O'DONNELL M E.
 PA (YUZH/) YUZHAKOV A.
 PA (YURI/) YURIEVA O.
 PA (JERU/) JERUZALMI D.
 PA (BRUC/) BRUCK I.
 PA (KURI/) KURIYAN J.
 Query Match 5.0%; Score 49.6; DB 12; Length 3729;
 Best Local Similarity 44.7%; Pred. No. 18;
 RESULT 629
 ID ABN59919 standard; cDNA; 5080 BP.
 DE Novel human coding sequence SEQ ID NO: 330.
 PN WO200222660-A2.
 PD 21-MAR-2002.
 PA (HYSE-) HYSEQ INC.
 Query Match 5.0%; Score 49.6; DB 6; Length 5080;
 Best Local Similarity 44.2%; Pred. No. 18;
 RESULT 630
 ID ADP82340 standard; DNA; 5081 BP.
 DE Leukaemia-related DNA sequence #2896.
 PN WO2003039443-A2.
 PD 15-MAY-2003.
 PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
 PA (UYLU-) UNIV LUDWIG MAXIMILIANS.
 PA (HAFE-) HAFERLACH T.
 PA (SCHO/) SCHOCH C.
 PA (KERN/) KERN W.
 Query Match 5.0%; Score 49.6; DB 10; Length 5081;
 Best Local Similarity 44.2%; Pred. No. 18;
 RESULT 631
 ID AB668935 standard; DNA; 5181 BP.
 DE Kidney cancer related gene sequence SEQ ID NO:7272.
 PN WO200194629-A2.
 PD 13-DEC-2001.
 PA (AVAL-) AVALON PHARM.
 Query Match 5.0%; Score 49.6; DB 6; Length 5181;
 Best Local Similarity 47.2%; Pred. No. 18;
 RESULT 632
 ID ADJ11677 standard; DNA; 951 BP.
 DE Rice DNA modulated by post-transcriptional gene silencing SeqID 313.
 PN US2003135888-A1.
 PD 17-JUL-2003.
 PA (ZHUT/) ZHU T.
 PA (WANG/) WANG X.
 PA (CHAN/) CHANG H.
 PA (BRIG/) BRIGGS S P.
 PA (COOP/) COOPER B.
 PA (GLAZ/) GLAZEBROOK J.
 PA (GOFF/) GOFF S A.
 PA (KATA/) KATAGIRI F.
 PA (KREP/) KREPS J.
 PA (MOUG/) MOUGHAMER T.
 PA (PROV/) PROVART N.
 PA (RICK/) RICKE D.
 Query Match 5.0%; Score 49.4; DB 11; Length 951;
 Best Local Similarity 44.3%; Pred. No. 20;
 RESULT 633
 ID AB237556 standard; DNA; 1029 BP.
 DE Streptomyces viridochromogenes AviG74 encoding polynucleotide.
 PN WO200268436-A1.
 PD 06-SEP-2002.
 PA (COMB-) COMBINATURE BIOPHARM AG.
 Query Match 5.0%; Score 49.4; DB 8; Length 1029;
 Best Local Similarity 47.8%; Pred. No. 20;
 RESULT 634
 ID ADP88594 standard; DNA; 1149 BP.
 DE Human POU domain factor Brn3a gene exon 2.
 PN WO2004052186-A2.
 PD 24-JUN-2004.
 PA (FORS-) FORSYTH INST.
 Query Match 5.0%; Score 49.4; DB 12; Length 1149;
 Best Local Similarity 46.7%; Pred. No. 20;
 RESULT 635
 ID ACA38093 standard; DNA; 1173 BP.
 DE Prokaryotic essential gene #19750.
 PN WO200277183-A2.
 PD 03-OCT-2002.
 PA (ELIT-) ELITRA PHARM INC.
 Query Match 5.0%; Score 49.4; DB 8; Length 1173;
 Best Local Similarity 45.2%; Pred. No. 20;
 RESULT 636
 ID ACA27337 standard; DNA; 1191 BP.
 DE Prokaryotic essential gene #8994.
 PN WO200277183-A2.
 PD 03-OCT-2002.
 PA (ELIT-) ELITRA PHARM INC.
 Query Match 5.0%; Score 49.4; DB 8; Length 1191;
 Best Local Similarity 53.8%; Pred. No. 20;
 RESULT 637
 ID AAX09010 standard; cDNA; 1272 BP.
 DE Brn-3a polynucleotide.
 PN WO9905272-A1.
 PD 04-FEB-1999.
 PA (UNLO) UNIV COLLEGE LONDON.
 Query Match 5.0%; Score 49.4; DB 2; Length 1272;
 Best Local Similarity 46.7%; Pred. No. 20;
 RESULT 638
 ID AAZ9006 standard; cDNA; 1272 BP.
 DE Human transcription factor Brn-3a coding sequence.
 PN WO20034466-A1.
 PD 15-JUN-2000.
 PA (UNLO) UNIV COLLEGE LONDON.
 Query Match 5.0%; Score 49.4; DB 3; Length 1272;
 Best Local Similarity 46.7%; Pred. No. 20;
 RESULT 639
 ID ADM80093 standard; DNA; 1398 BP.
 DE Spiramycin biosynthesis orf13c, SEQ ID 60.
 PN FR2845394-A1.
 PD 09-APR-2004.
 PA (AVET) AVENTIS PHARMA SA.
 PA (CNRS) CNRS CENT NAT RECH SCI.
 Query Match 5.0%; Score 49.4; DB 12; Length 1398;
 Best Local Similarity 45.0%; Pred. No. 20;
 RESULT 640
 ID ADN97609 standard; DNA; 1398 BP.
 DE S ambofaciens spiramycin biosynthetic gene ORF13c.

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PN WO2004033689-A2.
PD 22-APR-2004.
PA (AVET ) AVENTIS PHARMA SA.
PA (CNRS ) CNRS.
Query Match 5.0%; Score 49.4; DB 12; Length 1398;
Best Local Similarity 45.0%; Pred. No. 20;
RESULT 641
ID ABD01548 standard; DNA; 1419 BP.
DE Pseudomonas aeruginosa polynucleotide #152.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.0%; Score 49.4; DB 11; Length 1419;
Best Local Similarity 46.2%; Pred. No. 20;
RESULT 642
ID ACA40703 standard; DNA; 1587 BP.
DE Prokaryotic essential gene #22360.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.0%; Score 49.4; DB 8; Length 1587;
Best Local Similarity 47.6%; Pred. No. 20;
RESULT 643
ID ACA38400 standard; DNA; 1590 BP.
DE Prokaryotic essential gene #20057.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.0%; Score 49.4; DB 8; Length 1590;
Best Local Similarity 47.6%; Pred. No. 20;
RESULT 644
ID ABD01553 standard; DNA; 1692 BP.
DE Pseudomonas aeruginosa polynucleotide #157.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.0%; Score 49.4; DB 11; Length 1692;
Best Local Similarity 46.2%; Pred. No. 20;
RESULT 645
ID ABD01582 standard; DNA; 1698 BP.
DE Pseudomonas aeruginosa polynucleotide #186.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.0%; Score 49.4; DB 11; Length 1698;
Best Local Similarity 46.2%; Pred. No. 20;
RESULT 646
ID AAT40082 standard; DNA; 1724 BP.
DE M. tuberculosis RNA polymerase Group I sigma subunit sigA gene.
PN GB2298862-A.
PD 18-SEP-1996.
PA (ASTR ) ASTRA AB.
Query Match 5.0%; Score 49.4; DB 2; Length 1724;
Best Local Similarity 47.6%; Pred. No. 20;
RESULT 647
ID ADG75006 standard; DNA; 2091 BP.
DE Human herpesvirus 2 UL47 DNA - SEQ ID 78.
PN WO2003086308-A2.
PD 23-OCT-2003.
PA (CORI-) CORIXA CORP.
Query Match 5.0%; Score 49.4; DB 10; Length 2091;
Best Local Similarity 45.8%; Pred. No. 20;
RESULT 648
ID ADG75154 standard; DNA; 2091 BP.
DE Human herpesvirus 2 strain HG52 UL47 DNA - SEQ ID 226.
PN WO2003086308-A2.
PD 23-OCT-2003.
PA (CORI-) CORIXA CORP.
Query Match 5.0%; Score 49.4; DB 10; Length 2091;
Best Local Similarity 45.8%; Pred. No. 20;
RESULT 649
ID ADG75015 standard; DNA; 2118 BP.
DE Human herpesvirus 2 UL47 coding region DNA - SEQ ID 87.
PN WO2003086308-A2.
PD 23-OCT-2003.
PA (CORI-) CORIXA CORP.
Query Match 5.0%; Score 49.4; DB 10; Length 2118;
Best Local Similarity 45.8%; Pred. No. 20;
RESULT 650
ID ADG75014 standard; DNA; 2211 BP.
DE Human herpesvirus 2 UL47-His construct DNA - SEQ ID 86.
PN WO2003086308-A2.
PD 23-OCT-2003.
PA (CORI-) CORIXA CORP.
Query Match 5.0%; Score 49.4; DB 10; Length 2211;
Best Local Similarity 45.8%; Pred. No. 20;
RESULT 651
ID AAV22682 standard; DNA; 2214 BP.
DE New DNA sequence isolated from Pinctada fucata.
PN JPI0080285-A.
PD 31-MAR-1998.
PA (MIKI-) MIKIMOTO SEIYAKU KK.
Query Match 5.0%; Score 49.4; DB 2; Length 2214;
Best Local Similarity 47.1%; Pred. No. 20;
RESULT 652
ID ADC30095 standard; cDNA; 2382 BP.
DE Human novel cDNA sequence, SEQ ID NO:177.
PN WO2003029271-A2.
PD 10-APR-2003.
PA (HYSE-) HYSEQ INC.
Query Match 5.0%; Score 49.4; DB 10; Length 2382;
Best Local Similarity 45.6%; Pred. No. 20;
RESULT 653
ID ACA30032 standard; DNA; 2502 BP.
DE Prokaryotic essential gene #11689.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.0%; Score 49.4; DB 8; Length 2502;
Best Local Similarity 55.6%; Pred. No. 20;
RESULT 654
ID AAQ92657 standard; DNA; 2745 BP.
DE Virulence determinant rpoV gene.
PN WO9517511-A2.
PD 29-JUN-1995.
PA (AGRE-) AGRESEARCH NEW ZEALAND PASTORAL AGRIC.
PA (YESH ) UNIV YESHIVA EINSTEIN COLLEGE.
Query Match 5.0%; Score 49.4; DB 2; Length 2745;
Best Local Similarity 47.6%; Pred. No. 19;
RESULT 655
ID AAQ92656 standard; DNA; 2745 BP.
DE Virulence determinant rpoV gene.
PN WO9517511-A2.
PD 29-JUN-1995.
PA (AGRE-) AGRESEARCH NEW ZEALAND PASTORAL AGRIC.
PA (YESH ) UNIV YESHIVA EINSTEIN COLLEGE.
Query Match 5.0%; Score 49.4; DB 2; Length 2745;
Best Local Similarity 47.6%; Pred. No. 19;
RESULT 656
ID AAV38109 standard; DNA; 2745 BP.
DE Mycobacterium bovis large ORF WAG200 DNA sequence.
PN US5783386-A.
PD 21-JUL-1998.
PA (YESH ) UNIV YESHIVA EINSTEIN COLLEGE.
PA (AGRE-) AGRESEARCH NEW ZEALAND PASTORAL AGRIC.
Query Match 5.0%; Score 49.4; DB 2; Length 2745;
Best Local Similarity 47.6%; Pred. No. 19;
RESULT 657
ID AAV38108 standard; DNA; 2745 BP.
DE Mycobacterium bovis virulence restoring DNA sequence.
PN US5783386-A.
PD 21-JUL-1998.
PA (YESH ) UNIV YESHIVA EINSTEIN COLLEGE.
PA (AGRE-) AGRESEARCH NEW ZEALAND PASTORAL AGRIC.
Query Match 5.0%; Score 49.4; DB 2; Length 2745;
Best Local Similarity 47.6%; Pred. No. 19;
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RESULT 658
 ID AAS14697 standard; DNA; 3038 BP.
 DE Human CDNA encoding neuroendocrine VGF.
 PN WO200174298-A2.
 PD 11-OCT-2001.
 PA (UYBR-) UNIV BROWN RESEARCH FOUND.
 PA (HUGH-) HUGHES HOWARD MED INST.
 Query Match 5.0%; Score 49.4; DB 4; Length 3038;
 Best Local Similarity 44.2%; Pred. No. 19;
 RESULT 659
 ID ADD14800 standard; cDNA; 3038 BP.
 DE Human src biomarker polynucleotide SEQ ID NO:194.
 PN WO2003062395-A2.
 PD 31-JUL-2003.
 PA (BRIM-) BRISTOL-MYERS SQUIBB CO.
 Query Match 5.0%; Score 49.4; DB 10; Length 3038;
 Best Local Similarity 44.2%; Pred. No. 19;
 RESULT 660
 ID AAV22683 standard; cDNA to mRNA; 3331 BP.
 DE New DNA sequence isolated from Pinctada fucata.
 PN JP10080285-A.
 PD 31-MAR-1998.
 PA (MIKI-) MIKIMOTO SEIYAKU KK.
 Query Match 5.0%; Score 49.4; DB 2; Length 3331;
 Best Local Similarity 47.1%; Pred. No. 19;
 RESULT 661
 ID AA232021 standard; DNA; 3331 BP.
 DE Human METH1 related EST D86074.
 PN WO9937660-A1.
 PD 29-JUL-1999.
 PA (IRUE/) IRUELA-ARISPE L.
 PA (HAST/) HASTINGS G A.
 PA (RUBE/) RUBEN S M.
 Query Match 5.0%; Score 49.4; DB 2; Length 3331;
 Best Local Similarity 47.1%; Pred. No. 19;
 RESULT 662
 ID AAC90078 standard; DNA; 3331 BP.
 DE D86074 cDNA clone.
 PN WO200071577-A1.
 PD 30-NOV-2000.
 PA (HUMA-) HUMAN GENOME SCI INC.
 PA (SMIK-) SMITHKLINE BEECHAM CORP.
 PA (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
 PA (IRUE/) IRUELA-ARISPE L.
 PA (HAST/) HASTINGS G A.
 PA (RUBE/) RUBEN S M.
 PA (JONA/) JONAK Z L.
 PA (TRUL/) TRULLI S H.
 PA (FORN/) FORNWALD J A.
 PA (TERR/) TERRETT J A.
 Query Match 5.0%; Score 49.4; DB 5; Length 3331;
 Best Local Similarity 47.1%; Pred. No. 19;
 RESULT 663
 ID AA30290 standard; DNA; 3489 BP.
 DE Kaposi's sarcoma-associated herpesvirus LANA gene.
 PN WO20029626-A1.
 PD 25-MAY-2000.
 PA (KIEF/) KIEFF E D.
 PA (BALL/) BALLESTAS M E.
 PA (KAYE/) KAYE K M.
 Query Match 5.0%; Score 49.4; DB 3; Length 3489;
 Best Local Similarity 42.9%; Pred. No. 19;
 RESULT 664
 ID AAF82901 standard; DNA; 3489 BP.
 DE Nucleotide sequence of KSHV tethering protein, LANA.
 PN WO200125484-A2.
 PD 12-APR-2001.
 PA (UNMI-) UNIV MICHIGAN.
 Query Match 5.0%; Score 49.4; DB 4; Length 3489;
 Best Local Similarity 42.9%; Pred. No. 19;
 RESULT 665
 ID ABA93487 standard; DNA; 3489 BP.
 DE Kaposi's sarcoma-associated herpesvirus LANA protein encoding DNA.

PN US6322792-B1.
 PD 27-NOV-2001.
 PA (KIEF/) KIEFF E D.
 Query Match 5.0%; Score 49.4; DB 6; Length 3489;
 Best Local Similarity 42.9%; Pred. No. 19;
 RESULT 666
 ID ADJ65095 standard; DNA; 3489 BP.
 DE HHV8 DNA encoding latency-associated nuclear antigen, LANA.
 PN US2004037847-A1.
 PD 26-FEB-2004.
 PA (KIEF/) KIEFF E D.
 PA (BALL/) BALLESTAS M E.
 PA (KAYE/) KAYE K M.
 Query Match 5.0%; Score 49.4; DB 12; Length 3489;
 Best Local Similarity 42.9%; Pred. No. 19;
 RESULT 667
 ID ACA27005 standard; DNA; 4255 BP.
 DE Prokaryotic essential gene #8662.
 PN WO200277183-A2.
 PD 03-OCT-2002.
 PA (ELIT-) ELITRA PHARM INC.
 Query Match 5.0%; Score 49.4; DB 8; Length 4255;
 Best Local Similarity 45.5%; Pred. No. 19;
 RESULT 668
 ID AAV33912 standard; cDNA; 4524 BP.
 DE Nucleotide sequence of the SIAx DP2-64 (Oct-T1) gene.
 PN WO9849299-A1.
 PD 05-NOV-1998.
 PA (LUDW-) LUDWIG INST CANCER RES.
 Query Match 5.0%; Score 49.4; DB 2; Length 4524;
 Best Local Similarity 47.5%; Pred. No. 19;
 RESULT 669
 ID AAV62152 standard; DNA; 10211 BP.
 DE HSV-2 strain SB5 Contig ID 99 DNA sequence.
 PN WO9820016-A1.
 PD 14-MAY-1998.
 PA (SMIK-) SMITHKLINE BEECHAM CORP.
 Query Match 5.0%; Score 49.4; DB 2; Length 10211;
 Best Local Similarity 45.8%; Pred. No. 19;
 RESULT 670
 ID ABV93363 standard; DNA; 14061 BP.
 DE Human NOV13b coding sequence.
 PN WO200272771-A2.
 PD 19-SEP-2002.
 PA (CURA-) CURAGEN CORP.
 Query Match 5.0%; Score 49.4; DB 6; Length 14061;
 Best Local Similarity 44.7%; Pred. No. 19;
 RESULT 671
 ID AAV73805 standard; DNA; 32207 BP.
 DE KSHV LUR DNA (nucleotides 105,301-137,507).
 PN US5849564-A.
 PD 15-DEC-1998.
 PA (UYCO-) UNIV COLUMBIA NEW YORK.
 Query Match 5.0%; Score 49.4; DB 2; Length 32207;
 Best Local Similarity 42.9%; Pred. No. 18;
 RESULT 672
 ID ADO51695 standard; DNA; 32329 BP.
 DE Streptomyces cattleya NRRL 8057 thienamycin biosynthetic gene cluster.
 PN US2004038250-A1.
 PD 26-FEB-2004.
 PA (ASTU-) ASTUR-PHARMA SA.
 PA (UYOV-) UNIV OVIEDO.
 Query Match 5.0%; Score 49.4; DB 12; Length 32329;
 Best Local Similarity 44.7%; Pred. No. 18;
 RESULT 673
 ID AB237516 standard; DNA; 59816 BP.
 DE Streptomyces viridochromogenes Avi gene cluster sense strand.
 PN WO200268436-A1.
 PD 06-SEP-2002.
 PA (COMB-) COMBINATURE BIOPHARM AG.
 Query Match 5.0%; Score 49.4; DB 8; Length 59816;
 Best Local Similarity 47.8%; Pred. No. 18;
 RESULT 674

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ID ABZ37515 standard; DNA; 59816 BP.
DE Streptomyces viridochromogenes Avi gene cluster sense strand.
PN WO200268436-A1.
PD 06-SEP-2002.
PA (COMB-) COMBINATURE BIOPHARM AG.
Query Match 5.0%; Score 49.4; DB 8; Length 59816;
Best Local Similarity 47.8%; Pred. No. 18;
RESULT 675
ID ABX04971 standard; DNA; 103599 BP.
DE S. cinnamomensis monensin type I polyketide synthase gene cluster.
PN WO200168867-A1.
PD 20-SEP-2001.
PA (BIOT-) BIOTICA TECHNOLOGY LTD.
Query Match 5.0%; Score 49.4; DB 4; Length 103599;
Best Local Similarity 47.8%; Pred. No. 18;
RESULT 676
ID AAS08693 standard; DNA; 109519 BP.
DE Micromonospora DNA encoding biosynthetic enzymes for Evernimycin.
PN WO9804576-A1.
PD 03-FEB-1998.
PA (UYCO) UNIV COLUMBIA NEW YORK.
Query Match 5.0%; Score 49.4; DB 2; Length 137507;
Best Local Similarity 42.9%; Pred. No. 17;
RESULT 680
ID ADN12162 standard; DNA; 137508 BP.
DE Human herpesvirus 8.
PN WO2004027036-A2.
PD 01-APR-2004.
PA (UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
Query Match 5.0%; Score 49.4; DB 12; Length 137508;
Best Local Similarity 42.9%; Pred. No. 17;
RESULT 681
ID ABD17309 standard; DNA; 789 BP.
DE Pseudomonas aeruginosa polynucleotide #15913.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.0%; Score 49.2; DB 11; Length 789;
Best Local Similarity 48.3%; Pred. No. 22;
RESULT 682
ID ABD13248 standard; DNA; 795 BP.
DE Pseudomonas aeruginosa polynucleotide #11852.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.0%; Score 49.2; DB 11; Length 795;
Best Local Similarity 46.1%; Pred. No. 22;
RESULT 683
ID ABD17908 standard; DNA; 888 BP.
DE Pseudomonas aeruginosa polynucleotide #16512.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.0%; Score 49.2; DB 11; Length 888;
Best Local Similarity 50.7%; Pred. No. 22;
RESULT 684
ID AAS72681 standard; cDNA; 1074 BP.
DE DNA encoding novel human diagnostic protein #8485.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC. 5.0%; Score 49.2; DB 5; Length 1074;
Query Match

Best Local Similarity 42.4%; Pred. No. 22;
RESULT 685
ID ABD12927 standard; DNA; 1221 BP.
DE Pseudomonas aeruginosa polynucleotide #11531.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.0%; Score 49.2; DB 11; Length 1221;
Best Local Similarity 46.1%; Pred. No. 22;
RESULT 686
ID ABD15054 standard; DNA; 1263 BP.
DE Pseudomonas aeruginosa polynucleotide #13658.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.0%; Score 49.2; DB 11; Length 1263;
Best Local Similarity 45.6%; Pred. No. 22;
RESULT 687
ID ABD14863 standard; DNA; 1263 BP.
DE Pseudomonas aeruginosa polynucleotide #13467.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.0%; Score 49.2; DB 11; Length 1263;
Best Local Similarity 45.6%; Pred. No. 22;
RESULT 688
ID AAX09011 standard; cDNA; 1266 BP.
DE Brn-3a polynucleotide.
PN WO9905272-A1.
PD 04-FEB-1999.
PA (UNLO) UNIV COLLEGE LONDON.
Query Match 5.0%; Score 49.2; DB 2; Length 1266;
Best Local Similarity 47.4%; Pred. No. 22;
RESULT 689
ID AAA29007 standard; cDNA; 1266 BP.
DE Murine transcription factor Brn-3a coding sequence.
PN WO200034466-A1.
PD 15-JUN-2000.
PA (UNLO) UNIV COLLEGE LONDON.
Query Match 5.0%; Score 49.2; DB 3; Length 1266;
Best Local Similarity 47.4%; Pred. No. 22;
RESULT 690
ID ABD17488 standard; DNA; 1512 BP.
DE Pseudomonas aeruginosa polynucleotide #16092.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.0%; Score 49.2; DB 11; Length 1512;
Best Local Similarity 50.7%; Pred. No. 21;
RESULT 691
ID ABD17174 standard; DNA; 1521 BP.
DE Pseudomonas aeruginosa polynucleotide #15778.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.0%; Score 49.2; DB 11; Length 1521;
Best Local Similarity 48.3%; Pred. No. 21;
RESULT 692
ID ABD17253 standard; DNA; 1569 BP.
DE Pseudomonas aeruginosa polynucleotide #15857.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.0%; Score 49.2; DB 11; Length 1569;
Best Local Similarity 48.3%; Pred. No. 21;
RESULT 693
ID AAD11112 standard; DNA; 1602 BP.
DE Human small cell lung cancer associated gene, ZIC2.
PN WO200153349-A2.
PD 26-JUL-2001.
PA (LUDW-) LUDWIG INST CANCER RES.
PA (SLOK) SLOAN KETTERING INST CANCER RES.
PA (CORR) CORNELL RES FOUND INC.

Query Match 5.0%; Score 49.2; DB 4; Length 1602;
 Best Local Similarity 53.0%; Pred. No. 21;
 RESULT 694
 ID AAS61863 standard; cDNA; 1602 BP.
 DE Lung small cell carcinoma antigen, cDNA #404.
 PN WO200177168-A2.
 PD 18-OCT-2001.
 PA (CORI-) CORIXA CORP.
 Query Match 5.0%; Score 49.2; DB 6; Length 1602;
 Best Local Similarity 53.0%; Pred. No. 21;
 RESULT 695
 ID ADD15207 standard; DNA; 1602 BP.
 DE DNA encoding the human zinc finger protein ZIC2.
 PN WO2003039490-A2.
 PD 15-MAY-2003.
 PA (UYTE-) UNIV OFFICE TECHNOLOGY LICENSING STANFORD.
 Query Match 5.0%; Score 49.2; DB 10; Length 1602;
 Best Local Similarity 53.0%; Pred. No. 21;
 RESULT 696
 ID ADQ03085 standard; DNA; 1713 BP.
 DE P. aeruginosa virulence gene, VIR17.
 PN US2004122212-A1.
 PD 24-JUN-2004.
 PA (COSS/) COSSON P.
 PA (KOH/) KOHLER T.
 PA (BENG/) BENGHEZAL M.
 PA (MARC/) MARCHETTI A.
 PA (DELD/) DELDEN C V.
 Query Match 5.0%; Score 49.2; DB 12; Length 1713;
 Best Local Similarity 43.8%; Pred. No. 21;
 RESULT 697
 ID ADP98591 standard; DNA; 2160 BP.
 DE Murine class V POU transcription factor Brn3a gene.
 PN WO2004052186-A2.
 PD 24-JUN-2004.
 PA (FORS-) FORSYTH INST.
 Query Match 5.0%; Score 49.2; DB 12; Length 2160;
 Best Local Similarity 47.4%; Pred. No. 21;
 RESULT 698
 ID ABD17387 standard; DNA; 2400 BP.
 DE Pseudomonas aeruginosa polynucleotide #15991.
 PN US6551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Query Match 5.0%; Score 49.2; DB 11; Length 2400;
 Best Local Similarity 50.7%; Pred. No. 21;
 RESULT 699
 ID ABK63479 standard; cDNA; 2455 BP.
 DE Rat sequence differentially expressed in response to a hepatotoxin #1386.
 PN WO200210453-A2.
 PD 07-FEB-2002.
 PA (GENE-) GENE LOGIC INC.
 Query Match 5.0%; Score 49.2; DB 6; Length 2455;
 Best Local Similarity 43.7%; Pred. No. 21;
 RESULT 700
 ID ADB58687 standard; DNA; 2455 BP.
 DE Toxicity-related gene, SEQ ID 3713.
 PN WO2003064624-A2.
 PD 07-AUG-2003.
 PA (GENE-) GENE LOGIC INC.
 Query Match 5.0%; Score 49.2; DB 10; Length 2455;
 Best Local Similarity 43.7%; Pred. No. 21;
 RESULT 701
 ID ADB53374 standard; DNA; 2455 BP.
 DE Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:3916.
 PN WO2003065993-A2.
 PD 14-AUG-2003.
 PA (GENE-) GENE LOGIC INC.
 Query Match 5.0%; Score 49.2; DB 10; Length 2455;
 Best Local Similarity 43.7%; Pred. No. 21;
 RESULT 702
 ID ADF30464 standard; cDNA; 2455 BP.
 DE Rat angiogenesis modulating protein cDNA #9.

PN US2003162706-A1.
 PD 28-AUG-2003.
 PA (PROC) PROCTER & GAMBLE CO.
 Query Match 5.0%; Score 49.2; DB 10; Length 2455;
 Best Local Similarity 43.7%; Pred. No. 21;
 RESULT 703
 ID ABT42262 standard; DNA; 2455 BP.
 DE Toxicity modelling related rat gene SEQ ID NO 1964.
 PN WO200295000-A2.
 PD 28-NOV-2002.
 PA (GENE-) GENE LOGIC INC.
 Query Match 5.0%; Score 49.2; DB 10; Length 2455;
 Best Local Similarity 43.7%; Pred. No. 21;
 RESULT 704
 ID ADP72601 standard; DNA; 2455 BP.
 DE Renal toxin progression gene marker #1190.
 PN WO2004048598-A2.
 PD 10-JUN-2004.
 PA (GENE-) GENE LOGIC INC.
 Query Match 5.0%; Score 49.2; DB 12; Length 2455;
 Best Local Similarity 43.7%; Pred. No. 21;
 RESULT 705
 ID ADE25609 standard; cDNA; 2607 BP.
 DE Human cDNA differentially expressed in foam cells #13.
 PN US2003194721-A1.
 PD 16-OCT-2003.
 PA (INCY-) INCYTE GENOMICS INC.
 Query Match 5.0%; Score 49.2; DB 10; Length 2607;
 Best Local Similarity 42.4%; Pred. No. 21;
 RESULT 706
 ID ADK70215 standard; cDNA; 2680 BP.
 DE Human oesophageal cancer antigen cDNA SEQ ID NO:11.
 PN JP2003259872-A.
 PD 16-SEP-2003.
 PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
 Query Match 5.0%; Score 49.2; DB 12; Length 2680;
 Best Local Similarity 53.0%; Pred. No. 21;
 RESULT 707
 ID ADQ25191 standard; DNA; 2717 BP.
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 8011.
 PN WO2004048938-A2.
 PD 10-JUN-2004.
 PA (PROT-) PROTEIN DESIGN LABS INC.
 Query Match 5.0%; Score 49.2; DB 12; Length 2717;
 Best Local Similarity 53.0%; Pred. No. 21;
 RESULT 708
 ID ABA02191 standard; cDNA; 3318 BP.
 DE Human C/EBP alpha-encoding cDNA.
 PN US6306655-B1.
 PD 23-OCT-2001.
 PA (ISIS-) ISIS PHARM INC.
 Query Match 5.0%; Score 49.2; DB 6; Length 3318;
 Best Local Similarity 42.4%; Pred. No. 21;
 RESULT 709
 ID ADI39068 standard; DNA; 3597 BP.
 DE S. coelicolor meth DNA.
 PN WO2003087386-A2.
 PD 23-OCT-2003.
 PA (BADI) BASF AG.
 Query Match 5.0%; Score 49.2; DB 10; Length 3597;
 Best Local Similarity 47.0%; Pred. No. 21;
 RESULT 710
 ID ADI39145 standard; DNA; 8787 BP.
 DE Plasmid pCPHadh meth_Sc DNA.
 PN WO2003087386-A2.
 PD 23-OCT-2003.
 PA (BADI) BASF AG.
 Query Match 5.0%; Score 49.2; DB 10; Length 8787;
 Best Local Similarity 47.0%; Pred. No. 20;
 RESULT 711
 ID ABI50991 standard; DNA; 35133 BP.
 DE Thermus caldophilus GK24 cosmid clone 3 nucleotide sequence.
 PN KR2001019888-A.

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PA (OTOG-) OTOGENE AG.
Query Match 5.0%; Score 49; DB 6; Length 1355;
Best Local Similarity 50.2%; Pred. No. 23;
RESULT 721
ID AAH26499 standard; DNA; 1614 BP.
DE Human low density lipoprotein binding protein 2 (LBP-2) DNA.
PN WO200164874-A2.
PD 07-SEP-2001.
PA (BOST-) BOSTON HEART FOUND INC.
Query Match 5.0%; Score 49; DB 5; Length 1614;
Best Local Similarity 43.7%; Pred. No. 23;
RESULT 722
ID ABS58306 standard; cDNA; 1852 BP.
DE Spider dragline cDNA repetitive nucleotide sequence.
PN US2002137211-A1.
PD 26-SEP-2002.
PA (YISI-) UNIV SICHUAN TIANYOU BIOLOGIC ENG CO LTD.
Query Match 5.0%; Score 49; DB 10; Length 1852;
Best Local Similarity 46.6%; Pred. No. 23;
RESULT 723
ID ADM47862 standard; DNA; 1891 BP.
DE Polynucleotide sequence #280 useful in producing transgenic plants.
PN US2003233670-A1.
PD 18-DEC-2003.
PA (EDGE/) EDGERTON M D.
PA (CHOM/) CHOMET P S.
PA (LACC/) LACCETTI L B.
Query Match 5.0%; Score 49; DB 12; Length 1891;
Best Local Similarity 50.6%; Pred. No. 23;
RESULT 724
ID ADA71938 standard; DNA; 2000 BP.
DE Rice gene, SEQ ID 5263.
PN WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 5.0%; Score 49; DB 8; Length 2000;
Best Local Similarity 9.7%; Pred. No. 23;
RESULT 725
ID AAH98717 standard; cDNA; 4486 BP.
DE Human EST-derived coding sequence SEQ ID NO: 574.
PN WO200154477-A2.
PD 02-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 5.0%; Score 49; DB 4; Length 4486;
Best Local Similarity 47.5%; Pred. No. 22;
RESULT 726
ID AAV62153 standard; DNA; 7361 BP.
DE HSV-2 strain SB5 Contig ID 1 DNA sequence.
PN WO9820016-A1.
PD 14-MAY-1998.
PA (SMIK) SMITHKLINE BEECHAM CORP.
Query Match 5.0%; Score 49; DB 2; Length 7361;
Best Local Similarity 42.8%; Pred. No. 22;
RESULT 727
ID AAV62130 standard; DNA; 8952 BP.
DE HSV-2 strain SB5 Contig ID 100 DNA sequence.
PN WO9820016-A1.
PD 14-MAY-1998.
PA (SMIK) SMITHKLINE BEECHAM CORP.
Query Match 5.0%; Score 49; DB 2; Length 8952;
Best Local Similarity 42.8%; Pred. No. 22;
RESULT 728
ID AAL61171 standard; DNA; 9222 BP.
DE Actinosynnema pretiosum polyketide synthase (PKS) gene #2.
PN WO2003045312-A2.
PD 05-JUN-2003.
PA (UNIW) UNIV WASHINGTON.
Query Match 5.0%; Score 49; DB 8; Length 9222;
Best Local Similarity 46.0%; Pred. No. 22;
RESULT 729
ID AAH26495 standard; DNA; 12425 BP.
DE Human low density lipoprotein binding protein 2 (LBP-2) gene.
PN WO200164874-A2.

PA (KORE-) KOREA RES INST BIOSCIENCE & BIOTECHNOLOG.
Query Match 5.0%; Score 49.2; DB 4; Length 35133;
Best Local Similarity 44.4%; Pred. No. 20;
RESULT 712
ID ABL50990 standard; DNA; 35134 BP.
DE Thermus caldophilus GK24 cosmid clone 3 SEQ ID NO.1.
PN KR2001019888-A.
PD 15-MAR-2001.
PA (KORE-) KOREA RES INST BIOSCIENCE & BIOTECHNOLOG.
Query Match 5.0%; Score 49.2; DB 4; Length 35134;
Best Local Similarity 44.4%; Pred. No. 20;
RESULT 713
ID ADP74816 standard; DNA; 137560 BP.
DE Parapoxvirus ovis genome DNA sequence SeqID1.
DE Parapoxvirus ovis genome DNA sequence SeqID1.
Query Match 5.0%; Score 49.2; DB 12; Length 137560;
Best Local Similarity 44.9%; Pred. No. 19;
RESULT 714
ID AAA68100 standard; DNA; 399 BP.
DE E. grandis caffeoyl CoA methyl transferase DNA sequence SEQ ID NO.193.
PN WO200022099-A1.
PD 20-APR-2000.
PA (GENE-) GENESIS RES & DEV CORP LTD.
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.
Query Match 5.0%; Score 49; DB 3; Length 399;
Best Local Similarity 57.5%; Pred. No. 24;
RESULT 715
ID ADD41850 standard; DNA; 399 BP.
DE Caffeoyl CoA methyl transferase DNA #1.
PN US2003131373-A1.
PD 10-JUL-2003.
PA (BLOK/) BLOKSBERG L N.
PA (HAVU/) HAVUKKALA I.
Query Match 5.0%; Score 49; DB 10; Length 399;
Best Local Similarity 57.5%; Pred. No. 24;
RESULT 716
ID ACA37827 standard; DNA; 717 BP.
DE Prokaryotic essential gene #19484.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.0%; Score 49; DB 8; Length 717;
Best Local Similarity 44.8%; Pred. No. 24;
RESULT 717
ID ABX56042 standard; DNA; 843 BP.
DE M. echinospora calicheamicin biosynthesis gene calR.
PN WO200279465-A2.
PD 10-OCT-2002.
PA (SLOK) SLOAN KETTERING INST CANCER RES.
Query Match 5.0%; Score 49; DB 8; Length 843;
Best Local Similarity 47.9%; Pred. No. 23;
RESULT 718
ID AAZ51697 standard; DNA; 1044 BP.
DE Burkholderia cepacia recA gene (1).
PN WO200014274-A1.
PD 16-MAR-2000.
PA (UYBR-) UNIV BRITISH COLUMBIA.
Query Match 5.0%; Score 49; DB 3; Length 1044;
Best Local Similarity 43.8%; Pred. No. 23;
RESULT 719
ID AAT44494 standard; cDNA; 1355 BP.
DE Murine cyclin-dependent kinase inhibitor p57KIP2 cDNA.
PN WO9631534-A1.
PD 10-OCT-1996.
PA (SLOK) SLOAN KETTERING INST CANCER RES.
Query Match 5.0%; Score 49; DB 2; Length 1355;
Best Local Similarity 50.2%; Pred. No. 23;
RESULT 720
ID AAI72395 standard; cDNA; 1355 BP.
DE P57-KIP2 cDNA.
PN WO200204605-A2.
PD 17-JAN-2002.
PA (OTOG-) OTOGENE USA INC.

PD 07-SEP-2001.
PA (BOST-) BOSTON HEART FOUND INC.
Query Match 5.0%; Score 49; DB 5; Length 12425;
Best Local Similarity 43.7%; Pred. No. 22;
RESULT 730
ID AAA14651 standard; DNA; 77536 BP.
DE Nucleotide sequence of the FK-520 biosynthetic gene cluster.
Query Match 5.0%; Score 49; DB 3; Length 77536;
Best Local Similarity 44.4%; Pred. No. 21;
RESULT 731
Query Match 5.0%; Score 49; DB 4; Length 110000;
Best Local Similarity 50.6%; Pred. No. 21;
RESULT 732
Query Match 5.0%; Score 49; DB 4; Length 110000;
Best Local Similarity 45.0%; Pred. No. 21;
RESULT 733
Query Match 5.0%; Score 49; DB 4; Length 110000;
Best Local Similarity 45.0%; Pred. No. 21;
RESULT 734
ID AAV62176 standard; DNA; 117213 BP.
DE HSV-2 strain SB5 Contig ID 15 DNA sequence.
Query Match 5.0%; Score 49; DB 2; Length 117213;
Best Local Similarity 42.8%; Pred. No. 20;
RESULT 735
ID ABD09003 standard; DNA; 852 BP.
DE Pseudomonas aeruginosa polynucleotide #7607.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 4.9%; Score 48.8; DB 11; Length 852;
Best Local Similarity 49.2%; Pred. No. 25;
RESULT 736
ID ABD10213 standard; DNA; 1083 BP.
DE Pseudomonas aeruginosa polynucleotide #8817.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 4.9%; Score 48.8; DB 11; Length 1083;
Best Local Similarity 50.3%; Pred. No. 25;
RESULT 737
ID ADC36141 standard; DNA; 1188 BP.
DE Weed controller metabolism associated gene SEQ ID NO:8.
PN WO2003040370-A1.
PD 15-MAY-2003.
PA (SUMO) SUMITOMO CHEM CO LTD.
Query Match 4.9%; Score 48.8; DB 10; Length 1188;
Best Local Similarity 47.1%; Pred. No. 25;
RESULT 738
ID ACF06125 standard; DNA; 1194 BP.
DE Bacterial P450 enzyme encoding DNA SEQ ID NO:33.
PN WO2003052050-A2.
PD 26-JUN-2003.
PA (DIVE-) DIVERSA CORP.
Query Match 4.9%; Score 48.8; DB 9; Length 1194;
Best Local Similarity 44.8%; Pred. No. 25;
RESULT 739
ID AAS09830 standard; DNA; 1209 BP.
DE Pseudorabies virus DNA encoding glycoprotein 50, gp50.
PN US6251634-B1.
PD 26-JUN-2001.
PA (PHAA) PHARMACIA & UPJOHN CO.
Query Match 4.9%; Score 48.8; DB 4; Length 1209;
Best Local Similarity 44.9%; Pred. No. 25;
RESULT 740
ID ABD10628 standard; DNA; 1227 BP.
DE Pseudomonas aeruginosa polynucleotide #9232.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 4.9%; Score 48.8; DB 11; Length 1227;
Best Local Similarity 50.3%; Pred. No. 25;
RESULT 741
ID ABZ66800 standard; DNA; 1272 BP.

DE Orthosomycin biosynthetic polynucleotide SEQ ID NO 262.
PN WO200279505-A2.
PD 10-OCT-2002.
PA (ECOP-) ECOPIA BIOSCIENCES INC.
Query Match 4.9%; Score 48.8; DB 10; Length 1272;
Best Local Similarity 47.6%; Pred. No. 25;
RESULT 742
ID ABD10546 standard; DNA; 1296 BP.
DE Pseudomonas aeruginosa polynucleotide #9150.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 4.9%; Score 48.8; DB 11; Length 1296;
Best Local Similarity 50.3%; Pred. No. 25;
RESULT 743
ID ADC36144 standard; DNA; 1418 BP.
DE Weed controller metabolism associated gene SEQ ID NO:11.
PN WO2003040370-A1.
PD 15-MAY-2003.
PA (SUMO) SUMITOMO CHEM CO LTD.
Query Match 4.9%; Score 48.8; DB 10; Length 1418;
Best Local Similarity 47.1%; Pred. No. 25;
RESULT 744
ID ADC36202 standard; DNA; 1418 BP.
DE Weed controller metabolism associated gene SEQ ID NO:69.
PN WO2003040370-A1.
PD 15-MAY-2003.
PA (SUMO) SUMITOMO CHEM CO LTD.
Query Match 4.9%; Score 48.8; DB 10; Length 1418;
Best Local Similarity 47.1%; Pred. No. 25;
RESULT 745
ID ACC47259 standard; cDNA; 1427 BP.
DE Human SCAP encoding cDNA-Incyte Id. 6891852CB1.
PN WO2003008625-A2.
PD 30-JAN-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 4.9%; Score 48.8; DB 8; Length 1427;
Best Local Similarity 48.0%; Pred. No. 25;
RESULT 746
ID ABD13152 standard; DNA; 2232 BP.
DE Pseudomonas aeruginosa polynucleotide #11756.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 4.9%; Score 48.8; DB 11; Length 2232;
Best Local Similarity 43.4%; Pred. No. 25;
RESULT 747
ID ABD13005 standard; DNA; 2274 BP.
DE Pseudomonas aeruginosa polynucleotide #11609.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 4.9%; Score 48.8; DB 11; Length 2274;
Best Local Similarity 43.4%; Pred. No. 25;
RESULT 748
ID ABD13232 standard; DNA; 2613 BP.
DE Pseudomonas aeruginosa polynucleotide #11836.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 4.9%; Score 48.8; DB 11; Length 2613;
Best Local Similarity 43.4%; Pred. No. 25;
RESULT 749
ID ABD10111 standard; DNA; 2715 BP.
DE Pseudomonas aeruginosa polynucleotide #8715.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 4.9%; Score 48.8; DB 11; Length 2715;
Best Local Similarity 50.3%; Pred. No. 25;
RESULT 750
ID ABX93509 standard; DNA; 4826 BP.
DE DNA fragment containing poly-beta-hydroxybutyrate, PHB, synthesis genes.

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PN US2002146785-A1.
PD 10-OCT-2002.
PA (MAHI/) MAHISHI L H.
PA (TRIP/) TRIPATHI G.
PA (RAMC/) RAMCHANDER T V N.
PA (RAWA/) RAWAL S K.
Query Match
Best Local Similarity 4.9%; Score 48.8; DB 8; Length 4826;
Best Local Similarity 45.7%; Pred. No. 24;
RESULT 751
ID ABK91609 standard; DNA; 7897 BP.
DE Modified HIV protein-encoding plasmid DNA #161.
PN WO200232943-A2.
PD 25-APR-2002.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA (CHAD/) CHADRABARTI B K.
Query Match
Best Local Similarity 4.9%; Score 48.8; DB 6; Length 7897;
Best Local Similarity 47.9%; Pred. No. 24;
RESULT 752
ID ABK91616 standard; DNA; 9166 BP.
DE Modified HIV protein-encoding plasmid DNA #168.
PN WO200232943-A2.
PD 25-APR-2002.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA (CHAD/) CHADRABARTI B K.
Query Match
Best Local Similarity 4.9%; Score 48.8; DB 6; Length 9166;
Best Local Similarity 47.9%; Pred. No. 24;
RESULT 753
ID ABK91619 standard; DNA; 9167 BP.
DE Modified HIV protein-encoding plasmid DNA #171.
PN WO200232943-A2.
PD 25-APR-2002.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA (CHAD/) CHADRABARTI B K.
Query Match
Best Local Similarity 4.9%; Score 48.8; DB 6; Length 9167;
Best Local Similarity 47.9%; Pred. No. 24;
RESULT 754
ID ABK91617 standard; DNA; 9169 BP.
DE Modified HIV protein-encoding plasmid DNA #169.
PN WO200232943-A2.
PD 25-APR-2002.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA (CHAD/) CHADRABARTI B K.
Query Match
Best Local Similarity 4.9%; Score 48.8; DB 6; Length 9169;
Best Local Similarity 47.9%; Pred. No. 24;
RESULT 755
ID ABK91614 standard; DNA; 9170 BP.
DE Modified HIV protein-encoding plasmid DNA #166.
PN WO200232943-A2.
PD 25-APR-2002.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA (CHAD/) CHADRABARTI B K.
Query Match
Best Local Similarity 4.9%; Score 48.8; DB 6; Length 9170;
Best Local Similarity 47.9%; Pred. No. 24;
RESULT 756
ID ABK91607 standard; DNA; 9189 BP.
DE Modified HIV protein-encoding plasmid DNA #159.
PN WO200232943-A2.
PD 25-APR-2002.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA (CHAD/) CHADRABARTI B K.
Query Match
Best Local Similarity 4.9%; Score 48.8; DB 6; Length 9189;
Best Local Similarity 47.9%; Pred. No. 24;
RESULT 757
ID ABK91612 standard; DNA; 9194 BP.
DE Modified HIV protein-encoding plasmid DNA #164.
PN WO200232943-A2.
PD 25-APR-2002.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA (CHAD/) CHADRABARTI B K.
Query Match
Best Local Similarity 4.9%; Score 48.8; DB 6; Length 9194;
Best Local Similarity 47.9%; Pred. No. 24;
ID ABK91611 standard; DNA; 9194 BP.
DE Modified HIV protein-encoding plasmid DNA #163.
PN WO200232943-A2.
PD 25-APR-2002.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA (CHAD/) CHADRABARTI B K.
Query Match
Best Local Similarity 4.9%; Score 48.8; DB 6; Length 9194;
Best Local Similarity 47.9%; Pred. No. 24;
RESULT 759
ID ABK91623 standard; DNA; 9407 BP.
DE Modified HIV protein-encoding plasmid DNA #175.
PN WO200232943-A2.
PD 25-APR-2002.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA (CHAD/) CHADRABARTI B K.
Query Match
Best Local Similarity 4.9%; Score 48.8; DB 6; Length 9407;
Best Local Similarity 47.9%; Pred. No. 24;
RESULT 760
ID ABK91621 standard; DNA; 9782 BP.
DE Modified HIV protein-encoding plasmid DNA #173.
PN WO200232943-A2.
PD 25-APR-2002.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA (CHAD/) CHADRABARTI B K.
Query Match
Best Local Similarity 4.9%; Score 48.8; DB 6; Length 9782;
Best Local Similarity 47.9%; Pred. No. 24;
RESULT 761
ID ABK91620 standard; DNA; 9783 BP.
DE Modified HIV protein-encoding plasmid DNA #172.
PN WO200232943-A2.
PD 25-APR-2002.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA (CHAD/) CHADRABARTI B K.
Query Match
Best Local Similarity 4.9%; Score 48.8; DB 6; Length 9783;
Best Local Similarity 47.9%; Pred. No. 24;
RESULT 762
ID ABK91624 standard; DNA; 9785 BP.
DE Modified HIV protein-encoding plasmid DNA #176.
PN WO200232943-A2.
PD 25-APR-2002.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA (CHAD/) CHADRABARTI B K.
Query Match
Best Local Similarity 4.9%; Score 48.8; DB 6; Length 9785;
Best Local Similarity 47.9%; Pred. No. 24;
RESULT 763
ID ABK91622 standard; DNA; 9788 BP.
DE Modified HIV protein-encoding plasmid DNA #174.
PN WO200232943-A2.
PD 25-APR-2002.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA (CHAD/) CHADRABARTI B K.
Query Match
Best Local Similarity 4.9%; Score 48.8; DB 6; Length 9788;
Best Local Similarity 47.9%; Pred. No. 24;
RESULT 764
ID ABK91618 standard; DNA; 9792 BP.
DE Modified HIV protein-encoding plasmid DNA #170.
PN WO200232943-A2.
PD 25-APR-2002.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA (CHAD/) CHADRABARTI B K.
Query Match
Best Local Similarity 4.9%; Score 48.8; DB 6; Length 9792;
Best Local Similarity 47.9%; Pred. No. 24;
RESULT 765
ID ABZ66813 standard; DNA; 10035 BP.
DE Orthosomycin biosynthetic gene cluster SEQ ID NO 282.
PN WO200279505-A2.
PD 10-OCT-2002.
PA (ECOP-) ECOPIA BIOSCIENCES INC.
Query Match
Best Local Similarity 4.9%; Score 48.8; DB 10; Length 10035;
Best Local Similarity 47.6%; Pred. No. 24;
RESULT 766
ID ABK91613 standard; DNA; 12411 BP.
DE Modified HIV protein-encoding plasmid DNA #165.
PN WO200232943-A2.
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PD 25-APR-2002.
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 PA (CHAD/) CHADRABARTI B K.
 Query Match 4.9%; Score 48.8; DB 6; Length 12411;
 Best Local Similarity 47.9%; Pred. No. 24;
 RESULT 767
 ID ABX34289 standard; DNA; 135638 BP.
 DE S. atroolivaceus leinamycin biosynthesis gene cluster.
 PN WO20027179-A2.
 PD 03-OCT-2002.
 PA (REGC) UNIV CALIFORNIA.
 PA (KYOW) KYOWA HAKKO KOGYO KK.
 Query Match 4.9%; Score 48.8; DB 10; Length 135638;
 Best Local Similarity 44.7%; Pred. No. 22;
 RESULT 768
 ID ABS63423 standard; cDNA; 528 BP.
 DE DNA encoding soybean caffeoyl-CoA O-methyltransferase (CCOMT).
 PN US2002081693-A1.
 PD 27-JUN-2002.
 PA (CAHO/) CAHOON R E.
 PA (FADE/) FADER G M.
 PA (RAPA/) RAFALSKI J A.
 Query Match 4.9%; Score 48.6; DB 6; Length 528;
 Best Local Similarity 50.2%; Pred. No. 28;
 RESULT 769
 ID ACA38429 standard; DNA; 687 BP.
 DE Prokaryotic essential gene #20086.
 PN WO20027183-A2.
 PD 03-OCT-2002.
 PA (ELIT-) ELITRA PHARM INC.
 Query Match 4.9%; Score 48.6; DB 8; Length 687;
 Best Local Similarity 45.3%; Pred. No. 28;
 RESULT 770
 ID ACA40639 standard; DNA; 690 BP.
 DE Prokaryotic essential gene #22296.
 PN WO20027183-A2.
 PD 03-OCT-2002.
 PA (ELIT-) ELITRA PHARM INC.
 Query Match 4.9%; Score 48.6; DB 8; Length 690;
 Best Local Similarity 45.3%; Pred. No. 28;
 RESULT 771
 ID ABX56068 standard; DNA; 1320 BP.
 DE M. echinospira calicheamicin biosynthesis gene orfVIII.
 PN WO200279465-A2.
 PD 10-OCT-2002.
 PA (SLOK) SLOAN KETTERING INST CANCER RES.
 Query Match 4.9%; Score 48.6; DB 8; Length 1320;
 Best Local Similarity 45.1%; Pred. No. 27;
 RESULT 772
 ID ACC82989 standard; DNA; 1397 BP.
 DE HIV-1 subtype C isolate Dui51 reverse transcriptase codon optimised DNA.
 PN WO2003037919-A2.
 PD 08-MAY-2003.
 PA (SAME-) SOUTH AFRICAN MEDICAL RES COUNCIL.
 PA (UYCA-) UNIV CAPE TOWN.
 Query Match 4.9%; Score 48.6; DB 8; Length 1397;
 Best Local Similarity 47.8%; Pred. No. 27;
 RESULT 773
 ID AAT90471 standard; cDNA; 1479 BP.
 DE Human agrin cDNA.
 PN WO9721811-A2.
 PD 19-JUN-1997.
 PA (REGE-) REGENERON PHARM INC.
 Query Match 4.9%; Score 48.6; DB 2; Length 1479;
 Best Local Similarity 43.8%; Pred. No. 27;
 RESULT 774
 ID ADL61985 standard; DNA; 1533 BP.
 DE Human ovarian cancer DNA marker #20197.
 PN WO200170979-A2.
 PD 27-SEP-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Query Match 4.9%; Score 48.6; DB 5; Length 1533;
 Best Local Similarity 48.4%; Pred. No. 27;

RESULT 775
 ID ABD12608 standard; DNA; 1575 BP.
 DE Pseudomonas aeruginosa polynucleotide #11212.
 PN US6551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Query Match 4.9%; Score 48.6; DB 11; Length 1575;
 Best Local Similarity 46.6%; Pred. No. 27;
 RESULT 776
 ID ABD12542 standard; DNA; 1620 BP.
 DE Pseudomonas aeruginosa polynucleotide #11146.
 PN US6551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Query Match 4.9%; Score 48.6; DB 11; Length 1620;
 Best Local Similarity 46.6%; Pred. No. 27;
 RESULT 777
 ID AAT62137 standard; DNA; 2040 BP.
 DE Leishmania braziliensis Lbhsp83 antigen cDNA.
 PN WO9711180-A1.
 PD 27-MAR-1997.
 PA (CORI-) CORIXA CORP.
 Query Match 4.9%; Score 48.6; DB 2; Length 2040;
 Best Local Similarity 44.4%; Pred. No. 27;
 RESULT 778
 ID AAV47557 standard; DNA; 2040 BP.
 DE Leishmania antigen Lbhsp83 coding sequence.
 PN WO9835045-A2.
 PD 13-AUG-1998.
 PA (CORI-) CORIXA CORP.
 Query Match 4.9%; Score 48.6; DB 2; Length 2040;
 Best Local Similarity 44.4%; Pred. No. 27;
 RESULT 779
 ID AAD47114 standard; DNA; 2040 BP.
 DE Leishmania sp. 6H (Lbhsp83) DNA.
 PN WO200272792-A2.
 PD 19-SEP-2002.
 PA (CORI-) CORIXA CORP.
 Query Match 4.9%; Score 48.6; DB 6; Length 2040;
 Best Local Similarity 44.4%; Pred. No. 27;
 RESULT 780
 ID AAD40284 standard; DNA; 2040 BP.
 DE Leishmania braziliensis hsp83 antigenic protein encoding DNA.
 PN US6375955-B1.
 PD 23-APR-2002.
 PA (CORI-) CORIXA CORP.
 Query Match 4.9%; Score 48.6; DB 6; Length 2040;
 Best Local Similarity 44.4%; Pred. No. 27;
 RESULT 781
 ID AAS96021 standard; cDNA; 2040 BP.
 DE Leishmania antigen Lbhsp83 DNA.
 PN WO200179276-A2.
 PD 25-OCT-2001.
 PA (CORI-) CORIXA CORP.
 Query Match 4.9%; Score 48.6; DB 6; Length 2040;
 Best Local Similarity 44.4%; Pred. No. 27;
 RESULT 782
 ID ABK81732 standard; cDNA; 2040 BP.
 DE Leishmania antigenic polynucleotide #3.
 PN US6365165-B1.
 PD 02-APR-2002.
 PA (CORI-) CORIXA CORP.
 Query Match 4.9%; Score 48.6; DB 6; Length 2040;
 Best Local Similarity 44.4%; Pred. No. 27;
 RESULT 783
 ID AAF88523 standard; DNA; 2040 BP.
 DE L. braziliensis Hsp83 antigen DNA SEQ ID 5.
 PN US2002081320-A1.
 PD 27-JUN-2002.
 PA (REED/) REED S G.
 PA (CAMP/) CAMPOS-NETO A.
 PA (WEBB/) WEBB J R.
 PA (DILL/) DILLON D C.

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PA (SKEI/) SKEIKY Y A W.
PA (BHAT/) BHATIA A.
PA (COLE/) COLER R N.
PA (PROB/) PROBST P.
PA (BRAN/) BRANNON M. 4.9%; Score 48.6; DB 6; Length 2040;
Best Local Similarity 44.4%; Pred. No. 27;
RESULT 784
ID ADB78768 standard; cDNA; 2040 BP.
DE Leishmania DNA encoding antigen Lhsp83.
PN US2002169285-A1.
PD 14-NOV-2002.
PA (REED/) REED S G.
PA (CAMP/) CAMPOS-NETO A.
PA (WEBB/) WEBB J R.
PA (DILL/) DILLON D C.
Query Match 4.9%; Score 48.6; DB 9; Length 2040;
Best Local Similarity 44.4%; Pred. No. 27;
RESULT 785
ID AAH14403 standard; cDNA; 2279 BP.
DE Human cDNA sequence SEQ ID NO:11841.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 4.9%; Score 48.6; DB 4; Length 2279;
Best Local Similarity 47.3%; Pred. No. 27;
RESULT 786
ID ABX08845 standard; cDNA; 2279 BP.
DE Angiogenesis-associated human polynucleotide sequence #107.
PN WO200279492-A2.
PD 10-OCT-2002.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 4.9%; Score 48.6; DB 10; Length 2279;
Best Local Similarity 47.3%; Pred. No. 27;
RESULT 787
ID AAH17825 standard; cDNA; 2454 BP.
DE Human cDNA sequence SEQ ID NO:17498.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 4.9%; Score 48.6; DB 4; Length 2454;
Best Local Similarity 47.3%; Pred. No. 27;
RESULT 788
ID ABD12439 standard; DNA; 2472 BP.
DE Pseudomonas aeruginosa polynucleotide #11043.
PN US6551793-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 4.9%; Score 48.6; DB 11; Length 2472;
Best Local Similarity 46.6%; Pred. No. 27;
RESULT 789
ID AAL41592 standard; DNA; 2577 BP.
DE HIV-1 subtype C isolate Dui51 pol gene.
PN WO200204494-A2.
PD 17-JAN-2002.
PA (MEDI-) MEDICAL RES COUNCIL.
PA (UYCA-) UNIV CAPE TOWN.
PA (UYNC-) UNIV NORTH CAROLINA.
Query Match 4.9%; Score 48.6; DB 6; Length 2577;
Best Local Similarity 47.8%; Pred. No. 27;
RESULT 790
ID AAQ06825 standard; DNA; 2712 BP.
DE Streptomyces albidoflavus endochitinase DNA.
PN WO9942594-A1.
PD 26-AUG-1999.
PA (CORR) CORNELL RES FOUND INC.
Query Match 4.9%; Score 48.6; DB 2; Length 2712;
Best Local Similarity 47.6%; Pred. No. 27;
RESULT 791
ID AAH74538 standard; DNA; 2712 BP.
DE Nucleotide sequence of an endochitinase polypeptide.
PN WO200146387-A1.
PD 28-JUN-2001.

PA (CORR) CORNELL RES FOUND INC.
Query Match 4.9%; Score 48.6; DB 4; Length 2712;
Best Local Similarity 47.6%; Pred. No. 27;
RESULT 792
ID ABA95198 standard; cDNA; 3298 BP.
DE Human MICAPRUB-2 polypeptide encoding cDNA (clone ID: 1593855CB1).
PN WO200216587-A2.
PD 28-FEB-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 4.9%; Score 48.6; DB 6; Length 3298;
Best Local Similarity 47.3%; Pred. No. 26;
RESULT 793
ID ACC82987 standard; DNA; 3687 BP.
DE HIV-1 Gtttnc DNA construct.
PN WO2003037919-A2.
PD 08-MAY-2003.
PA (SAME-) SOUTH AFRICAN MEDICAL RES COUNCIL.
PA (UYCA-) UNIV CAPE TOWN.
Query Match 4.9%; Score 48.6; DB 8; Length 3687;
Best Local Similarity 47.8%; Pred. No. 26;
RESULT 794
ID ADO85410 standard; DNA; 3720 BP.
DE Streptomyces phoK/phoR::omegaaac double mutant, seq id 5.
PN FR2848567-A1.
PD 18-JUN-2004.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 4.9%; Score 48.6; DB 12; Length 3720;
Best Local Similarity 49.4%; Pred. No. 26;
RESULT 795
ID ADC39155 standard; cDNA; 4760 BP.
DE Novel human NOVX polypeptide coding sequence SEQ ID NO: 97.
PN WO2003010327-A2.
PD 06-FEB-2003.
PA (CURA-) CURAGEN CORP.
Query Match 4.9%; Score 48.6; DB 10; Length 4760;
Best Local Similarity 43.8%; Pred. No. 26;
RESULT 796
ID ADH72283 standard; DNA; 4760 BP.
DE Human gene of the invention NOV60d SEQ ID NO:1179.
PN WO20030102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 4.9%; Score 48.6; DB 12; Length 4760;
Best Local Similarity 43.8%; Pred. No. 26;
RESULT 797
ID ADO85408 standard; DNA; 4860 BP.
DE Streptomyces phoK::omegaaac mutant, seq id 3.
PN FR2848567-A1.
PD 18-JUN-2004.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 4.9%; Score 48.6; DB 12; Length 4860;
Best Local Similarity 49.4%; Pred. No. 26;
RESULT 798
ID AAH48730 standard; cDNA; 5065 BP.
DE Human HCN4 cDNA.
PN WO200159153-A2.
PD 16-AUG-2001.
PA (AVET) AVENTIS PHARMA DEUT GMBH.
Query Match 4.9%; Score 48.6; DB 4; Length 5065;
Best Local Similarity 50.6%; Pred. No. 26;
RESULT 799
ID ABA09197 standard; cDNA; 5499 BP.
DE Human cation channel hHCN4 homologue cDNA, SEQ ID NO:973.
PN WO200157188-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 4.9%; Score 48.6; DB 4; Length 5499;
Best Local Similarity 50.6%; Pred. No. 26;
RESULT 800
ID ADC39153 standard; cDNA; 6224 BP.
DE Novel human NOVX polypeptide coding sequence SEQ ID NO: 95.
PN WO2003010327-A2.
PD 06-FEB-2003.

PA (CURA-) CURAGEN CORP. 4.9%; Score 48.6; DB 10; Length 6224;
Query Match Best Local Similarity 43.8%; Pred. No. 26;
RESULT 801
ID ADH72277 standard; DNA; 6224 BP.
DE Human gene of the invention NOV60a SEQ ID NO:1173.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP. 4.9%; Score 48.6; DB 12; Length 6224;
Query Match Best Local Similarity 43.8%; Pred. No. 26;
RESULT 802
ID ADM74234 standard; DNA; 6224 BP.
DE Human NOV8A gene sequence SeqID73.
PN WO2004015079-A2.
PD 19-FEB-2004.
PA (CURA-) CURAGEN CORP. 4.9%; Score 48.6; DB 12; Length 6224;
Query Match Best Local Similarity 43.8%; Pred. No. 26;
RESULT 803
ID ADC39163 standard; cDNA; 6494 BP.
DE Novel human NOVX polypeptide coding sequence SEQ ID NO: 105.
PN WO2003010327-A2.
PD 06-FEB-2003.
PA (CURA-) CURAGEN CORP. 4.9%; Score 48.6; DB 10; Length 6494;
Query Match Best Local Similarity 43.8%; Pred. No. 26;
RESULT 804
ID ADH72291 standard; DNA; 6494 BP.
DE Human gene of the invention NOV60h SEQ ID NO:1187.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP. 4.9%; Score 48.6; DB 12; Length 6494;
Query Match Best Local Similarity 43.8%; Pred. No. 26;
RESULT 805
Query Match 4.9%; Score 48.6; DB 4; Length 110000;
Best Local Similarity 45.3%; Pred. No. 24;
RESULT 806
ID AAV23873 standard; DNA; 562 BP.
DE Plant OMT enzyme DNA sequence.
PN WO9811205-A2.
PD 14-SEP-1999.
PA (GENE-) GENESIS RES & DEV CORP LTD.
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD. 4.9%; Score 48.4; DB 2; Length 562;
Query Match Best Local Similarity 49.2%; Pred. No. 30;
RESULT 807
ID AA206876 standard; cDNA; 562 BP.
DE Fine O-methyl transferase (OMT) partial cDNA 2.
PN US5952486-A.
PD 14-SEP-1999.
PA (GENE-) GENESIS RES & DEV CORP LTD.
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD. 4.9%; Score 48.4; DB 2; Length 562;
Query Match Best Local Similarity 49.2%; Pred. No. 30;
RESULT 808
ID AAA69580 standard; cDNA; 562 BP.
DE Pinus radiata O-methyltransferase cDNA SEQ ID NO:54.
PN WO200036081-A2.
PD 22-JUN-2000.
PA (GENE-) GENESIS RES & DEV CORP LTD.
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD. 4.9%; Score 48.4; DB 3; Length 562;
Query Match Best Local Similarity 49.2%; Pred. No. 30;
RESULT 809
ID AAA67960 standard; DNA; 562 BP.
DE Pinus radiata OMT nucleotide sequence SEQ ID NO:53.
PN WO200022099-A1.
PD 20-APR-2000.
PA (GENE-) GENESIS RES & DEV CORP LTD.
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD. 4.9%; Score 48.4; DB 3; Length 562;
Query Match

Best Local Similarity 49.2%; Pred. No. 30;
RESULT 810
ID ADD41710 standard; DNA; 562 BP.
DE O-methyl transferase DNA #6.
PN US2003131373-A1.
PD 10-JUL-2003.
PA (BLOK/) BLOKSBERG L N.
PA (HAVU/) HAVUKALA I.
Query Match 4.9%; Score 48.4; DB 10; Length 562;
Best Local Similarity 49.2%; Pred. No. 30;
RESULT 811
ID AA043032 standard; DNA; 756 BP.
DE Collagen-like polymer DCP3-C2(AB12)C2 coding sequence.
PN WO9310154-A1.
PD 27-MAY-1993.
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
Query Match 4.9%; Score 48.4; DB 2; Length 756;
Best Local Similarity 44.3%; Pred. No. 30;
RESULT 812
ID AAT16766 standard; DNA; 756 BP.
DE Collagen-like polymer sequence D gene 2 encoding unit C2A24C2.
PN US5496712-A.
PD 05-MAR-1996.
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
Query Match 4.9%; Score 48.4; DB 2; Length 756;
Best Local Similarity 44.3%; Pred. No. 30;
RESULT 813
ID AAA02484 standard; cDNA; 1000 BP.
DE Human colon cancer cell line polynucleotide sequence SEQ ID NO:2475.
PN WO9558675-A2.
PD 18-NOV-1999.
PA (CHIR) CHIRON CORP.
PA (HYSE-) HYSEQ INC. 4.9%; Score 48.4; DB 3; Length 1000;
Query Match Best Local Similarity 33.5%; Pred. No. 29;
RESULT 814
ID ADA70207 standard; DNA; 1059 BP.
DE Rice gene, SEQ ID 3530.
PN WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG. 4.9%; Score 48.4; DB 8; Length 1059;
Query Match Best Local Similarity 43.8%; Pred. No. 29;
RESULT 815
ID ADJ11579 standard; DNA; 1059 BP.
DE Rice DNA modulated by post-transcriptional gene silencing SeqID 215.
PN US2003135888-A1.
PD 17-JUL-2003.
PA (ZHUT/) ZHU T.
PA (WANG/) WANG X.
PA (CHAN/) CHANG H.
PA (BRIG/) BRIGGS S P.
PA (COOP/) COOPER B.
PA (GLAZ/) GLAZEBROOK J.
PA (GOFF/) GOFF S A.
PA (KATA/) KATAGIRI F.
PA (KREP/) KREPS J.
PA (MOUG/) MOUGHAMER T.
PA (PROV/) PROVART N.
PA (RICK/) RICKE D.
Query Match 4.9%; Score 48.4; DB 11; Length 1059;
Best Local Similarity 43.8%; Pred. No. 29;
RESULT 816
ID ADA71187 standard; DNA; 1482 BP.
DE Rice gene, SEQ ID 4510.
PN WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG. 4.9%; Score 48.4; DB 8; Length 1482;
Query Match Best Local Similarity 44.0%; Pred. No. 29;
RESULT 817
ID AAZ35999 standard; DNA; 1646 BP.
DE S. kitasatoensis macrolide antibiotic acylation enzyme gene.

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PN JPI1285384-A.
PD 19-OCT-1999.
PA (ASAH) ASAHI KASEI KOGYO KK.
Query Match 4.9%; Score 48.4; DB 3; Length 1646;
Best Local Similarity 50.4%; Pred. No. 29;
RESULT 818
ID ACA37821 standard; DNA; 1650 BP.
DE Prokaryotic essential gene #19478.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 4.9%; Score 48.4; DB 8; Length 1650;
Best Local Similarity 45.0%; Pred. No. 29;
RESULT 819
ID ACA27358 standard; DNA; 2523 BP.
DE Prokaryotic essential gene #9015.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 4.9%; Score 48.4; DB 8; Length 2523;
Best Local Similarity 47.4%; Pred. No. 29;
RESULT 820
ID ADA70538 standard; DNA; 2562 BP.
DE Rice gene, SEQ ID 3861.
PN WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 4.9%; Score 48.4; DB 8; Length 2562;
Best Local Similarity 47.3%; Pred. No. 29;
RESULT 821
ID AAS06333 standard; cDNA; 2898 BP.
DE DNA encoding human glutamate receptor-like protein, MEM2.
PN WO200144473-A2.
PD 21-JUN-2001.
PA (CURA-) CURAGEN CORP.
Query Match 4.9%; Score 48.4; DB 4; Length 2898;
Best Local Similarity 43.0%; Pred. No. 29;
RESULT 822
ID AAD7033 standard; DNA; 3690 BP.
DE Methyllobacterium extorquens PHA synthase DNA.
PN WO200123596-A2.
PD 05-APR-2001.
PA (PION-) PIONEER HI-BRED INT INC.
PA (PION-) DU PONT DE NEMOURS & CO E I.
Query Match 4.9%; Score 48.4; DB 4; Length 3690;
Best Local Similarity 48.2%; Pred. No. 28;
RESULT 823
ID AAZ09496 standard; DNA; 4751 BP.
DE Human heart tissue Ih ion channel DNA.
PN WO9942574-A1.
PD 26-AUG-1999.
PA (KERJ) FORSCHUNGSZENTRUM JUELICH GMBH.
Query Match 4.9%; Score 48.4; DB 2; Length 4751;
Best Local Similarity 53.8%; Pred. No. 28;
RESULT 824
ID AAD29757 standard; DNA; 4751 BP.
DE Human hyperpolarisation-activated cyclic nucleotide-gated channel 4 DNA.
PN WO200202630-A2.
PD 10-JAN-2002.
PA (SMIK) SMITHKLINE BEECHAM PLC.
Query Match 4.9%; Score 48.4; DB 6; Length 4751;
Best Local Similarity 53.8%; Pred. No. 28;
RESULT 825
ID ACA37735 standard; DNA; 4833 BP.
DE Prokaryotic essential gene #19392.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 4.9%; Score 48.4; DB 8; Length 4833;
Best Local Similarity 50.3%; Pred. No. 28;
RESULT 826
ID AAD54223 standard; DNA; 24081 BP.
DE Streptomyces platensis subspecies rosaceus dorrigocin ORF6 DNA.
PN WO200288176-A2.
PD 07-NOV-2002.
PA (ECOP-) ECOPIA BIOSCIENCES INC.
Query Match 4.9%; Score 48.4; DB 10; Length 24081;
Best Local Similarity 51.1%; Pred. No. 27;
RESULT 827
ID ACA37577 standard; DNA; 31263 BP.
DE Prokaryotic essential gene #19234.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 4.9%; Score 48.4; DB 8; Length 31263;
Best Local Similarity 46.2%; Pred. No. 27;
RESULT 828
ID AAD54217 standard; DNA; 52101 BP.
DE Streptomyces platensis subspecies rosaceus dorrigocin DNA.
PN WO200288176-A2.
PD 07-NOV-2002.
PA (ECOP-) ECOPIA BIOSCIENCES INC.
Query Match 4.9%; Score 48.4; DB 10; Length 52101;
Best Local Similarity 51.1%; Pred. No. 26;
RESULT 829
ID AAD57189 standard; DNA; 600 BP.
DE Mycobacterium avium subspecies paratuberculosis protein gene #2.
PN WO2003058248-A2.
PD 17-JUL-2003.
PA (IDLE-) ID-LELYSTAD INST DIERHOUDRIJ EN DIERGEZ.
Query Match 4.9%; Score 48.2; DB 9; Length 600;
Best Local Similarity 48.4%; Pred. No. 32;
RESULT 831
ID ADC30820 standard; cDNA; 663 BP.
DE Human novel cDNA sequence, SEQ ID NO:902.
PN WO2003029271-A2.
PD 10-APR-2003.
PA (HYSE-) HYSEQ INC.
Query Match 4.9%; Score 48.2; DB 10; Length 663;
Best Local Similarity 52.7%; Pred. No. 32;
RESULT 832
ID ADK52175 standard; cDNA; 663 BP.
DE Full length cDNA clone MasP1 clone 3.
PN WO2004016651-A2.
PD 26-FEB-2004.
PA (UYVO-) UNIV YORK.
Query Match 4.9%; Score 48.2; DB 12; Length 663;
Best Local Similarity 44.0%; Pred. No. 32;
RESULT 833
ID ADJ39458 standard; cDNA; 786 BP.
DE Plant cDNA #458.
PN US2004016025-A1.
PD 22-JAN-2004.
PA (BUDW/) BUDWORTH P.
PA (MOUG/) MOUGHAMER T.
PA (BRIG/) BRIGGS S P.
PA (COOP/) COOPER B.
PA (GLAZ/) GLAZERBOOK J.
PA (GOFF/) GOFF S A.
PA (KATA/) KATAGIRI F.
PA (KREP/) KREPS J.
PA (PROV/) PROVART N.
PA (RICK/) RICHE D.
PA (ZHUT/) ZHU T.
Query Match 4.9%; Score 48.2; DB 12; Length 786;
Best Local Similarity 49.8%; Pred. No. 32;
RESULT 834
ID ACC68993 standard; cDNA; 811 BP.
DE Human neurotransmission-associated protein NTRAN-15 cDNA SEQ ID NO:40.
PN WO2003025129-A2.
PD 27-MAR-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 4.9%; Score 48.2; DB 10; Length 811;

Best Local Similarity 52.7%; Pred. No. 32;
RESULT 835
ID ABD13103 standard; DNA; 822 BP.
DE Pseudomonas aeruginosa polynucleotide #11707.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 4.9%; Score 48.2; DB 11; Length 822;
Best Local Similarity 46.5%; Pred. No. 32;
RESULT 836
ID ADG10464 standard; cDNA; 823 BP.
DE Human STAT6-activating protein-encoding cDNA, SEQ ID NO:54.
PN WO200296943-A1.
PD 05-DEC-2002.
PA (ASAH) ASAH KASEI KOGYO KK.
Query Match 4.9%; Score 48.2; DB 10; Length 823;
Best Local Similarity 52.7%; Pred. No. 32;
RESULT 837
ID ADG10466 standard; cDNA; 823 BP.
DE Human STAT6-activating protein-encoding cDNA, SEQ ID NO:56.
PN WO200296943-A1.
PD 05-DEC-2002.
PA (ASAH) ASAH KASEI KOGYO KK.
Query Match 4.9%; Score 48.2; DB 10; Length 823;
Best Local Similarity 52.7%; Pred. No. 32;
RESULT 838
ID ACA37950 standard; DNA; 825 BP.
DE Prokaryotic essential gene #19607.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 4.9%; Score 48.2; DB 8; Length 825;
Best Local Similarity 48.9%; Pred. No. 32;
RESULT 839
ID AAI58255 standard; cDNA; 920 BP.
DE Human polynucleotide SEQ ID NO 458.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 4.9%; Score 48.2; DB 4; Length 920;
Best Local Similarity 52.7%; Pred. No. 32;
RESULT 840
ID ADQ98462 standard; cDNA; 920 BP.
DE DNA encoding human GPCR-like protein seqid 132.
PN US6569662-B1.
PD 27-MAY-2003.
PA (HYSE-) HYSEQ INC.
Query Match 4.9%; Score 48.2; DB 5; Length 920;
Best Local Similarity 52.7%; Pred. No. 32;
RESULT 841
ID ADB48222 standard; cDNA; 920 BP.
DE Novel human cDNA SEQ ID NO 132.
PN US2003104529-A1.
PD 05-JUN-2003.
PA (ZHOU/) ZHOU P.
PA (TANG/) TANG Y T.
PA (LIUC/) LIU C.
PA (ASUN/) ASUNDI V.
PA (DRNA/) DRMANAC R T.
Query Match 4.9%; Score 48.2; DB 9; Length 920;
Best Local Similarity 52.7%; Pred. No. 32;
RESULT 842
ID ACA42680 standard; DNA; 930 BP.
DE Prokaryotic essential gene #24337.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 4.9%; Score 48.2; DB 8; Length 930;
Best Local Similarity 48.1%; Pred. No. 32;
RESULT 843
ID ABK51403 standard; DNA; 969 BP.
DE DNA encoding human CCAAT enhancer binding protein beta-2.
PN WO200160973-A2.

PD 23-AUG-2001.
PA (UYVA-) UNIV VANDERBILT.
Query Match 4.9%; Score 48.2; DB 4; Length 969;
Best Local Similarity 47.2%; Pred. No. 32;
RESULT 844
ID AAD19381 standard; DNA; 969 BP.
DE Human CCAAT/enhancer binding protein (C/EBP) beta-2 isoform DNA.
PN WO200160320-A2.
PD 23-AUG-2001.
PA (UYVA-) UNIV VANDERBILT.
Query Match 4.9%; Score 48.2; DB 4; Length 969;
Best Local Similarity 47.2%; Pred. No. 32;
RESULT 845
ID ABK51402 standard; DNA; 1038 BP.
DE DNA encoding human CCAAT enhancer binding protein beta-1.
PN WO200160973-A2.
PD 23-AUG-2001.
PA (UYVA-) UNIV VANDERBILT.
Query Match 4.9%; Score 48.2; DB 4; Length 1038;
Best Local Similarity 47.2%; Pred. No. 32;
RESULT 846
ID AAD19380 standard; DNA; 1038 BP.
DE Human CCAAT/enhancer binding protein (C/EBP) beta-1 isoform DNA.
PN WO200160320-A2.
PD 23-AUG-2001.
PA (UYVA-) UNIV VANDERBILT.
Query Match 4.9%; Score 48.2; DB 4; Length 1038;
Best Local Similarity 47.2%; Pred. No. 32;
RESULT 847
ID AAS14696 standard; DNA; 1038 BP.
DE Human cDNA encoding transcription factor C/EBPbeta.
PN WO200174298-A2.
PD 11-OCT-2001.
PA (UYBR-) UNIV BROWN RESEARCH FOUND.
PA (HUGH-) HUGHES HOWARD MED INST.
Query Match 4.9%; Score 48.2; DB 4; Length 1038;
Best Local Similarity 47.2%; Pred. No. 32;
RESULT 848
ID AAL44084 standard; DNA; 1038 BP.
DE Human C/EBP-beta protein coding sequence 3.
PN WO200254938-A2.
PD 18-JUL-2002.
PA (REGC) UNIV CALIFORNIA.
Query Match 4.9%; Score 48.2; DB 6; Length 1038;
Best Local Similarity 47.2%; Pred. No. 32;
RESULT 849
ID ABK51997 standard; DNA; 1038 BP.
DE DNA encoding wild-type human C/EBPbeta protein #3.
PN WO200246218-A2.
PD 13-JUN-2002.
PA (REGC) UNIV CALIFORNIA.
Query Match 4.9%; Score 48.2; DB 6; Length 1038;
Best Local Similarity 47.2%; Pred. No. 32;
RESULT 850
ID ACF36516 standard; DNA; 1038 BP.
DE Human wild-type C/EBPbeta polypeptide encoding DNA.
PN WO2003072031-A2.
PD 04-SEP-2003.
PA (REGC) UNIV CALIFORNIA.
Query Match 4.9%; Score 48.2; DB 10; Length 1038;
Best Local Similarity 47.2%; Pred. No. 32;
RESULT 851
ID ABK51410 standard; DNA; 1042 BP.
DE Human CCAAT enhancer binding protein (C/EBP) gene mutant.
PN WO200160973-A2.
PD 23-AUG-2001.
PA (UYVA-) UNIV VANDERBILT.
Query Match 4.9%; Score 48.2; DB 4; Length 1042;
Best Local Similarity 47.2%; Pred. No. 32;
RESULT 852
ID ADK71964 standard; DNA; 1260 BP.
DE Human I Kappa B kinase (IKK) gamma DNA SeqID 22.
PN WO2004016781-A1.

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DE Human cDNA differentially expressed in granulocytic cells #1134.
PN WO200228999-A2.
PD 11-APR-2002.
PA (RIKE) RIKEN KK.
PA (KAZU-) KAZUSA DNA RES INST.
Query Match 4.9%; Score 48.2; DB 12; Length 1260;
Best Local Similarity 47.8%; Pred. No. 32;
RESULT 853
ID AAD55721 standard; DNA; 1336 BP.
DE Argiope trifasciata major ampullate spidroin 2 (MasP2) DNA.
PN WO2003020916-A2.
PD 13-MAR-2003.
PA (UYWY-) UNIV WYOMING.
Query Match 4.9%; Score 48.2; DB 8; Length 1336;
Best Local Similarity 43.2%; Pred. No. 32;
RESULT 854
ID ADP09651 standard; DNA; 1413 BP.
DE Rice cinnamic acid 5-hydroxylase ORF DNA without the T-DNA insert Seq 42.
PN WO2004046357-A1.
PD 03-JUN-2004.
PA (POSC-) POSCO.
PA (POST-) POSTECH FOUND.
Query Match 4.9%; Score 48.2; DB 12; Length 1413;
Best Local Similarity 49.8%; Pred. No. 31;
RESULT 855
ID ADP75211 standard; cDNA; 1701 BP.
DE Human ADAMTS2 cDNA splice variant 2.
PN WO2003031594-A2.
PD 17-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 4.9%; Score 48.2; DB 11; Length 1701;
Best Local Similarity 44.0%; Pred. No. 31;
RESULT 856
ID AAA35065 standard; DNA; 1910 BP.
DE Human adenosine receptor related polynucleotide SEQ ID NO:2754.
PN WO200009525-A2.
PD 24-FEB-2000.
PA (UYEC-) UNIV EAST CAROLINA.
Query Match 4.9%; Score 48.2; DB 3; Length 1910;
Best Local Similarity 47.2%; Pred. No. 31;
RESULT 857
ID AAF21187 standard; DNA; 1910 BP.
DE Human low adenosine antisense oligonucleotide related sequence #2754.
PN WO200062736-A2.
PD 26-OCT-2000.
PA (UYEC-) UNIV EAST CAROLINA.
PA (NYCE-) NYCE J W.
Query Match 4.9%; Score 48.2; DB 3; Length 1910;
Best Local Similarity 47.2%; Pred. No. 31;
RESULT 858
ID ABK51401 standard; DNA; 1910 BP.
DE Human CCAAT enhancer binding protein (C/EBPB) gene.
PN WO200160973-A2.
PD 23-AUG-2001.
PA (UYVA-) UNIV VANDERBILT.
Query Match 4.9%; Score 48.2; DB 4; Length 1910;
Best Local Similarity 47.2%; Pred. No. 31;
RESULT 859
ID AAD19379 standard; DNA; 1910 BP.
DE Human CCAAT/enhancer binding protein (C/EBP) beta DNA.
PN WO200160320-A2.
PD 23-AUG-2001.
PA (UYVA-) UNIV VANDERBILT.
Query Match 4.9%; Score 48.2; DB 4; Length 1910;
Best Local Similarity 47.2%; Pred. No. 31;
RESULT 860
ID AAL44083 standard; DNA; 1910 BP.
DE Human C/EBP-beta protein coding sequence 2.
PN WO200254938-A2.
PD 18-JUL-2002.
PA (REGC) UNIV CALIFORNIA.
Query Match 4.9%; Score 48.2; DB 6; Length 1910;
Best Local Similarity 47.2%; Pred. No. 31;
RESULT 861
ID ABK84563 standard; cDNA; 1910 BP.
DE Human cDNA differentially expressed in granulocytic cells #1134.
PN WO200228999-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 4.9%; Score 48.2; DB 6; Length 1910;
Best Local Similarity 47.2%; Pred. No. 31;
RESULT 862
ID ABL94237 standard; cDNA; 1910 BP.
DE Human C/EBP beta-encoding cDNA, SEQ ID NO:3.
PN US6271030-B1.
PD 07-AUG-2001.
PA (ISIS-) ISIS PHARM INC.
Query Match 4.9%; Score 48.2; DB 6; Length 1910;
Best Local Similarity 47.2%; Pred. No. 31;
RESULT 863
ID ABK51996 standard; DNA; 1910 BP.
DE DNA encoding wild-type human C/EBPbeta protein #2.
PN WO200246218-A2.
PD 13-JUN-2002.
PA (REGC) UNIV CALIFORNIA.
Query Match 4.9%; Score 48.2; DB 6; Length 1910;
Best Local Similarity 47.2%; Pred. No. 31;
RESULT 864
ID ACF36515 standard; DNA; 1910 BP.
DE Human wild-type C/EBPbeta polypeptide encoding DNA.
PN WO2003072031-A2.
PD 04-SEP-2003.
PA (REGC) UNIV CALIFORNIA.
Query Match 4.9%; Score 48.2; DB 10; Length 1910;
Best Local Similarity 47.2%; Pred. No. 31;
RESULT 865
ID ABZ96881 standard; DNA; 1910 BP.
DE Human nucleic acid sequence.
PN WO200285308-A2.
PD 31-OCT-2002.
PA (EPIG-) EPIGENESIS PHARM INC.
Query Match 4.9%; Score 48.2; DB 10; Length 1910;
Best Local Similarity 47.2%; Pred. No. 31;
RESULT 866
ID ABD20730 standard; DNA; 1910 BP.
DE Human pulmonary and inflammatory target DNA #341.
PN WO200285309-A2.
PD 31-OCT-2002.
PA (EPIG-) EPIGENESIS PHARM INC.
Query Match 4.9%; Score 48.2; DB 11; Length 1910;
Best Local Similarity 47.2%; Pred. No. 31;
RESULT 867
ID AAQ15015 standard; DNA; 1913 BP.
DE Nuclear factor C/EBP2 DNA.
PN JP03236782-A.
PD 22-OCT-1991.
PA (CHUZ-) CHUZO KISH IMOTO.
Query Match 4.9%; Score 48.2; DB 2; Length 1913;
Best Local Similarity 47.2%; Pred. No. 31;
RESULT 868
ID ADA44712 standard; DNA; 1975 BP.
DE Human inhibitor-kappa B kinase-gamma encoding DNA #SEQ ID 10.
PN WO2003031576-A2.
PD 17-APR-2003.
PA (ISIS-) ISIS PHARM INC.
Query Match 4.9%; Score 48.2; DB 8; Length 1975;
Best Local Similarity 47.8%; Pred. No. 31;
RESULT 869
ID AAC81426 standard; cDNA; 1994 BP.
DE Human I-kappa-B kinase gamma-subunit (IKK-gamma) cDNA.
PN JP2000253884-A.
PD 19-SEP-2000.
PA (TOAG) TOA GOSEI CHEM IND LTD.
Query Match 4.9%; Score 48.2; DB 3; Length 1994;
Best Local Similarity 47.8%; Pred. No. 31;
RESULT 870
ID AAA35027 standard; DNA; 1994 BP.
DE Human adenosine receptor related polynucleotide SEQ ID NO:2716.

PN WO200009525-A2.
PD 24-FEB-2000.
PA (UYEC-) UNIV EAST CAROLINA.
Query Match 4.9%; Score 48.2; DB 3; Length 1994;
Best Local Similarity 47.8%; Pred. No. 31;
RESULT 871
ID AAP21149 standard; DNA; 1994 BP.
DE Human low adenosine antisense oligonucleotide related sequence #2716.
PN WO200062736-A2.
PD 26-OCT-2000.
PA (UYEC-) UNIV EAST CAROLINA.
PA (UYEC-) NYCE J W.
Query Match 4.9%; Score 48.2; DB 3; Length 1994;
Best Local Similarity 47.8%; Pred. No. 31;
RESULT 872
ID ADA44705 standard; DNA; 1994 BP.
DE Human inhibitor-kappa B kinase-gamma encoding DNA #SEQ ID 3.
PN WO2003031576-A2.
PD 17-APR-2003.
PA (ISIS-) ISIS PHARM INC.
Query Match 4.9%; Score 48.2; DB 8; Length 1994;
Best Local Similarity 47.8%; Pred. No. 31;
RESULT 873
ID ABZ96843 standard; DNA; 1994 BP.
DE Human nucleic acid sequence.
PN WO200285308-A2.
PD 31-OCT-2002.
PA (EPIG-) EPIGENESIS PHARM INC.
Query Match 4.9%; Score 48.2; DB 10; Length 1994;
Best Local Similarity 47.8%; Pred. No. 31;
RESULT 874
ID ABV75393 standard; DNA; 1994 BP.
DE Human NEMO polypeptide encoding DNA.
PN WO200292761-A2.
PD 21-NOV-2002.
PA (IMVX) IMMUNEX CORP.
Query Match 4.9%; Score 48.2; DB 10; Length 1994;
Best Local Similarity 47.8%; Pred. No. 31;
RESULT 875
ID ABD20692 standard; DNA; 1994 BP.
DE Human pulmonary and inflammatory target DNA #303.
PN WO200285309-A2.
PD 31-OCT-2002.
PA (EPIG-) EPIGENESIS PHARM INC.
Query Match 4.9%; Score 48.2; DB 11; Length 1994;
Best Local Similarity 47.8%; Pred. No. 31;
RESULT 876
ID AAZ07513 standard; DNA; 2009 BP.
DE Human RIP-associated protein (RAP-2) encoding DNA.
PN WO9947672-A1.
PD 23-SEP-1999.
PA (YEDA) YEDA RES & DEV CO LTD.
PA (YESH) UNIV YESHIVA EINSTEIN COLLEGE.
Query Match 4.9%; Score 48.2; DB 2; Length 2009;
Best Local Similarity 47.8%; Pred. No. 31;
RESULT 877
ID AAV06593 standard; cDNA; 2023 BP.
DE Human N-proteinase (short form) cDNA.
PN WO9800555-A1.
PD 08-JAN-1998.
PA (PROCK) PROCKOP D J.
PA (COLI) COLIGE A.
PA (LAPI) LAPIERE C.
Query Match 4.9%; Score 48.2; DB 2; Length 2023;
Best Local Similarity 44.0%; Pred. No. 31;
RESULT 878
ID ABS57455 standard; cDNA; 2023 BP.
DE Human short form N-proteinase cDNA.
PN US6428998-B1.
PD 06-AUG-2002.
PA (UYLI-) UNIV LIEGE.
Query Match 4.9%; Score 48.2; DB 10; Length 2023;
Best Local Similarity 44.0%; Pred. No. 31;

RESULT 879
ID AAZ07514 standard; DNA; 2034 BP.
DE Human RIP-associated protein (RAP-2) clone #41072 nucleotide sequence.
PN WO9947672-A1.
PD 23-SEP-1999.
PA (YEDA) YEDA RES & DEV CO LTD.
PA (YESH) UNIV YESHIVA EINSTEIN COLLEGE.
Query Match 4.9%; Score 48.2; DB 2; Length 2034;
Best Local Similarity 47.8%; Pred. No. 31;
RESULT 880
ID ACD23012 standard; cDNA; 2035 BP.
DE Human NEMO cDNA.
PN US2003032055-A1.
PD 13-FEB-2003.
PA (KENW) KENWICK S J.
PA (WOPF) WOPFENDIN H.
PA (MUNN) MUNNICH A.
PA (SMAH) SMARI A.
PA (ISRA) ISRAEL A.
PA (POUS) POUTKA A.
PA (HEIS) HEISS N.
PA (DURS) D'URSO M.
PA (LEWI) LEWIS R A.
PA (NELS) NELSON D L.
PA (ARAD) ARADHYA S.
PA (LEVY) LEVY M.
Query Match 4.9%; Score 48.2; DB 9; Length 2035;
Best Local Similarity 47.8%; Pred. No. 31;
RESULT 881
ID AAA35066 standard; DNA; 2171 BP.
DE Human adenosine receptor related polynucleotide SEQ ID NO:2755.
PN WO200009525-A2.
PD 24-FEB-2000.
PA (UYEC-) UNIV EAST CAROLINA.
Query Match 4.9%; Score 48.2; DB 3; Length 2171;
Best Local Similarity 47.2%; Pred. No. 31;
RESULT 882
ID AAF21188 standard; DNA; 2171 BP.
DE Human low adenosine antisense oligonucleotide related sequence #2755.
PN WO200062736-A2.
PD 26-OCT-2000.
PA (UYEC-) UNIV EAST CAROLINA.
PA (NYCE) NYCE J W.
Query Match 4.9%; Score 48.2; DB 3; Length 2171;
Best Local Similarity 47.2%; Pred. No. 31;
RESULT 883
ID AB296882 standard; DNA; 2171 BP.
DE Human nucleic acid sequence.
PN WO200285308-A2.
PD 31-OCT-2002.
PA (EPIG-) EPIGENESIS PHARM INC.
Query Match 4.9%; Score 48.2; DB 10; Length 2171;
Best Local Similarity 47.2%; Pred. No. 31;
RESULT 884
ID ABD20731 standard; DNA; 2171 BP.
DE Human pulmonary and inflammatory target DNA #342.
PN WO200285309-A2.
PD 31-OCT-2002.
PA (EPIG-) EPIGENESIS PHARM INC.
Query Match 4.9%; Score 48.2; DB 11; Length 2171;
Best Local Similarity 47.2%; Pred. No. 31;
RESULT 885
ID ACA27128 standard; DNA; 2595 BP.
DE Prokaryotic essential gene #8785.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 4.9%; Score 48.2; DB 8; Length 2595;
Best Local Similarity 46.3%; Pred. No. 31;
RESULT 886
ID AAD28564 standard; DNA; 3350 BP.
DE Herpes simplex virus type 2 G10_UL37consensus DNA.
PN WO200202131-A2.

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PD 10-JAN-2002.
PA (CORI-) CORIXA CORP. 4.9%; Score 48.2; DB 6; Length 3350;
Query Match 44.5%; Pred. No. 31;
Best Local Similarity 44.5%; Pred. No. 31;
RESULT 887
ID ADG74976 standard; DNA; 3350 BP.
DE Human herpesvirus 2 isolated clone DNA - SEQ ID 48.
PN WO2003086308-A2.
PD 23-OCT-2003.
PA (CORI-) CORIXA CORP. 4.9%; Score 48.2; DB 10; Length 3350;
Query Match 44.5%; Pred. No. 31;
Best Local Similarity 44.5%; Pred. No. 31;
RESULT 888
ID AAS77503 standard; cDNA; 3633 BP.
DE DNA encoding novel human diagnostic protein #13307.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC. 4.9%; Score 48.2; DB 5; Length 3633;
Query Match 44.0%; Pred. No. 31;
Best Local Similarity 44.0%; Pred. No. 31;
RESULT 889
ID ACC72669 standard; cDNA; 3636 BP.
DE Human cancer related protein encoding cDNA SEQ ID NO:8.
PN WO2003025138-A2.
PD 27-MAR-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC. 4.9%; Score 48.2; DB 10; Length 3636;
Query Match 44.0%; Pred. No. 31;
Best Local Similarity 44.0%; Pred. No. 31;
RESULT 890
ID ACA040841 standard; DNA; 4146 BP.
DE Prokaryotic essential gene #22498.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC. 4.9%; Score 48.2; DB 8; Length 4146;
Query Match 46.1%; Pred. No. 31;
Best Local Similarity 46.1%; Pred. No. 31;
RESULT 891
ID ACA0804 standard; DNA; 4542 BP.
DE Prokaryotic essential gene #22461.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC. 4.9%; Score 48.2; DB 8; Length 4542;
Query Match 43.2%; Pred. No. 30;
Best Local Similarity 43.2%; Pred. No. 30;
RESULT 892
ID ADP09634 standard; DNA; 4941 BP.
DE Rice cinnamic acid 5-hydroxylase genomic DNA without the T-DNA SeqID 25.
PN WO2004046357-A1.
PD 03-JUN-2004.
PA (POSC-) POSCO. 4.9%; Score 48.2; DB 12; Length 4941;
PA (POST-) POSTECH FOUND. 49.8%; Pred. No. 30;
Query Match 49.8%; Pred. No. 30;
Best Local Similarity 49.8%; Pred. No. 30;
RESULT 893
ID ADO10048 standard; cDNA; 5204 BP.
DE Novel human protein Novid cDNA.
PN US2004052806-A1.
PD 18-MAR-2004.
PA (KEKU/) KEKUDA R. 4.9%; Score 48.2; DB 3; Length 8631;
PA (ALSO/) ALSOROOK J P. 4.9%; Score 48.2; DB 3; Length 8631;
PA (TCH-) TCHERNEV V T. 4.9%; Score 48.2; DB 3; Length 8631;
PA (LIUX/) LIU X. 4.9%; Score 48.2; DB 3; Length 8631;
PA (SPYT/) SPYTEK K A. 4.9%; Score 48.2; DB 3; Length 8631;
PA (PAT/) PATURAJAN M. 4.9%; Score 48.2; DB 3; Length 8631;
PA (GROS/) GROSSE W M. 4.9%; Score 48.2; DB 3; Length 8631;
PA (LEPL/) LEFLEY D M. 4.9%; Score 48.2; DB 3; Length 8631;
PA (BURG/) BURGESS C E. 4.9%; Score 48.2; DB 3; Length 8631;
PA (VERN/) VERNET C A M. 4.9%; Score 48.2; DB 3; Length 8631;
PA (LILL/) LI L. 4.9%; Score 48.2; DB 3; Length 8631;
PA (GORM/) GORMAN L. 4.9%; Score 48.2; DB 3; Length 8631;
PA (EDIN/) EDINGER S R. 4.9%; Score 48.2; DB 3; Length 8631;
PA (SCIO/) SCIORE P. 4.9%; Score 48.2; DB 3; Length 8631;
PA (ELLE/) ELLERMAN K. 4.9%; Score 48.2; DB 3; Length 8631;

PA (MAL/) MARYANKAR U M. 4.9%; Score 48.2; DB 12; Length 5204;
PA (ROTH/) ROTHENBERG M E. 4.9%; Score 48.2; DB 12; Length 5204;
PA (STON/) STONE D J. 4.9%; Score 48.2; DB 12; Length 5204;
PA (BOLD/) BOLDOG F L. 4.9%; Score 48.2; DB 12; Length 5204;
PA (GUOX/) GUO X. 4.9%; Score 48.2; DB 12; Length 5204;
PA (SHEN/) SHENOY S G. 4.9%; Score 48.2; DB 12; Length 5204;
PA (ANDE/) ANDERSON D W. 4.9%; Score 48.2; DB 12; Length 5204;
PA (PADI/) PADIGARU M. 4.9%; Score 48.2; DB 12; Length 5204;
PA (TAUP/) TAUPIER R J. 4.9%; Score 48.2; DB 12; Length 5204;
PA (MILL/) MILLER C E. 4.9%; Score 48.2; DB 12; Length 5204;
PA (EISE/) EISEN A. 4.9%; Score 48.2; DB 12; Length 5204;
Query Match 48.9%; Pred. No. 30;
Best Local Similarity 48.9%; Pred. No. 30;
RESULT 894
ID ADP75209 standard; cDNA; 6642 BP.
DE Human ADAMTS2 cDNA splice variant 1.
PN WO2003031594-A2.
PD 17-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP. 4.9%; Score 48.2; DB 11; Length 6642;
Query Match 44.0%; Pred. No. 30;
Best Local Similarity 44.0%; Pred. No. 30;
RESULT 895
ID AAV06592 standard; cDNA; 6692 BP.
DE Human N-proteinase (long form) cDNA.
PN WO9800555-A1.
PD 08-JAN-1998.
PA (PROC/) PROCKOP D J. 4.9%; Score 48.2; DB 2; Length 6692;
PA (COLI/) COLIGE A. 4.9%; Score 48.2; DB 2; Length 6692;
PA (LAPI/) LAPIERE C. 4.9%; Score 48.2; DB 2; Length 6692;
Query Match 44.0%; Pred. No. 30;
Best Local Similarity 44.0%; Pred. No. 30;
RESULT 896
ID ABS57451 standard; cDNA; 6692 BP.
DE Human long form N-proteinase cDNA.
PN US6428998-B1.
PD 06-AUG-2002.
PA (UVIL-) UNIV LIEGE. 4.9%; Score 48.2; DB 10; Length 6692;
Query Match 44.0%; Pred. No. 30;
Best Local Similarity 44.0%; Pred. No. 30;
RESULT 897
ID AAA35028 standard; DNA; 8631 BP.
DE Human adenosine receptor related polynucleotide SEQ ID NO:2717.
PN WO200009525-A2.
PD 24-FEB-2000.
PA (UYEC-) UNIV EAST CAROLINA. 4.9%; Score 48.2; DB 3; Length 8631;
Query Match 47.8%; Pred. No. 30;
Best Local Similarity 47.8%; Pred. No. 30;
RESULT 898
ID AAF21150 standard; DNA; 8631 BP.
DE Human low adenosine antisense oligonucleotide related sequence #2717.
PN WO200062736-A2.
PD 26-OCT-2000.
PA (UYEC-) UNIV EAST CAROLINA. 4.9%; Score 48.2; DB 3; Length 8631;
PA (NYCE/) NYCE J W. 4.9%; Score 48.2; DB 3; Length 8631;
Query Match 47.8%; Pred. No. 30;
Best Local Similarity 47.8%; Pred. No. 30;
RESULT 899
ID ABZ96844 standard; DNA; 8631 BP.
DE Human nucleic acid sequence.
PN WO200285308-A2.
PD 31-OCT-2002.
PA (EPIG-) EPIGENESIS PHARM INC. 4.9%; Score 48.2; DB 10; Length 8631;
Query Match 47.8%; Pred. No. 30;
Best Local Similarity 47.8%; Pred. No. 30;
RESULT 900
ID ABD20693 standard; DNA; 8631 BP.
DE Human pulmonary and inflammatory target DNA #304.
PN WO200285309-A2.
PD 31-OCT-2002.
PA (EPIG-) EPIGENESIS PHARM INC. 4.9%; Score 48.2; DB 11; Length 8631;
Query Match 47.8%; Pred. No. 30;
Best Local Similarity 47.8%; Pred. No. 30;
RESULT 901

ID AAD54222 standard; DNA; 9579 BP.
DE Streptomyces platensis subspecies rosaceus dorrigocin ORF5 DNA.
PN WO200288176-A2.
PD 07-NOV-2002.
PA (ECOP-) ECOPIA BIOSCIENCES INC.
Query Match 4.9%; Score 48.2; DB 10; Length 9579;
Best Local Similarity 47.2%; Pred. No. 30;
RESULT 902
ID ADC26981 standard; DNA; 20922 BP.
DE Sorangium cellulosum tmbA gene cluster tmbB DNA.
PN US2003054547-A1.
PD 20-MAR-2003.
PA (JULI/) JULIEN B.
Query Match 4.9%; Score 48.2; DB 10; Length 20922;
Best Local Similarity 46.3%; Pred. No. 29;
RESULT 903
ID AAD17185 standard; DNA; 27541 BP.
DE Streptomyces noursei nys2 DNA of nystatin PKS gene cluster.
PN WO200159126-A2.
PD 16-AUG-2001.
PA (UYNO-) UNIV NORGES TEKNISK NATURVITENSKAPELIGE.
PA (SNTF) SINTEF STIFTELSEN IND TEK FORSK.
PA (ALPH-) ALPHARMA AS.
PA (SINV-) SINVENT AS.
PA (DZIE/) DZIEGLEWSKA H.
PA (ZOTC/) ZOTCHEV S B.
PA (SEKU/) SEKUROVA O N.
PA (FJAE/) FJAEVRIK E.
PA (BRAU/) BRAUTASET T.
PA (STRO/) STROM A R.
PA (VALL/) VALLA S.
Query Match 4.9%; Score 48.2; DB 4; Length 27541;
Best Local Similarity 47.0%; Pred. No. 29;
RESULT 904
ID AAD54217 standard; DNA; 52101 BP.
DE Streptomyces platensis subspecies rosaceus dorrigocin DNA.
PN WO200288176-A2.
PD 07-NOV-2002.
PA (ECOP-) ECOPIA BIOSCIENCES INC.
Query Match 4.9%; Score 48.2; DB 10; Length 52101;
Best Local Similarity 47.2%; Pred. No. 28;
RESULT 905
ID ADC26995 standard; DNA; 67251 BP.
DE Sorangium cellulosum tmbA gene cluster.
PN US2003054547-A1.
PD 20-MAR-2003.
PA (JULI/) JULIEN B.
Query Match 4.9%; Score 48.2; DB 10; Length 67251;
Best Local Similarity 46.4%; Pred. No. 28;
RESULT 906
ID AAL60437 standard; DNA; 70383 BP.
DE Human kinase splice form 1 genomic DNA.
Query Match 4.9%; Score 48.2; DB 9; Length 70383;
Best Local Similarity 45.5%; Pred. No. 28;
RESULT 907
ID AD139160 standard; DNA; 86941 BP.
DE Streptomyces hygroscopicus herbimycin gene cluster, SEQ ID NO:2.
PN WO2003106653-A2.
PD 24-DEC-2003.
PA (KOSA-) KOSAN BIOSCIENCES INC.
PA (REID/) REID R C.
Query Match 4.9%; Score 48.2; DB 12; Length 86941;
Best Local Similarity 45.9%; Pred. No. 28;
RESULT 908
Query Match 4.9%; Score 48.2; DB 4; Length 110000;
Best Local Similarity 43.2%; Pred. No. 28;
RESULT 909
Query Match 4.9%; Score 48.2; DB 4; Length 110000;
Best Local Similarity 43.2%; Pred. No. 28;
RESULT 910
ID ABD03629 standard; DNA; 465 BP.
DE Pseudomonas aeruginosa polynucleotide #2233.
PN US5551795-B1.

PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 4.9%; Score 48; DB 11; Length 465;
Best Local Similarity 50.0%; Pred. No. 35;
RESULT 911
ID ACF39326 standard; DNA; 660 BP.
DE Mycobacterium tuberculosis mycobacterial antigen DNA SEQ ID NO:28.
PN WO2003033530-A2.
PD 24-APR-2003.
PA (MICR-) MICROBIOLOGICAL RES AUTHORITY.
Query Match 4.9%; Score 48; DB 8; Length 660;
Best Local Similarity 51.4%; Pred. No. 35;
RESULT 912
ID ABQ40859 standard; DNA; 712 BP.
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 27450.
PN WO200218632-A2.
PD 07-MAR-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.9%; Score 48; DB 6; Length 712;
Best Local Similarity 45.5%; Pred. No. 35;
RESULT 913
ID ABQ40858 standard; DNA; 712 BP.
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 27449.
PN WO200218632-A2.
PD 07-MAR-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.9%; Score 48; DB 6; Length 712;
Best Local Similarity 45.5%; Pred. No. 35;
RESULT 914
ID AB266735 standard; DNA; 756 BP.
DE Orthosomycin biosynthetic polynucleotide SEQ ID NO 132.
PN WO200279505-A2.
PD 10-OCT-2002.
PA (ECOP-) ECOPIA BIOSCIENCES INC.
Query Match 4.9%; Score 48; DB 10; Length 756;
Best Local Similarity 48.5%; Pred. No. 35;
RESULT 915
ID ABD08476 standard; DNA; 822 BP.
DE Pseudomonas aeruginosa polynucleotide #7080.
PN US5551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 4.9%; Score 48; DB 11; Length 822;
Best Local Similarity 45.2%; Pred. No. 34;
RESULT 916
ID ABD03843 standard; DNA; 852 BP.
DE Pseudomonas aeruginosa polynucleotide #2447.
PN US5551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 4.9%; Score 48; DB 11; Length 852;
Best Local Similarity 50.0%; Pred. No. 34;
RESULT 917
ID ABD03031 standard; DNA; 1071 BP.
DE Pseudomonas aeruginosa polynucleotide #1635.
PN US5551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 4.9%; Score 48; DB 11; Length 1071;
Best Local Similarity 50.0%; Pred. No. 34;
RESULT 918
ID AAA02477 standard; cDNA; 1127 BP.
DE Human colon cancer cell line polynucleotide sequence SEQ ID NO:2468.
PN WO9958675-A2.
PD 18-NOV-1999.
PA (CHIR) CHIRON CORP.
PA (HYSE-) HYSEQ INC.
Query Match 4.9%; Score 48; DB 3; Length 1127;
Best Local Similarity 34.2%; Pred. No. 34;
RESULT 919
ID AAZ10560 standard; DNA; 1128 BP.
DE DNA encoding G protein-coupled receptor protein designated SREB1.
PN WO9946378-A1.

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PD 16-SEP-1999.
PA (YAWA) YAMANOUCHI PHARM CO LTD.
Query Match 4.9%; Score 48; DB 2; Length 1128;
Best Local Similarity 45.1%; Pred. No. 34;
RESULT 920
ID AAA46026 standard; cDNA; 1128 BP.
DE Human G protein coupled receptor hGPCR27 encoding cDNA SEQ ID NO:17.
PN WO200022131-A2.
PD 20-APR-2000.
PA (AREN-) ARENA PHARM INC.
Query Match 4.9%; Score 48; DB 3; Length 1128;
Best Local Similarity 45.1%; Pred. No. 34;
RESULT 921
ID AAD01125 standard; cDNA; 1128 BP.
DE Human orphan G protein-coupled receptor hGPCR27 cDNA.
PN WO200031258-A2.
PD 02-JUN-2000.
PA (AREN-) ARENA PHARM INC.
Query Match 4.9%; Score 48; DB 3; Length 1128;
Best Local Similarity 45.1%; Pred. No. 34;
RESULT 922
ID AAD27892 standard; DNA; 1128 BP.
DE Human G-protein coupled receptor 14266 DNA.
PN WO200212344-A2.
PD 14-FEB-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 4.9%; Score 48; DB 6; Length 1128;
Best Local Similarity 45.1%; Pred. No. 34;
RESULT 923
ID AAS98049 standard; DNA; 1128 BP.
DE Human DNA for potential G protein-coupled receptor #7.
PN WO200185791-A1.
PD 15-NOV-2001.
PA (LIFE-) LIFESPAN BIOSCIENCES INC.
Query Match 4.9%; Score 48; DB 6; Length 1128;
Best Local Similarity 45.1%; Pred. No. 34;
RESULT 924
ID ACA93263 standard; cDNA; 1128 BP.
DE Human cDNA encoding GPCR hGPCR27.
PN US2003017528-A1.
PD 23-JAN-2003.
PA (CHEN/) CHEN R.
PA (DANG/) DANG H T.
PA (LIAN/) LIAN C W.
PA (LINI/) LIN I.
Query Match 4.9%; Score 48; DB 8; Length 1128;
Best Local Similarity 45.1%; Pred. No. 34;
RESULT 925
ID AB242853 standard; DNA; 1128 BP.
DE Human G protein-coupled receptor GPR27 nucleotide SEQ ID NO:493.
PN WO200261087-A2.
PD 08-AUG-2002.
PA (LIFE-) LIFESPAN BIOSCIENCES INC.
Query Match 4.9%; Score 48; DB 8; Length 1128;
Best Local Similarity 45.1%; Pred. No. 34;
RESULT 926
ID ADG98761 standard; cDNA; 1128 BP.
DE Human orphan GPCR cDNA, GPCR27.
PN US2003148450-A1.
PD 07-AUG-2003.
PA (CHEN/) CHEN R.
PA (DANG/) DANG H T.
PA (LIAN/) LIAN C W.
PA (LINI/) LIN I.
Query Match 4.9%; Score 48; DB 10; Length 1128;
Best Local Similarity 45.1%; Pred. No. 34;
RESULT 927
ID ADJ26924 standard; cDNA; 1128 BP.
DE Human endogenous orphan G-protein coupled receptor (GPCR) 27 cDNA.
PN US2003175891-A1.
PD 18-SEP-2003.
PA (CHEN/) CHEN R.
PA (DANG/) DANG H T.

PA (LIAN/) LIAN C W.
PA (LINI/) LIN I.
Query Match 4.9%; Score 48; DB 11; Length 1128;
Best Local Similarity 45.1%; Pred. No. 34;
RESULT 928
ID ADN39803 standard; cDNA; 1128 BP.
DE Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:CI75.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 4.9%; Score 48; DB 11; Length 1128;
Best Local Similarity 45.1%; Pred. No. 34;
RESULT 929
ID ADG86378 standard; DNA; 1128 BP.
DE Human endogenous orphan GPCR hGPCR27 DNA.
PN US2003229216-A1.
PD 11-DEC-2003.
PA (CHEN/) CHEN R.
PA (LIAN/) LIAN C W.
PA (LOWI/) LOWITZ K.
PA (CHAL/) CHALMERS D T.
PA (BEHA/) BEHAN D P.
Query Match 4.9%; Score 48; DB 12; Length 1128;
Best Local Similarity 45.1%; Pred. No. 34;
RESULT 930
ID ADO29912 standard; cDNA; 1128 BP.
DE Human GPCR GPR27 polynucleotide, SEQ ID NO:1014.
PN WO2004040000-A2.
PD 13-MAY-2004.
PA (PRIM-) PRIMAL INC.
Query Match 4.9%; Score 48; DB 12; Length 1128;
Best Local Similarity 45.1%; Pred. No. 34;
RESULT 931
ID ADP20171 standard; cDNA; 1128 BP.
DE Human G protein coupled receptor hGPCR27 cDNA.
PN US2004110238-A1.
PD 10-JUN-2004.
PA (CHEN/) CHEN R.
PA (LIAN/) LIAN C W.
PA (LOWI/) LOWITZ K.
PA (CHAL/) CHALMERS D T.
PA (BEHA/) BEHAN D P.
Query Match 4.9%; Score 48; DB 12; Length 1128;
Best Local Similarity 45.1%; Pred. No. 34;
RESULT 932
ID ACC59401 standard; DNA; 1188 BP.
DE Microbial resistance gene PA1877 coding sequence.
PN WO2003041483-A2.
PD 22-MAY-2003.
PA (DART-) DARTMOUTH COLLEGE.
Query Match 4.9%; Score 48; DB 9; Length 1188;
Best Local Similarity 46.8%; Pred. No. 34;
RESULT 933
ID ADC36366 standard; DNA; 1197 BP.
DE Weed controller metabolism associated gene SEQ ID NO:234.
PN WO2003040370-A1.
PD 15-MAY-2003.
PA (SUMO-) SUMITOMO CHEM CO LTD.
Query Match 4.9%; Score 48; DB 10; Length 1197;
Best Local Similarity 44.1%; Pred. No. 34;
RESULT 934
ID ACA37909 standard; DNA; 1275 BP.
DE Prokaryotic essential gene #19566.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 4.9%; Score 48; DB 8; Length 1275;
Best Local Similarity 46.0%; Pred. No. 34;
RESULT 935
ID ABD03924 standard; DNA; 1359 BP.
DE Pseudomonas aeruginosa polynucleotide #2528.
PN US6551795-B1.
PD 22-APR-2003.

PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 4.9%; Score 48; DB 11; Length 1359;
Best Local Similarity 50.0%; Pred. No. 34;
RESULT 936
ID ADC36376 standard; DNA; 1411 BP.
DE Weed controller metabolism associated gene SEQ ID NO:244.
PN WO2003040370-A1.
PD 15-MAY-2003.
PA (SUMO) SUMITOMO CHEM CO LTD.
Query Match 4.9%; Score 48; DB 10; Length 1411;
Best Local Similarity 44.1%; Pred. No. 34;
RESULT 937
ID ABD03787 standard; DNA; 1473 BP.
DE Pseudomonas aeruginosa polynucleotide #2391.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 4.9%; Score 48; DB 11; Length 1473;
Best Local Similarity 50.0%; Pred. No. 34;
RESULT 938
ID ABD03082 standard; DNA; 1695 BP.
DE Pseudomonas aeruginosa polynucleotide #1686.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 4.9%; Score 48; DB 11; Length 1695;
Best Local Similarity 50.0%; Pred. No. 34;
RESULT 939
ID ABD02888 standard; DNA; 1740 BP.
DE Pseudomonas aeruginosa polynucleotide #1492.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 4.9%; Score 48; DB 11; Length 1740;
Best Local Similarity 50.0%; Pred. No. 34;
RESULT 940
ID AC25954 standard; DNA; 1782 BP.
DE Prokaryotic essential gene #7611.
PN WO20027183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 4.9%; Score 48; DB 8; Length 1782;
Best Local Similarity 50.0%; Pred. No. 34;
RESULT 941
ID ABD02930 standard; DNA; 1806 BP.
DE Pseudomonas aeruginosa polynucleotide #1534.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 4.9%; Score 48; DB 11; Length 1806;
Best Local Similarity 50.0%; Pred. No. 34;
RESULT 942
ID ADF70581 standard; DNA; 1842 BP.
DE Orphan receptor ligand-related human protein gene SeqID204.
PN WO2003071272-A1.
PD 28-AUG-2003.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 4.9%; Score 48; DB 10; Length 1842;
Best Local Similarity 45.1%; Pred. No. 34;
RESULT 943
ID AAX90924 standard; DNA; 1925 BP.
DE Epstein Barr Virus Nuclear Antigen 1 (EBNA 1) DNA.
PN WO9947647-A1.
PD 23-SEP-1999.
PA (PHAR-) PHARMACOEPIA INC.
Query Match 4.9%; Score 48; DB 2; Length 1925;
Best Local Similarity 51.4%; Pred. No. 34;
RESULT 944
ID ABD08413 standard; DNA; 1929 BP.
DE Pseudomonas aeruginosa polynucleotide #7017.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 4.9%; Score 48; DB 11; Length 1929;
Best Local Similarity 45.2%; Pred. No. 34;
RESULT 945
ID ABD08507 standard; DNA; 1947 BP.
DE Pseudomonas aeruginosa polynucleotide #7111.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 4.9%; Score 48; DB 11; Length 1947;
Best Local Similarity 45.2%; Pred. No. 34;
RESULT 946
ID ABD08587 standard; DNA; 2253 BP.
DE Pseudomonas aeruginosa polynucleotide #7191.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 4.9%; Score 48; DB 11; Length 2253;
Best Local Similarity 45.5%; Pred. No. 34;
RESULT 947
ID ABD08649 standard; DNA; 2409 BP.
DE Pseudomonas aeruginosa polynucleotide #7253.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 4.9%; Score 48; DB 11; Length 2409;
Best Local Similarity 45.5%; Pred. No. 33;
RESULT 948
ID ADO24486 standard; cDNA; 2485 BP.
DE Human PRO87344 encoding cDNA SEQ ID NO:125.
PN WO2004043397-A2.
PD 27-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 4.9%; Score 48; DB 12; Length 2485;
Best Local Similarity 45.1%; Pred. No. 33;
RESULT 949
ID ABD08843 standard; DNA; 2490 BP.
DE Pseudomonas aeruginosa polynucleotide #7447.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 4.9%; Score 48; DB 11; Length 2490;
Best Local Similarity 45.5%; Pred. No. 33;
RESULT 950
ID AAS54094 standard; DNA; 3489 BP.
DE Pseudomonas aeruginosa DNA for cellular proliferation protein #225.
PN WO200170955-A2.
PD 27-SEP-2001.
PA (ELIT-) ELITRA PHARM INC.
Query Match 4.9%; Score 48; DB 4; Length 3489;
Best Local Similarity 45.1%; Pred. No. 33;
RESULT 951
ID ACA42240 standard; DNA; 3489 BP.
DE Prokaryotic essential gene #23897.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 4.9%; Score 48; DB 8; Length 3489;
Best Local Similarity 45.1%; Pred. No. 33;
RESULT 952
ID AAS08699 standard; DNA; 12152 BP.
DE M. carbonacea DNA encoding Everninomicin biosynthetic enzymes.
PN WO200151639-A2.
PD 19-JUL-2001.
PA (SCHE) SCHERING CORP.
Query Match 4.9%; Score 48; DB 5; Length 12152;
Best Local Similarity 48.5%; Pred. No. 32;
RESULT 953
ID AAS17367 standard; DNA; 33529 BP.
DE DNA sequence of S. cellulosum polyketide synthase cosmid, pKOS28-26.
PN US6280599-B1.
PD 28-AUG-2001.
PA (KOSA-) KOSAN BIOSCIENCE.
Query Match 4.9%; Score 48; DB 5; Length 33529;

Best Local Similarity 46.4%; Pred. No. 31;
RESULT 954
ID ABZ66810 standard; DNA; 37116 BP.
DE Orthosmycin biosynthetic gene cluster SEQ ID NO 279.
PN WO200279505-A2.
PD 10-OCT-2002.
PA (ECOP-) ECOPIA BIOSCIENCES INC.
Query Match 4.9%; Score 48; DB 10; Length 37116;
Best Local Similarity 48.5%; Pred. No. 31;
RESULT 955
ID ADP64454 standard; DNA; 76994 BP.
DE Sorangium cellulosum disorazole polyketide synthase gene cluster DNA.
PN WO2004053065-A2.
PD 24-JUN-2004.
PA (KOSA-) KOSAN BIOSCIENCES INC.
Query Match 4.9%; Score 48; DB 12; Length 76994;
Best Local Similarity 44.4%; Pred. No. 30;
RESULT 956
ID ABD08121 standard; DNA; 309 BP.
DE Pseudomonas aeruginosa polynucleotide #6725.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 4.8%; Score 47.8; DB 11; Length 309;
Best Local Similarity 49.4%; Pred. No. 38;
RESULT 957
ID ADI42790 standard; DNA; 487 BP.
DE Plant transcription factor polynucleotide #800.
PN US2004019927-A1.
PD 29-JAN-2004.
PA (SHER-) SHERMAN B K.
PA (RIEC-) RIECHMANN J L.
PA (JIANG-) JIANG C.
PA (HEAR-) HEARD J E.
PA (HAAR-) HAARKE V.
PA (CREE-) CREELMAN R A.
PA (RATC-) RATCLIFFE O.
PA (ADAM-) ADAM L J.
PA (REUB-) REUBER T L.
PA (KEDD-) KEDDIE J.
PA (BROU-) BROUN P E.
PA (PILG-) PILGRIM M L.
PA (DUBE-) DUBELL A N.
PA (PINE-) PINEDA O.
PA (YUGG-) YU G.
Query Match 4.8%; Score 47.8; DB 12; Length 487;
Best Local Similarity 45.1%; Pred. No. 38;
RESULT 958
ID ABK35609 standard; DNA; 777 BP.
DE Gene encoding novel human secreted or membrane-associated protein #28.
PN WO200204600-A2.
PD 17-JAN-2002.
PA (SMIK-) SMITHKLINE BEECHAM CORP.
PA (GLAX-) GLAXO GROUP LTD.
Query Match 4.8%; Score 47.8; DB 6; Length 777;
Best Local Similarity 51.8%; Pred. No. 37;
RESULT 959
ID ADF58345 standard; cDNA; 777 BP.
DE Human polynucleotide sequence SEQ ID NO:712.
PN WO2003080795-A2.
PD 02-OCT-2003.
PA (HYSE-) HYSEQ INC.
Query Match 4.8%; Score 47.8; DB 10; Length 777;
Best Local Similarity 51.8%; Pred. No. 37;
RESULT 960
ID ABD17337 standard; DNA; 801 BP.
DE Pseudomonas aeruginosa polynucleotide #15941.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 4.8%; Score 47.8; DB 11; Length 801;
Best Local Similarity 47.5%; Pred. No. 37;

RESULT 961
ID ABD15977 standard; DNA; 819 BP.
DE Pseudomonas aeruginosa polynucleotide #14581.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 4.8%; Score 47.8; DB 11; Length 819;
Best Local Similarity 47.1%; Pred. No. 37;
RESULT 962
ID AAL61183 standard; DNA; 885 BP.
DE Actinosynnema pretiosum methyltransferase gene #2.
PN WO2003045312-A2.
PD 05-JUN-2003.
PA (UNIW-) UNIV WASHINGTON.
Query Match 4.8%; Score 47.8; DB 8; Length 885;
Best Local Similarity 44.9%; Pred. No. 37;
RESULT 963
ID ABD08291 standard; DNA; 966 BP.
DE Pseudomonas aeruginosa polynucleotide #6895.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 4.8%; Score 47.8; DB 11; Length 966;
Best Local Similarity 49.4%; Pred. No. 37;
RESULT 964
ID ACA37720 standard; DNA; 1029 BP.
DE Prokaryotic essential gene #19377.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 4.8%; Score 47.8; DB 8; Length 1029;
Best Local Similarity 45.6%; Pred. No. 37;
RESULT 965
ID ADB80220 standard; DNA; 1173 BP.
DE Mycobacterium tuberculosis nutrient starvation-inducible gene #129.
PN WO2003004520-A2.
PD 16-JAN-2003.
PA (MITCR-) MICROBIOLOGICAL RES AUTHORITY.
Query Match 4.8%; Score 47.8; DB 10; Length 1173;
Best Local Similarity 47.0%; Pred. No. 37;
RESULT 966
ID ABD17849 standard; DNA; 1218 BP.
DE Pseudomonas aeruginosa polynucleotide #16453.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 4.8%; Score 47.8; DB 11; Length 1218;
Best Local Similarity 47.5%; Pred. No. 37;
RESULT 967
ID ACA26886 standard; DNA; 1287 BP.
DE Prokaryotic essential gene #8543.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 4.8%; Score 47.8; DB 8; Length 1287;
Best Local Similarity 45.4%; Pred. No. 37;
RESULT 968
ID ABL15825 standard; cDNA; 1291 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 41957.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE-) PE CORP NY.
Query Match 4.8%; Score 47.8; DB 4; Length 1291;
Best Local Similarity 47.8%; Pred. No. 37;
RESULT 969
ID ABA16862 standard; DNA; 1343 BP.
DE Human nervous system related polynucleotide SEQ ID NO 9193.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.8%; Score 47.8; DB 5; Length 1343;
Best Local Similarity 51.8%; Pred. No. 37;
RESULT 970

ID ABA19759 standard; DNA; 1343 BP.
DE Human nervous system related polynucleotide SEQ ID NO 12090.
FN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.8%; Score 47.8; DB 5; Length 1343;
Best Local Similarity 51.8%; Pred. No. 37;
RESULT 971
ID ACA37836 standard; DNA; 1404 BP.
DE Prokaryotic essential gene #19493.
FN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 4.8%; Score 47.8; DB 8; Length 1404;
Best Local Similarity 46.8%; Pred. No. 37;
RESULT 972
ID ABD08211 standard; DNA; 1485 BP.
DE Pseudomonas aeruginosa polynucleotide #6815.
FN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 4.8%; Score 47.8; DB 11; Length 1485;
Best Local Similarity 49.4%; Pred. No. 37;
RESULT 973
ID ABD08326 standard; DNA; 1509 BP.
DE Pseudomonas aeruginosa polynucleotide #6930.
FN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 4.8%; Score 47.8; DB 11; Length 1509;
Best Local Similarity 49.4%; Pred. No. 37;
RESULT 974
ID ACAJ37879 standard; DNA; 1527 BP.
DE Prokaryotic essential gene #19536.
FN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 4.8%; Score 47.8; DB 8; Length 1527;
Best Local Similarity 47.2%; Pred. No. 37;
RESULT 975
ID AAD36877 standard; DNA; 1686 BP.
DE S. clavuligerus clavulanic acid biosynthesis enzyme encoding DNA, ORF15.
FN WO2003040372-A2.
PD 15-MAY-2003.
PA (SMIK-) SMITHKLINE BEECHAM PLC.
PA (UVAL-) UNIV ALBERTA.
Query Match 4.8%; Score 47.8; DB 8; Length 1686;
Best Local Similarity 46.3%; Pred. No. 37;
RESULT 976
ID AAT62138 standard; DNA; 1771 BP.
DE Leishmania tropica Lt-210 antigen cDNA.
FN WO9711180-A1.
PD 27-MAR-1997.
PA (CORI-) CORIXA CORP.
Query Match 4.8%; Score 47.8; DB 2; Length 1771;
Best Local Similarity 45.5%; Pred. No. 36;
RESULT 977
ID AAV47558 standard; DNA; 1771 BP.
DE Leishmania antigen Lt-210 coding sequence.
FN WO9835045-A2.
PD 13-AUG-1998.
PA (CORI-) CORIXA CORP.
Query Match 4.8%; Score 47.8; DB 2; Length 1771;
Best Local Similarity 45.5%; Pred. No. 36;
RESULT 978
ID AAZ5621 standard; DNA; 1771 BP.
DE Leishmania tropica Lt210 nucleotide sequence.
FN US965142-A.
PD 12-OCT-1999.
PA (CORI-) CORIXA CORP.
Query Match 4.8%; Score 47.8; DB 2; Length 1771;
Best Local Similarity 45.5%; Pred. No. 36;
RESULT 979

ID AAD40285 standard; DNA; 1771 BP.
DE Leishmania tropica Lt-1 antigenic protein encoding DNA.
FN US6375955-B1.
PD 23-APR-2002.
PA (CORI-) CORIXA CORP.
Query Match 4.8%; Score 47.8; DB 6; Length 1771;
Best Local Similarity 45.5%; Pred. No. 36;
RESULT 980
ID AAS96022 standard; cDNA; 1771 BP.
DE Leishmania antigen Lt-1 DNA.
FN WO200179276-A2.
PD 25-OCT-2001.
PA (CORI-) CORIXA CORP.
Query Match 4.8%; Score 47.8; DB 6; Length 1771;
Best Local Similarity 45.5%; Pred. No. 36;
RESULT 981
ID ABK81733 standard; DNA; 1771 BP.
DE Leishmania antigenic polynucleotide #4.
FN US6365165-B1.
PD 02-APR-2002.
PA (CORI-) CORIXA CORP.
Query Match 4.8%; Score 47.8; DB 6; Length 1771;
Best Local Similarity 45.5%; Pred. No. 36;
RESULT 982
ID AAF88524 standard; DNA; 1771 BP.
DE L. tropica Lt-210 antigen DNA SEQ ID 7.
FN US2002081320-A1.
PD 27-JUN-2002.
PA (REED-) REED S G.
PA (CAMP-) CAMPOS-NETO A.
PA (WEBB-) WEBB J R.
PA (DILL-) DILLON D C.
PA (SKEI-) SKEIKY Y A W.
PA (BHAT-) BHATIA A.
PA (COLE-) COLER R N.
PA (PROB-) PROBST P.
PA (BRAN-) BRANNON M.
Query Match 4.8%; Score 47.8; DB 6; Length 1771;
Best Local Similarity 45.5%; Pred. No. 36;
RESULT 983
ID ADB78770 standard; DNA; 1771 BP.
DE Leishmania DNA encoding antigen Lt-210.
FN US2002169285-A1.
PD 14-NOV-2002.
PA (REED-) REED S G.
PA (CAMP-) CAMPOS-NETO A.
PA (WEBB-) WEBB J R.
PA (DILL-) DILLON D C.
Query Match 4.8%; Score 47.8; DB 9; Length 1771;
Best Local Similarity 45.5%; Pred. No. 36;
RESULT 984
ID ABD17433 standard; DNA; 1962 BP.
DE Pseudomonas aeruginosa polynucleotide #16037.
FN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 4.8%; Score 47.8; DB 11; Length 1962;
Best Local Similarity 47.5%; Pred. No. 36;
RESULT 985
ID ABD17959 standard; DNA; 2526 BP.
DE Pseudomonas aeruginosa polynucleotide #16563.
FN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 4.8%; Score 47.8; DB 11; Length 2526;
Best Local Similarity 47.5%; Pred. No. 36;
RESULT 986
ID AAL61203 standard; DNA; 3018 BP.
DE Actinosynnema pretiosum cytochrome P450 gene.
FN WO2003045312-A2.
PD 05-JUN-2003.
PA (UNIW) UNIV WASHINGTON.
Query Match 4.8%; Score 47.8; DB 8; Length 3018;

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Best Local Similarity 47.9%; Pred. No. 36;
RESULT 987
ID ABD10462 standard; DNA; 3126 BP.
DE Pseudomonas aeruginosa polynucleotide #9066.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 4.8%; Score 47.8; DB 11; Length 3126;
Best Local Similarity 51.1%; Pred. No. 36;
RESULT 988
ID AAL61181 standard; DNA; 3354 BP.
DE Actinosynnema pretiosum transcriptional regulator gene #1.
PN WO2003045312-A2.
PD 05-JUN-2003.
PA (UNIW) UNIV WASHINGTON.
Query Match 4.8%; Score 47.8; DB 8; Length 3354;
Best Local Similarity 41.5%; Pred. No. 36;
RESULT 989
ID ADQ19781 standard; DNA; 3824 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 2600.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 4.8%; Score 47.8; DB 12; Length 3824;
Best Local Similarity 47.3%; Pred. No. 36;
RESULT 990
ID ADQ23914 standard; DNA; 3824 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 6734.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 4.8%; Score 47.8; DB 12; Length 3824;
Best Local Similarity 47.3%; Pred. No. 36;
RESULT 991
ID ABD16585 standard; DNA; 5121 BP.
DE Pseudomonas aeruginosa polynucleotide #15189.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 4.8%; Score 47.8; DB 11; Length 5121;
Best Local Similarity 47.1%; Pred. No. 35;
RESULT 992
ID ABD16327 standard; DNA; 6327 BP.
DE Pseudomonas aeruginosa polynucleotide #14931.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 4.8%; Score 47.8; DB 11; Length 6327;
Best Local Similarity 47.1%; Pred. No. 35;
RESULT 993
ID ACF05731 standard; DNA; 7201 BP.
DE Plasmid pEAK12d-IPAA44548-6His.
PN WO2003055913-A2.
PD 10-JUL-2003.
PA (ARES-) ARES TRADING SA.
Query Match 4.8%; Score 47.8; DB 9; Length 7201;
Best Local Similarity 48.7%; Pred. No. 35;
RESULT 994
ID ACF06299 standard; DNA; 7231 BP.
DE Plasmid pEAK12d-IPAA26841-6His nucleotide sequence.
PN WO2003054012-A2.
PD 03-JUL-2003.
PA (ARES-) ARES TRADING SA.
Query Match 4.8%; Score 47.8; DB 9; Length 7231;
Best Local Similarity 48.7%; Pred. No. 35;
RESULT 995
ID ACF06300 standard; DNA; 7297 BP.
DE SigptdIPAA26841s-6His nucleotide sequence.
PN WO2003054012-A2.
PD 03-JUL-2003.
PA (ARES-) ARES TRADING SA.
Query Match 4.8%; Score 47.8; DB 9; Length 7297;
Best Local Similarity 48.7%; Pred. No. 35;

RESULT 996
ID ACF05558 standard; DNA; 7429 BP.
DE Plasmid pEAK12d-IPAA24020-6His.
PN WO2003055912-A2.
PD 10-JUL-2003.
PA (ARES-) ARES TRADING SA.
Query Match 4.8%; Score 47.8; DB 9; Length 7429;
Best Local Similarity 48.7%; Pred. No. 35;
RESULT 997
ID ACF06298 standard; DNA; 7456 BP.
DE Plasmid pEAK12d-IPAA26841long-6His nucleotide sequence.
PN WO2003054012-A2.
PD 03-JUL-2003.
PA (ARES-) ARES TRADING SA.
Query Match 4.8%; Score 47.8; DB 9; Length 7456;
Best Local Similarity 48.7%; Pred. No. 35;
RESULT 998
ID ADP28653 standard; DNA; 8973 BP.
DE Human secreted protein encoding sequence SEQ ID #651.
PN WO2004035732-A2.
PD 29-APR-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match 4.8%; Score 47.8; DB 12; Length 8973;
Best Local Similarity 44.6%; Pred. No. 35;
RESULT 999
ID AAD36874 standard; DNA; 29870 BP.
DE Streptomyces clavuligerus clavulanic acid biosynthesis gene cluster.
PN WO2003040372-A2.
PD 15-MAY-2003.
PA (SMIK) SMITHKLINE BEECHAM PLC.
PA (UYAL-) UNIV ALBERTA.
Query Match 4.8%; Score 47.8; DB 8; Length 29870;
Best Local Similarity 46.3%; Pred. No. 34;
RESULT 1000
ID AA29349 standard; DNA; 71989 BP.
DE Sorangium cellulosum epothilone polyketide synthase operon genomic DNA.
Query Match 4.8%; Score 47.8; DB 3; Length 71989;
Best Local Similarity 48.2%; Pred. No. 33;
RESULT 1001
ID AAL61224 standard; DNA; 82746 BP.
DE Actinosynnema pretiosum ansamitocin biosynthetic gene cluster I.
PN WO2003045312-A2.
PD 05-JUN-2003.
PA (UNIW) UNIV WASHINGTON.
Query Match 4.8%; Score 47.8; DB 8; Length 82746;
Best Local Similarity 44.9%; Pred. No. 33;
RESULT 1002
Query Match 4.8%; Score 47.8; DB 4; Length 110000;
Best Local Similarity 47.0%; Pred. No. 33;
RESULT 1003
Query Match 4.8%; Score 47.8; DB 4; Length 110000;
Best Local Similarity 45.4%; Pred. No. 33;
RESULT 1004
Query Match 4.8%; Score 47.8; DB 4; Length 110000;
Best Local Similarity 47.0%; Pred. No. 33;
RESULT 1005
ID ACL3251 standard; DNA; 422 BP.
DE DNA clone originating in barley containing SNP encoding sequence #13242.
PN WO2003057877-A1.
PD 17-JUL-2003.
PA (UYNI-) UNIV JAPAN OKAYAMA.
Query Match 4.8%; Score 47.8; DB 9; Length 422;
Best Local Similarity 59.7%; Pred. No. 41;
RESULT 1006
ID ACA19654 standard; DNA; 921 BP.
DE Prokaryotic essential gene #1311.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 4.8%; Score 47.6; DB 8; Length 921;
Best Local Similarity 47.8%; Pred. No. 40;
RESULT 1007
ID ABD17059 standard; DNA; 930 BP.

DE Pseudomonas aeruginosa polynucleotide #15663.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 4.8%; Score 47.6; DB 11; Length 930;
Best Local Similarity 47.8%; Pred. No. 40;
RESULT 1008
ID ADI45687 standard; cDNA; 1002 BP.
DE Corn isoprenoid biosynthesis-associated cDNA #30.
PN US2004010815-A1.
PD 15-JAN-2004.
PA (LANG/) LANGE B M.
PA (GHAS/) CHASSEMIAN M.
PA (BRIG/) BRIGGS S P.
PA (COOP/) COOPER B.
PA (GLAZ/) GLAZEROOK J.
PA (GOFF/) GOFF S A.
PA (KATA/) KATAGIRI F.
PA (KREP/) KREPS J.
PA (MOUG/) MOUGHAMER T.
PA (PROV/) PROVART N.
PA (RICK/) RICKE D.
PA (ZHUT/) ZHU T.
Query Match 4.8%; Score 47.6; DB 12; Length 1002;
Best Local Similarity 47.0%; Pred. No. 40;
RESULT 1009
ID ADF31999 standard; DNA; 1170 BP.
DE Transcriptional repressor of the ROK family.
PN WO2003099993-A2.
PD 04-DEC-2003.
PA (AVET) AVENTIS PHARM INC.
Query Match 4.8%; Score 47.6; DB 12; Length 1170;
Best Local Similarity 43.8%; Pred. No. 40;
RESULT 1010
ID ADF32000 standard; DNA; 1170 BP.
DE Transcriptional repressor of the ROK family complement.
PN WO2003099993-A2.
PD 04-DEC-2003.
PA (AVET) AVENTIS PHARM INC.
Query Match 4.8%; Score 47.6; DB 12; Length 1170;
Best Local Similarity 43.8%; Pred. No. 40;
RESULT 1011
ID ACA37852 standard; DNA; 1203 BP.
DE Prokaryotic essential gene #19509.
PN WO20027183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 4.8%; Score 47.6; DB 8; Length 1203;
Best Local Similarity 45.6%; Pred. No. 40;
RESULT 1012
ID ABD04031 standard; DNA; 1248 BP.
DE Pseudomonas aeruginosa polynucleotide #2635.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 4.8%; Score 47.6; DB 11; Length 1248;
Best Local Similarity 46.4%; Pred. No. 40;
RESULT 1013
ID ABD05292 standard; DNA; 1278 BP.
DE Pseudomonas aeruginosa polynucleotide #3896.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 4.8%; Score 47.6; DB 11; Length 1278;
Best Local Similarity 43.6%; Pred. No. 40;
RESULT 1014
ID ACA03563 standard; DNA; 1971 BP.
DE Synthetic DNA encoding immunogenic HIV peptide #46.
PN WO2003004657-A1.
PD 16-JAN-2003.
PA (CHIR) CHIRON CORP.
Query Match 4.8%; Score 47.6; DB 8; Length 1971;
Best Local Similarity 46.8%; Pred. No. 39;
RESULT 1015
ID ACA03557 standard; DNA; 1971 BP.
DE Synthetic DNA encoding immunogenic HIV peptide #40.
PN WO2003004657-A1.
PD 16-JAN-2003.
PA (CHIR) CHIRON CORP.
Query Match 4.8%; Score 47.6; DB 8; Length 1971;
Best Local Similarity 47.6%; Pred. No. 39;
RESULT 1016
ID ACC78513 standard; DNA; 1971 BP.
DE HIV protInaRT_YM.opt.SF2 nucleotide sequence.
PN WO2003020876-A2.
PD 13-MAR-2003.
PA (CHIR) CHIRON CORP.
Query Match 4.8%; Score 47.6; DB 8; Length 1971;
Best Local Similarity 47.6%; Pred. No. 39;
RESULT 1017
ID ADC13270 standard; DNA; 1971 BP.
DE DNA of HIV construct protInaRT_YM-opt_C SEQ ID NO 49.
PN WO2003004620-A2.
PD 16-JAN-2003.
PA (CHIR) CHIRON CORP.
Query Match 4.8%; Score 47.6; DB 10; Length 1971;
Best Local Similarity 46.8%; Pred. No. 39;
RESULT 1018
ID ABD03593 standard; DNA; 1971 BP.
DE Pseudomonas aeruginosa polynucleotide #2197.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 4.8%; Score 47.6; DB 11; Length 1971;
Best Local Similarity 46.4%; Pred. No. 39;
RESULT 1019
ID ABD05320 standard; DNA; 1977 BP.
DE Pseudomonas aeruginosa polynucleotide #3924.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 4.8%; Score 47.6; DB 11; Length 1977;
Best Local Similarity 43.6%; Pred. No. 39;
RESULT 1020
ID AAD55732 standard; DNA; 2078 BP.
DE Dolomides tenebrosus fibroin 2 DNA.
PN WO2003020916-A2.
PD 13-MAR-2003.
PA (UTWY-) UNIV WYOMING.
Query Match 4.8%; Score 47.6; DB 8; Length 2078;
Best Local Similarity 46.2%; Pred. No. 39;
RESULT 1021
ID ABD05412 standard; DNA; 2091 BP.
DE Pseudomonas aeruginosa polynucleotide #4016.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 4.8%; Score 47.6; DB 11; Length 2091;
Best Local Similarity 43.6%; Pred. No. 39;
RESULT 1022
ID ABD03873 standard; DNA; 2211 BP.
DE Pseudomonas aeruginosa polynucleotide #2477.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 4.8%; Score 47.6; DB 11; Length 2211;
Best Local Similarity 46.4%; Pred. No. 39;
RESULT 1023
ID AAAY0477 standard; DNA; 2305 BP.
DE HIV FS(+) ProtInact_RTpt_YM coding sequence.
PN WO20030302-A2.
PD 06-JUL-2000.
PA (CHIR) CHIRON CORP.
Query Match 4.8%; Score 47.6; DB 3; Length 2305;
Best Local Similarity 47.6%; Pred. No. 39;

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RESULT 1024
 ID AAY70479 standard; DNA; 2306 BP.
 DE HIV FS(-) ProtMod Rtppt_YM coding sequence.
 PN WO20039302-A2.
 PD 06-JUL-2000.
 PA (CHIR) CHIRON CORP.
 Query Match 4.8%; Score 47.6; DB 3; Length 2306;
 Best Local Similarity 47.6%; Pred. No. 39;
 RESULT 1025
 ID ACA37615 standard; DNA; 2337 BP.
 DE Prokaryotic essential gene #19272.
 PN WO200277183-A2.
 PD 03-OCT-2002.
 PA (ELIT-) ELITRA PHARM INC.
 Query Match 4.8%; Score 47.6; DB 8; Length 2337;
 Best Local Similarity 46.4%; Pred. No. 39;
 RESULT 1026
 ID ACA27167 standard; DNA; 2424 BP.
 DE Prokaryotic essential gene #8824.
 PN WO200277183-A2.
 PD 03-OCT-2002.
 PA (ELIT-) ELITRA PHARM INC.
 Query Match 4.8%; Score 47.6; DB 8; Length 2424;
 Best Local Similarity 43.9%; Pred. No. 39;
 RESULT 1027
 ID ACA03547 standard; DNA; 2457 BP.
 DE Synthetic DNA encoding immunogenic HIV peptide #30.
 PN WO2003004657-A1.
 PD 16-JAN-2003.
 PA (CHIR) CHIRON CORP.
 Query Match 4.8%; Score 47.6; DB 8; Length 2457;
 Best Local Similarity 46.8%; Pred. No. 39;
 RESULT 1028
 ID ADC13265 standard; DNA; 2457 BP.
 DE DNA of HIV construct p2Pol-Opt_YM_C SEQ ID NO 44.
 PN WO2003004620-A2.
 PD 16-JAN-2003.
 PA (CHIR) CHIRON CORP.
 Query Match 4.8%; Score 47.6; DB 10; Length 2457;
 Best Local Similarity 46.8%; Pred. No. 39;
 RESULT 1029
 ID ABL39960 standard; DNA; 2463 BP.
 DE Synthetic construct PR975YM SEQ ID NO:31.
 PN WO200204493-A2.
 PD 17-JAN-2002.
 PA (CHIR) CHIRON CORP.
 Query Match 4.8%; Score 47.6; DB 6; Length 2463;
 Best Local Similarity 46.8%; Pred. No. 39;
 RESULT 1030
 ID ADM73765 standard; DNA; 2463 BP.
 DE HIV-1 polynucleotide #8.
 PN US2003223961-A1.
 PD 04-DEC-2003.
 PA (MEGE/) MEGEDE J Z.
 PA (BARV/) BARNETT S W.
 PA (ENGE/) ENGELBRECHT S.
 PA (RENS/) RENSBERG E J V.
 Query Match 4.8%; Score 47.6; DB 12; Length 2463;
 Best Local Similarity 46.8%; Pred. No. 39;
 RESULT 1031
 ID ACA03542 standard; DNA; 2466 BP.
 DE Synthetic DNA encoding immunogenic HIV peptide #25.
 PN WO2003004657-A1.
 PD 16-JAN-2003.
 PA (CHIR) CHIRON CORP.
 Query Match 4.8%; Score 47.6; DB 8; Length 2466;
 Best Local Similarity 47.6%; Pred. No. 39;
 RESULT 1032
 ID AC78506 standard; DNA; 2466 BP.
 DE HIV p2Polinaopt_YM.SF2 nucleotide sequence.
 PN WO2003020876-A2.
 PD 10-JUN-2004.

PD 13-MAR-2003.
 PA (CHIR) CHIRON CORP.
 Query Match 4.8%; Score 47.6; DB 8; Length 2466;
 Best Local Similarity 47.6%; Pred. No. 39;
 RESULT 1033
 ID AD28560 standard; DNA; 2481 BP.
 DE Herpes simplex virus type 2 full-length HSV-2 RL2 gene.
 PN WO200202131-A2.
 PD 10-JAN-2002.
 PA (CORI-) CORIXA CORP.
 Query Match 4.8%; Score 47.6; DB 6; Length 2481;
 Best Local Similarity 51.4%; Pred. No. 39;
 RESULT 1034
 ID ADG74963 standard; DNA; 2481 BP.
 DE Human herpesvirus 2 RL2 DNA - SEQ ID 35.
 PN WO2003086308-A2.
 PD 23-OCT-2003.
 PA (CORI-) CORIXA CORP.
 Query Match 4.8%; Score 47.6; DB 10; Length 2481;
 Best Local Similarity 51.4%; Pred. No. 39;
 RESULT 1035
 ID ADG75080 standard; DNA; 3066 BP.
 DE Human herpesvirus 2 RL2 DNA - SEQ ID 152.
 PN WO2003086308-A2.
 PD 23-OCT-2003.
 PA (CORI-) CORIXA CORP.
 Query Match 4.8%; Score 47.6; DB 10; Length 3066;
 Best Local Similarity 51.4%; Pred. No. 39;
 RESULT 1036
 ID ADF30533 standard; cDNA; 3783 BP.
 DE Rat angiogenesis modulating protein cDNA #24.
 PN US2003162706-A1.
 PD 28-AUG-2003.
 PA (PROC) PROCTER & GAMBLE CO.
 Query Match 4.8%; Score 47.6; DB 10; Length 3783;
 Best Local Similarity 43.6%; Pred. No. 39;
 RESULT 1037
 ID ADE71207 standard; DNA; 5369 BP.
 DE Novel human protein coding sequence #23.
 PN JP2002345493-A.
 PD 03-DEC-2002.
 PA (KAZU-) ZH KAZUSA DNA KENKYUSHO.
 Query Match 4.8%; Score 47.6; DB 10; Length 5369;
 Best Local Similarity 45.6%; Pred. No. 38;
 RESULT 1038
 ID ADK18365 standard; DNA; 5780 BP.
 DE Human NOVX protein encoding gene #10.
 PN WO2003057854-A2.
 PD 17-JUL-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 4.8%; Score 47.6; DB 10; Length 5780;
 Best Local Similarity 46.4%; Pred. No. 38;
 RESULT 1039
 ID ABS78696 standard; DNA; 5802 BP.
 DE S. kaniharaensis DNA encoding PKSE.
 PN CA2387401-A1.
 PD 04-SEP-2002.
 PA (ECOP-) ECOPIA BIOSCIENCES INC.
 Query Match 4.8%; Score 47.6; DB 6; Length 5802;
 Best Local Similarity 46.0%; Pred. No. 38;
 RESULT 1040
 ID ADK18367 standard; DNA; 6008 BP.
 DE Human NOVX protein encoding gene #11.
 PN WO2003057854-A2.
 PD 17-JUL-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 4.8%; Score 47.6; DB 10; Length 6008;
 Best Local Similarity 46.4%; Pred. No. 38;
 RESULT 1041
 ID ADP13461 standard; DNA; 6008 BP.
 DE Renal cell carcinoma differentially expressed gene #197.
 PN WO2004048933-A2.
 PD 10-JUN-2004.

PA (AMHP) WYETH.
PA (TWIN/) TWINE N C.
PA (BURC/) BURCZYNSKI M E.
PA (TREP/) TREPICCHIO W L.
PA (DORN/) DORNER A.
PA (STOV/) STOVER J A.
PA (SLON/) SLONI D K.
Query Match 4.8%; Score 47.6; DB 12; Length 6008;
Best Local Similarity 46.4%; Pred. No. 38;
RESULT 1042
ID AAV58939 standard; DNA; 9960 BP.
DE Mycobacterium smegmatis embCAB operon.
PN WO9841533-A1.
PD 24-SEP-1998.
Query Match 4.8%; Score 47.4; DB 12; Length 504;
Best Local Similarity 45.2%; Pred. No. 44;
RESULT 1048
ID ADG93398 standard; DNA; 670 BP.
DE Maize lipoxygenase (LOX) DNA #15.
PN US2003168855-A1.
PD 04-SEP-2003.
PA (PTON-) PIONEER HI-BRED INT INC.
Query Match 4.8%; Score 47.4; DB 10; Length 670;
Best Local Similarity 49.0%; Pred. No. 44;
RESULT 1049
ID ADG93400 standard; DNA; 670 BP.
DE Maize lipoxygenase (LOX) DNA #16.
PN US2003168855-A1.
PD 04-SEP-2003.
PA (PTON-) PIONEER HI-BRED INT INC.
Query Match 4.8%; Score 47.4; DB 10; Length 670;
Best Local Similarity 49.0%; Pred. No. 44;
RESULT 1050
ID ABD10158 standard; DNA; 918 BP.
DE Pseudomonas aeruginosa polynucleotide #8762.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 4.8%; Score 47.4; DB 11; Length 918;
Best Local Similarity 46.3%; Pred. No. 43;
RESULT 1051
ID ABD10588 standard; DNA; 948 BP.
DE Pseudomonas aeruginosa polynucleotide #9192.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 4.8%; Score 47.4; DB 11; Length 948;
Best Local Similarity 46.3%; Pred. No. 43;
RESULT 1052
ID ABD07203 standard; DNA; 954 BP.
DE Pseudomonas aeruginosa polynucleotide #5807.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 4.8%; Score 47.4; DB 11; Length 954;
Best Local Similarity 44.2%; Pred. No. 43;
RESULT 1053
ID AAZ51701 standard; DNA; 1044 BP.
DE Burkholderia multivorans recA gene (1).
PN WO200014274-A1.
PD 16-MAR-2000.
PA (UYBR-) UNIV BRITISH COLUMBIA.
Query Match 4.8%; Score 47.4; DB 3; Length 1044;
Best Local Similarity 43.6%; Pred. No. 43;
RESULT 1054
ID ABD12320 standard; DNA; 1116 BP.
DE Pseudomonas aeruginosa polynucleotide #10924.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 4.8%; Score 47.4; DB 11; Length 1116;
Best Local Similarity 48.0%; Pred. No. 43;
RESULT 1055
ID ABD10379 standard; DNA; 1149 BP.

PA (AMHP) WYETH.
PA (TWIN/) TWINE N C.
PA (BURC/) BURCZYNSKI M E.
PA (TREP/) TREPICCHIO W L.
PA (DORN/) DORNER A.
PA (STOV/) STOVER J A.
PA (SLON/) SLONI D K.
Query Match 4.8%; Score 47.6; DB 12; Length 6008;
Best Local Similarity 46.4%; Pred. No. 38;
RESULT 1042
ID AAV58939 standard; DNA; 9960 BP.
DE Mycobacterium smegmatis embCAB operon.
PN WO9841533-A1.
PD 24-SEP-1998.
Query Match 4.8%; Score 47.4; DB 12; Length 504;
Best Local Similarity 45.1%; Pred. No. 38;
RESULT 1043
ID AAD17185 standard; DNA; 27541 BP.
DE Streptomyces noursei nys2 DNA of nystatin PKS gene cluster.
PN WO200159126-A2.
PD 16-AUG-2001.
PA (UYNO-) UNIV NORGES TEKNISK NATURVITENSKAPELIGE.
PA (SNTF) SINTEF STIFTELSEN IND TEK FORSK.
PA (ALPH-) ALPHARMA AS.
PA (SINV-) SINVENT AS.
PA (DZIE/) DZIEGLEWSKA H.
PA (ZOTC/) ZOTCHEV S B.
PA (SEKU/) SEKUROVA O N.
PA (FJAE/) FJAERVIK E.
PA (BRAU/) BRAUTASET T.
PA (STRO/) STROM A R.
PA (VALL/) VALLA S.
Query Match 4.8%; Score 47.6; DB 4; Length 27541;
Best Local Similarity 47.2%; Pred. No. 36;
RESULT 1044
ID AAS59516 standard; DNA; 29255 BP.
DE Propionibacterium acnes immunogenic protein encoding DNA #11.
PN WO200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match 4.8%; Score 47.6; DB 4; Length 29255;
Best Local Similarity 44.9%; Pred. No. 36;
RESULT 1045
ID ACF64445 standard; DNA; 29255 BP.
DE Propionibacterium acnes DNA contig sequence #11.
PN WO2003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match 4.8%; Score 47.6; DB 8; Length 29255;
Best Local Similarity 44.9%; Pred. No. 36;
RESULT 1046
ID ADJ12143 standard; DNA; 414 BP.
DE Maize cDNA modulated by post-transcriptional gene silencing SeqID 779.
PN US2003135888-A1.
PD 17-JUL-2003.
PA (ZHUT/) ZHU T.
PA (WANG/) WANG X.
PA (CHAN/) CHANG H.
PA (BRIG/) BRIGGS S P.
PA (COOP/) COOPER B.
PA (GLAZ/) GLAZEBROOK J.
PA (GOFF/) GOFF S A.
PA (KATA/) KATAGIRI F.
PA (KREP/) KREPS J.
PA (MOUG/) MOUGHAMER T.
PA (PROV/) PROVART N.
PA (RICK/) RICKS D.
Query Match 4.8%; Score 47.4; DB 11; Length 414;
Best Local Similarity 47.5%; Pred. No. 44;
RESULT 1047
ID ADJ444853 standard; cDNA; 504 BP.
DE Plant cDNA #5853.

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DE Pseudomonas aeruginosa polynucleotide #8983.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 4.8%; Score 47.4; DB 11; Length 1149;
Best Local Similarity 46.3%; Pred. No. 43;
RESULT 1056
ID ABD12534 standard; DNA; 1209 BP.
DE Pseudomonas aeruginosa polynucleotide #11138.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 4.8%; Score 47.4; DB 11; Length 1209;
Best Local Similarity 48.0%; Pred. No. 43;
RESULT 1057
ID ABX56037 standard; DNA; 1248 BP.
DE M. echinospora calicheamicin biosynthesis gene calM.
PN WO200279465-A2.
PD 10-OCT-2002.
PA (SLOK) SLOAN KETTERING INST CANCER RES.
Query Match 4.8%; Score 47.4; DB 8; Length 1248;
Best Local Similarity 49.3%; Pred. No. 43;
RESULT 1058
ID ABD07240 standard; DNA; 1251 BP.
DE Pseudomonas aeruginosa polynucleotide #5844.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 4.8%; Score 47.4; DB 11; Length 1251;
Best Local Similarity 44.2%; Pred. No. 43;
RESULT 1059
ID ACA27319 standard; DNA; 1404 BP.
DE Prokaryotic essential gene #8976.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 4.8%; Score 47.4; DB 8; Length 1404;
Best Local Similarity 44.6%; Pred. No. 43;
RESULT 1060
ID ABD04734 standard; DNA; 1650 BP.
DE Pseudomonas aeruginosa polynucleotide #3338.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 4.8%; Score 47.4; DB 11; Length 1650;
Best Local Similarity 43.9%; Pred. No. 43;
RESULT 1061
ID ACA37851 standard; DNA; 1734 BP.
DE Prokaryotic essential gene #19508.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 4.8%; Score 47.4; DB 8; Length 1734;
Best Local Similarity 52.8%; Pred. No. 43;
RESULT 1062
ID ABD04627 standard; DNA; 1869 BP.
DE Pseudomonas aeruginosa polynucleotide #3231.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 4.8%; Score 47.4; DB 11; Length 1869;
Best Local Similarity 43.9%; Pred. No. 42;
RESULT 1063
ID ABD12660 standard; DNA; 1881 BP.
DE Pseudomonas aeruginosa polynucleotide #11264.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 4.8%; Score 47.4; DB 11; Length 1881;
Best Local Similarity 48.0%; Pred. No. 42;
RESULT 1064
ID ABD07163 standard; DNA; 1986 BP.
DE Pseudomonas aeruginosa polynucleotide #5767.

PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 4.8%; Score 47.4; DB 11; Length 1986;
Best Local Similarity 44.2%; Pred. No. 42;
RESULT 1065
ID ABD04694 standard; DNA; 2283 BP.
DE Pseudomonas aeruginosa polynucleotide #3298.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 4.8%; Score 47.4; DB 11; Length 2283;
Best Local Similarity 43.9%; Pred. No. 42;
RESULT 1066
ID ADO26117 standard; DNA; 2354 BP.
DE Corn phenylalanine ammonia synthase (PAL) seqid 155.
PN WO2004046336-A2.
PD 03-JUN-2004.
PA (MONS) MONSANTO TECHNOLOGY LLC.
Query Match 4.8%; Score 47.4; DB 12; Length 2354;
Best Local Similarity 47.5%; Pred. No. 42;
RESULT 1067
ID ACA25940 standard; DNA; 2463 BP.
DE Prokaryotic essential gene #7597.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 4.8%; Score 47.4; DB 8; Length 2463;
Best Local Similarity 45.5%; Pred. No. 42;
RESULT 1068
ID ABD10506 standard; DNA; 2583 BP.
DE Pseudomonas aeruginosa polynucleotide #9110.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 4.8%; Score 47.4; DB 11; Length 2583;
Best Local Similarity 46.3%; Pred. No. 42;
RESULT 1069
ID AAQ39093 standard; DNA; 2634 BP.
DE Streptomyces nodosus 2634bp BamHI fragment.
PN WO9306219-A1.
PD 01-APR-1993.
PA (FARH) HOECHST AG.
Query Match 4.8%; Score 47.4; DB 2; Length 2634;
Best Local Similarity 44.9%; Pred. No. 42;
RESULT 1070
ID ACA23465 standard; DNA; 2883 BP.
DE Prokaryotic essential gene #5122.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 4.8%; Score 47.4; DB 8; Length 2883;
Best Local Similarity 44.9%; Pred. No. 42;
RESULT 1071
ID ADA71066 standard; DNA; 3153 BP.
DE Rice gene, SEQ ID 4389.
PN WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 4.8%; Score 47.4; DB 8; Length 3153;
Best Local Similarity 46.3%; Pred. No. 42;
RESULT 1072
ID ADA69900 standard; DNA; 3252 BP.
DE Rice gene, SEQ ID 3223.
PN WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 4.8%; Score 47.4; DB 8; Length 3252;
Best Local Similarity 45.4%; Pred. No. 42;
RESULT 1073
ID ADC68517 standard; cDNA; 3629 BP.
DE S. arundinaceus fructan biosynthesis protein cDNA SEQ ID NO:9.
PN WO2003040306-A2.

PD 15-MAY-2003.
PA (GENE-) GENESIS RES & DEV CORP LTD.
PA (WRIG-) WRIGHTSON SEEDS LTD.
Query Match 4.8%; Score 47.4; DB 10; Length 3629;
Best Local Similarity 46.1%; Pred. No. 42;
RESULT 1074
ID ADC68420 standard; cDNA; 3633 BP.
DE S. arundinaceus fructan biosynthesis protein cDNA SEQ ID NO:130.
PN WO2003040306-A2.
PD 15-MAY-2003.
PA (GENE-) GENESIS RES & DEV CORP LTD.
PA (WRIG-) WRIGHTSON SEEDS LTD.
Query Match 4.8%; Score 47.4; DB 10; Length 3633;
Best Local Similarity 46.1%; Pred. No. 42;
RESULT 1075
ID AAD47222 standard; DNA; 19016 BP.
DE Streptococcus sp. H021 DNA fragment for rabelomycin biosynthetic pathway.
PN WO200274800-A1.
PD 26-SEP-2002.
PA (GALI-) GALILAEUS OY.
Query Match 4.8%; Score 47.4; DB 8; Length 19016;
Best Local Similarity 43.3%; Pred. No. 40;
RESULT 1076
ID ADB86070 standard; DNA; 47988 BP.
DE Streptomyces hygroscopicus non-ribosomal peptide synthetase complex DNA.
PN WO2003082909-A1.
PD 09-OCT-2003.
PA (AMHP) WYETH.
Query Match 4.8%; Score 47.4; DB 10; Length 47988;
Best Local Similarity 44.2%; Pred. No. 39;
RESULT 1077
ID AAA09469 standard; DNA; 50937 BP.
DE Streptococcus oleandomycin gene cluster.
PN WO200026349-A2.
PD 11-MAY-2000.
PA (KOSA-) KOSAN BIOSCIENCES INC.
Query Match 4.8%; Score 47.4; DB 3; Length 50937;
Best Local Similarity 44.7%; Pred. No. 39;
RESULT 1078
ID AAA09469 standard; DNA; 50937 BP.
DE Streptococcus oleandomycin gene cluster.
PN WO200026349-A2.
PD 11-MAY-2000.
PA (KOSA-) KOSAN BIOSCIENCES INC.
Query Match 4.8%; Score 47.4; DB 3; Length 50937;
Best Local Similarity 45.7%; Pred. No. 39;
RESULT 1079
ID ADP74816 standard; DNA; 137560 BP.
DE Parapoxvirus ovis genome DNA sequence SeqID1.
Query Match 4.8%; Score 47.4; DB 12; Length 137560;
Best Local Similarity 47.9%; Pred. No. 38;
RESULT 1080
ID ADC76153 standard; DNA; 607 BP.
DE DNA homologous to phytopathogen resistance-related cDNA - SEQ ID 1422.
PN WO2003020905-A2.
PD 13-MAR-2003.
PA (DOWC) DOW CHEM CO.
Query Match 4.8%; Score 47.2; DB 10; Length 607;
Best Local Similarity 47.8%; Pred. No. 47;
RESULT 1081
ID ADD17151 standard; DNA; 607 BP.
DE DNA (SeqID 1219) that confers an altered visual phenotype in plants.
PN WO2003020741-A1.
PD 13-MAR-2003.
PA (DOWC) DOW CHEM CO.
Query Match 4.8%; Score 47.2; DB 10; Length 607;
Best Local Similarity 47.8%; Pred. No. 47;
RESULT 1082
ID ADD17811 standard; DNA; 607 BP.
DE DNA (SeqID 1879) that confers an altered visual phenotype in plants.
PN WO2003020741-A1.
PD 13-MAR-2003.

PA (DOWC) DOW CHEM CO.
PA (DOWC) DOW AGROSCIENCES LLC.
Query Match 4.8%; Score 47.2; DB 10; Length 607;
Best Local Similarity 47.8%; Pred. No. 47;
RESULT 1083
ID ADK58311 standard; DNA; 607 BP.
DE Plant DNA sequence which confers altered metabolic characteristic #5694.
PN WO2003020936-A1.
PD 13-MAR-2003.
PA (DOWC) DOW CHEM CO.
PA (DOWC) DOW AGROSCIENCES LLC.
Query Match 4.8%; Score 47.2; DB 10; Length 607;
Best Local Similarity 47.8%; Pred. No. 47;
RESULT 1084
ID ABD17417 standard; DNA; 714 BP.
DE Pseudomonas aeruginosa polynucleotide #16021.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 4.8%; Score 47.2; DB 11; Length 714;
Best Local Similarity 48.8%; Pred. No. 47;
RESULT 1085
ID ACA23687 standard; DNA; 852 BP.
DE Prokaryotic essential gene #5344.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 4.8%; Score 47.2; DB 8; Length 852;
Best Local Similarity 47.9%; Pred. No. 47;
RESULT 1086
ID ADC76149 standard; DNA; 873 BP.
DE DNA homologous to phytopathogen resistance-related cDNA - SEQ ID 1418.
PN WO2003020905-A2.
PD 13-MAR-2003.
PA (DOWC) DOW CHEM CO.
Query Match 4.8%; Score 47.2; DB 10; Length 873;
Best Local Similarity 47.8%; Pred. No. 47;
RESULT 1087
ID ADD17156 standard; DNA; 873 BP.
DE DNA (SeqID 1224) that confers an altered visual phenotype in plants.
PN WO2003020741-A1.
PD 13-MAR-2003.
PA (DOWC) DOW CHEM CO.
PA (DOWC) DOW AGROSCIENCES LLC.
Query Match 4.8%; Score 47.2; DB 10; Length 873;
Best Local Similarity 47.8%; Pred. No. 47;
RESULT 1088
ID ADK58312 standard; DNA; 873 BP.
DE Plant DNA sequence which confers altered metabolic characteristic #5695.
PN WO2003020936-A1.
PD 13-MAR-2003.
PA (DOWC) DOW CHEM CO.
PA (DOWC) DOW AGROSCIENCES LLC.
Query Match 4.8%; Score 47.2; DB 10; Length 873;
Best Local Similarity 47.8%; Pred. No. 47;
RESULT 1089
ID AAT59269 standard; cDNA; 888 BP.
DE Streptomyces pristinaespiralis papC gene.
PN WO9601901-A1.
PD 25-JAN-1996.
PA (RHON) RHONE POULENC RORER SA.
Query Match 4.8%; Score 47.2; DB 2; Length 888;
Best Local Similarity 45.3%; Pred. No. 47;
RESULT 1090
ID ABD02366 standard; DNA; 999 BP.
DE Pseudomonas aeruginosa polynucleotide #970.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 4.8%; Score 47.2; DB 11; Length 999;
Best Local Similarity 46.4%; Pred. No. 47;
RESULT 1091
ID ADA48950 standard; DNA; 1044 BP.

DE Wheat gene conferring disease resistance in plants.
PN WO2003000506-A2.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 4.8%; Score 47.2; DB 9; Length 1044;
Best Local Similarity 44.5%; Pred. No. 47;
RESULT 1092
ID ABD02410 standard; DNA; 1110 BP.
DE Pseudomonas aeruginosa polynucleotide #1014.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 4.8%; Score 47.2; DB 11; Length 1110;
Best Local Similarity 46.4%; Pred. No. 47;
RESULT 1093
ID ACA26954 standard; DNA; 1134 BP.
DE Prokaryotic essential gene #8611.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 4.8%; Score 47.2; DB 8; Length 1134;
Best Local Similarity 46.7%; Pred. No. 46;
RESULT 1094
ID ABX56038 standard; DNA; 1194 BP.
DE M. echinospira calicheamicin biosynthesis gene caln.
PN WO200279465-A2.
PD 10-OCT-2002.
PA (SLOK) SLOAN KETTERING INST CANCER RES.
Query Match 4.8%; Score 47.2; DB 8; Length 1194;
Best Local Similarity 43.0%; Pred. No. 46;
RESULT 1095
ID ABD02476 standard; DNA; 1275 BP.
DE Pseudomonas aeruginosa polynucleotide #1080.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 4.8%; Score 47.2; DB 11; Length 1275;
Best Local Similarity 46.4%; Pred. No. 46;
RESULT 1096
ID ABX56047 standard; DNA; 1347 BP.
DE M. echinospira calicheamicin biosynthesis gene calw.
PN WO200279465-A2.
PD 10-OCT-2002.
PA (SLOK) SLOAN KETTERING INST CANCER RES.
Query Match 4.8%; Score 47.2; DB 8; Length 1347;
Best Local Similarity 47.0%; Pred. No. 46;
RESULT 1097
ID ACA23577 standard; DNA; 1374 BP.
DE Prokaryotic essential gene #5234.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 4.8%; Score 47.2; DB 8; Length 1374;
Best Local Similarity 47.3%; Pred. No. 46;
RESULT 1098
ID ACA26528 standard; DNA; 1395 BP.
DE Prokaryotic essential gene #8185.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 4.8%; Score 47.2; DB 8; Length 1395;
Best Local Similarity 46.6%; Pred. No. 46;
RESULT 1099
ID ACA37685 standard; DNA; 1410 BP.
DE Prokaryotic essential gene #19342.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 4.8%; Score 47.2; DB 8; Length 1410;
Best Local Similarity 45.8%; Pred. No. 46;
RESULT 1100
ID ABQ55009 standard; cDNA; 1616 BP.
DE Human ovarian antigen HUKJ46 cDNA, SEQ ID NO:889.
PN WO2003020876-A2.
PN WO200200677-A1.
PD 03-JAN-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.8%; Score 47.2; DB 6; Length 1616;
Best Local Similarity 45.3%; Pred. No. 46;
RESULT 1101
ID ABL39997 standard; DNA; 1680 BP.
DE Synthetic RT polynucleotide sequence SEQ ID NO:76.
PN WO200204493-A2.
PD 17-JAN-2002.
PA (CHIR) CHIRON CORP.
Query Match 4.8%; Score 47.2; DB 6; Length 1680;
Best Local Similarity 47.6%; Pred. No. 46;
RESULT 1102
ID ADM73810 standard; DNA; 1680 BP.
DE HIV-1 polynucleotide #45.
PN US2003223961-A1.
PD 04-DEC-2003.
PA (MEGE/) MEGEDE J Z.
PA (BARN/) BARNETT S W.
PA (ENGE/) ENGELBRECHT S.
PA (RENS/) RENSBURG E J V.
Query Match 4.8%; Score 47.2; DB 12; Length 1680;
Best Local Similarity 47.6%; Pred. No. 46;
RESULT 1103
ID ACH91868 standard; DNA; 1737 BP.
DE Human genome derived single exon probe #25063.
PN US2003194704-A1.
PD 16-OCT-2003.
PA (PENN/) PENN S G.
PA (RANK/) RANK D R.
PA (HANZ/) HANZEL D K.
Query Match 4.8%; Score 47.2; DB 12; Length 1737;
Best Local Similarity 49.2%; Pred. No. 46;
RESULT 1104
ID ACH92275 standard; DNA; 1738 BP.
DE Human genome derived single exon probe #25470.
PN US2003194704-A1.
PD 16-OCT-2003.
PA (PENN/) PENN S G.
PA (RANK/) RANK D R.
PA (HANZ/) HANZEL D K.
Query Match 4.8%; Score 47.2; DB 12; Length 1738;
Best Local Similarity 49.2%; Pred. No. 46;
RESULT 1105
ID AAL40132 standard; DNA; 1896 BP.
DE Isoprenoid related nucleic acid sequence SEQ ID No 16.
PN WO200226933-A2.
PD 04-APR-2002.
PA (CRGI) CARGILL INC.
Query Match 4.8%; Score 47.2; DB 6; Length 1896;
Best Local Similarity 45.3%; Pred. No. 46;
RESULT 1106
ID ABD17641 standard; DNA; 1944 BP.
DE Pseudomonas aeruginosa polynucleotide #16245.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 4.8%; Score 47.2; DB 11; Length 1944;
Best Local Similarity 48.8%; Pred. No. 46;
RESULT 1107
ID ACA03560 standard; DNA; 1977 BP.
DE Synthetic DNA encoding immunogenic HIV peptide #43.
PN WO2003004657-A1.
PD 16-JAN-2003.
PA (CHIR) CHIRON CORP.
Query Match 4.8%; Score 47.2; DB 8; Length 1977;
Best Local Similarity 47.6%; Pred. No. 46;
RESULT 1108
ID ACC78516 standard; DNA; 1977 BP.
DE HIV proctrit-opt.SF2 nucleotide sequence.
PN WO2003020876-A2.

PD 13-MAR-2003.
PA (CHIR) CHIRON CORP.
Query Match 4.8%; Score 47.2; DB 8; Length 1977;
Best Local Similarity 47.6%; Pred. No. 46;
RESULT 1109
ID ADM73804 standard; DNA; 1977 BP.
DE HIV-1 polynucleotide #39.
PN US2003223961-A1.
PD 04-DEC-2003.
PA (MEGE/) MEGEDE J Z.
PA (BARN/) BARNETT S W.
PA (ENGE/) ENGELBRECHT S.
PA (RENS/) RENSBERG E J V.
Query Match 4.8%; Score 47.2; DB 12; Length 1977;
Best Local Similarity 47.6%; Pred. No. 46;
RESULT 1110
ID ABL39991 standard; DNA; 1978 BP.
DE Synthetic protease and RT polynucleotide sequence SEQ ID NO:70.
PN WO200204493-A2.
PD 17-JAN-2002.
PA (CHIR) CHIRON CORP.
Query Match 4.8%; Score 47.2; DB 6; Length 1978;
Best Local Similarity 47.6%; Pred. No. 46;
RESULT 1111
ID ACA03571 standard; DNA; 1989 BP.
DE Synthetic DNA encoding immunogenic HIV peptide #54.
PN WO2003004657-A1.
PD 16-JAN-2003.
PA (CHIR) CHIRON CORP.
Query Match 4.8%; Score 47.2; DB 8; Length 1989;
Best Local Similarity 47.6%; Pred. No. 46;
RESULT 1112
ID ACCT78522 standard; DNA; 1989 BP.
DE HIV RT-opt.SF2 (native) nucleotide sequence.
PN WO2003020876-A2.
PD 13-MAR-2003.
PA (CHIR) CHIRON CORP.
Query Match 4.8%; Score 47.2; DB 8; Length 1989;
Best Local Similarity 47.6%; Pred. No. 46;
RESULT 1113
ID ABD07303 standard; DNA; 2133 BP.
DE Pseudomonas aeruginosa polynucleotide #5907.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 4.8%; Score 47.2; DB 11; Length 2133;
Best Local Similarity 44.1%; Pred. No. 46;
RESULT 1114
ID ACA03552 standard; DNA; 2145 BP.
DE Synthetic DNA encoding immunogenic HIV peptide #35.
PN WO2003004657-A1.
PD 16-JAN-2003.
PA (CHIR) CHIRON CORP.
Query Match 4.8%; Score 47.2; DB 8; Length 2145;
Best Local Similarity 47.6%; Pred. No. 46;
RESULT 1115
ID ACCT78510 standard; DNA; 2145 BP.
DE HIV pol.opt.SF2 nucleotide sequence.
PN WO2003020876-A2.
PD 13-MAR-2003.
PA (CHIR) CHIRON CORP.
Query Match 4.8%; Score 47.2; DB 8; Length 2145;
Best Local Similarity 47.6%; Pred. No. 46;
RESULT 1116
ID AAAY0481 standard; DNA; 2312 BP.
DE HIV FS(-) ProtMod Rtopt(+) coding sequence.
PN WO2003039302-A2.
PD 06-JUL-2000.
PA (CHIR) CHIRON CORP.
Query Match 4.8%; Score 47.2; DB 3; Length 2312;
Best Local Similarity 47.6%; Pred. No. 46;
RESULT 1117

ID ACA03543 standard; DNA; 2472 BP.
DE Synthetic DNA encoding immunogenic HIV peptide #26.
PN WO2003004657-A1.
PD 16-JAN-2003.
PA (CHIR) CHIRON CORP.
Query Match 4.8%; Score 47.2; DB 8; Length 2472;
Best Local Similarity 47.6%; Pred. No. 45;
RESULT 1118
ID ACCT78507 standard; DNA; 2472 BP.
DE HIV p2Polopt.SF2 nucleotide sequence.
PN WO2003020876-A2.
PD 13-MAR-2003.
PA (CHIR) CHIRON CORP.
Query Match 4.8%; Score 47.2; DB 8; Length 2472;
Best Local Similarity 47.6%; Pred. No. 45;
RESULT 1119
ID ADA69874 standard; DNA; 2529 BP.
DE Rice gene. SEQ ID 3197.
PN WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 4.8%; Score 47.2; DB 8; Length 2529;
Best Local Similarity 44.5%; Pred. No. 45;
RESULT 1120
ID ADC72236 standard; DNA; 2691 BP.
DE Human NR3B gene SEQ ID NO:9.
PN WO2003016479-A2.
PD 27-FEB-2003.
PA (BURN-) BURNHAM INST.
PA (UYA) UNIV YALE.
PA (BGHM) BRIGHAM & WOMENS HOSPITAL.
Query Match 4.8%; Score 47.2; DB 10; Length 2691;
Best Local Similarity 43.7%; Pred. No. 45;
RESULT 1121
ID ADN49187 standard; cDNA; 2691 BP.
DE Human N-methyl-D-aspartate (NMDA) type 3B (NR3B) EST cDNA.
PN US2004033500-A1.
PD 19-FEB-2004.
PA (BURN-) BURNHAM INST.
PA (BGHM) BRIGHAM & WOMENS HOSPITAL INC.
Query Match 4.8%; Score 47.2; DB 12; Length 2691;
Best Local Similarity 43.7%; Pred. No. 45;
RESULT 1122
ID AAL47419 standard; cDNA; 2706 BP.
DE Human N-methyl-D-aspartate receptor coding sequence.
PN WO200240538-A2.
PD 23-MAY-2002.
PA (FARB) BAYER AG.
Query Match 4.8%; Score 47.2; DB 6; Length 2706;
Best Local Similarity 43.7%; Pred. No. 45;
RESULT 1123
ID ACC47899 standard; cDNA; 2706 BP.
DE Human NR3B subunit receptor polypeptide coding sequence.
PN WO2003033872-A2.
PD 24-APR-2003.
PA (RIKE) RIKEN KK.
Query Match 4.8%; Score 47.2; DB 8; Length 2706;
Best Local Similarity 43.7%; Pred. No. 45;
RESULT 1124
ID ACA38169 standard; DNA; 2751 BP.
DE Prokaryotic essential gene #19826.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 4.8%; Score 47.2; DB 8; Length 2751;
Best Local Similarity 47.1%; Pred. No. 45;
RESULT 1125
ID ADA69752 standard; DNA; 2763 BP.
DE Rice gene. SEQ ID 3075.
PN WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 4.8%; Score 47.2; DB 8; Length 2763;

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Best Local Similarity 48.2%; Pred. No. 45;
RESULT 1126
ID ABD17862 standard; DNA; 2808 BP.
DE Pseudomonas aeruginosa polynucleotide #16466.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 4.8%; Score 47.2; DB 11; Length 2808;
Best Local Similarity 48.8%; Pred. No. 45;
RESULT 1127
ID ABD12055 standard; DNA; 2862 BP.
DE Pseudomonas aeruginosa polynucleotide #10659.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 4.8%; Score 47.2; DB 11; Length 2862;
Best Local Similarity 43.1%; Pred. No. 45;
RESULT 1128
ID AAT59268 standard; cDNA; 2888 BP.
DE Streptomyces pristinaespiralis papA and papM intergenic region.
PN WO9601901-A1.
PD 25-JAN-1996.
PA (RHON) RHONE-POULENC RORER SA.
Query Match 4.8%; Score 47.2; DB 2; Length 2888;
Best Local Similarity 45.3%; Pred. No. 45;
RESULT 1129
ID ADN49407 standard; DNA; 2898 BP.
DE Human glutamate receptor (MEM2) DNA.
PN US2004086931-A1.
PD 06-MAY-2004.
PA (SPAD/) SPADERNA S K.
PA (QUIN/) QUINN K E.
PA (SHIM/) SHIMKETS R A.
PA (PADI/) PADIGARU M.
PA (SPYT/) SPYTEK K A.
Query Match 4.8%; Score 47.2; DB 12; Length 2898;
Best Local Similarity 43.7%; Pred. No. 45;
RESULT 1130
ID ABD11810 standard; DNA; 2910 BP.
DE Pseudomonas aeruginosa polynucleotide #10414.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 4.8%; Score 47.2; DB 11; Length 2910;
Best Local Similarity 43.1%; Pred. No. 45;
RESULT 1131
ID AAS06334 standard; cDNA; 2916 BP.
DE DNA encoding human glutamate receptor-like protein, MEM3.
PN WO20014473-A2.
PD 21-JUN-2001.
PA (CURA-) CURAGEN CORP.
Query Match 4.8%; Score 47.2; DB 4; Length 2916;
Best Local Similarity 43.7%; Pred. No. 45;
RESULT 1132
ID ADN49409 standard; DNA; 2916 BP.
DE Human glutamate receptor (MEM3) DNA.
PN US2004086931-A1.
PD 06-MAY-2004.
PA (SPAD/) SPADERNA S K.
PA (QUIN/) QUINN K E.
PA (SHIM/) SHIMKETS R A.
PA (PADI/) PADIGARU M.
PA (SPYT/) SPYTEK K A.
Query Match 4.8%; Score 47.2; DB 12; Length 2916;
Best Local Similarity 43.7%; Pred. No. 45;
RESULT 1133
ID AAZ52054 standard; DNA; 3012 BP.
DE Codon optimised Human immunodeficiency virus pol coding region.
PN WO200015819-A1.
PD 23-MAR-2000.
PA (CHIL-) CHILDRENS MEDICAL CENT.
Query Match 4.8%; Score 47.2; DB 3; Length 3012;
Best Local Similarity 47.6%; Pred. No. 45;
RESULT 1134
ID ABL39983 standard; DNA; 3015 BP.
DE Synthetic pol polynucleotide sequence SEQ ID NO:62.
PN WO200204493-A2.
PD 17-JAN-2002.
PA (CHIR) CHIRON CORP.
PA (UYST-) UNIV STELLENBOSCH.
Query Match 4.8%; Score 47.2; DB 6; Length 3015;
Best Local Similarity 47.6%; Pred. No. 45;
RESULT 1135
ID ACA03553 standard; DNA; 3015 BP.
DE Synthetic DNA encoding immunogenic HIV peptide #36.
PN WO2003004657-A1.
PD 16-JAN-2003.
PA (CHIR) CHIRON CORP.
Query Match 4.8%; Score 47.2; DB 8; Length 3015;
Best Local Similarity 47.6%; Pred. No. 45;
RESULT 1136
ID ADM73796 standard; DNA; 3015 BP.
DE HIV-1 polynucleotide #31.
PN US200323961-A1.
PD 04-DEC-2003.
PA (MEGE/) MEGEDE J Z.
PA (BARN/) BARNETT S W.
PA (ENGE/) ENGELBRECHT S.
PA (RENS/) RENSBURG E J V.
Query Match 4.8%; Score 47.2; DB 12; Length 3015;
Best Local Similarity 47.6%; Pred. No. 45;
RESULT 1137
ID ADC72232 standard; DNA; 3096 BP.
DE Human NR3B gene SEQ ID NO:5.
PN WO2003016479-A2.
PD 27-FEB-2003.
PA (BURN-) BURNHAM INST.
PA (UYVA) UNIV YALE.
PA (BGHM) BRIGHAM & WOMENS HOSPITAL.
Query Match 4.8%; Score 47.2; DB 10; Length 3096;
Best Local Similarity 43.7%; Pred. No. 45;
RESULT 1138
ID ADN49183 standard; cDNA; 3096 BP.
DE Human N-methyl-D-aspartate (NMDA) type 3B (NR3B) cDNA #1.
PN US2004033500-A1.
PD 19-FEB-2004.
PA (BURN-) BURNHAM INST.
PA (BGHM) BRIGHAM & WOMENS HOSPITAL INC.
Query Match 4.8%; Score 47.2; DB 12; Length 3096;
Best Local Similarity 43.7%; Pred. No. 45;
RESULT 1139
ID ADC72287 standard; DNA; 3097 BP.
DE Human NR3B gene SEQ ID NO:61.
PN WO2003016479-A2.
PD 27-FEB-2003.
PA (BURN-) BURNHAM INST.
PA (UYVA) UNIV YALE.
PA (BGHM) BRIGHAM & WOMENS HOSPITAL.
Query Match 4.8%; Score 47.2; DB 10; Length 3097;
Best Local Similarity 43.7%; Pred. No. 45;
RESULT 1140
ID ADN49238 standard; cDNA; 3097 BP.
DE Human N-methyl-D-aspartate (NMDA) type 3B (NR3B) cDNA #2.
PN US2004033500-A1.
PD 19-FEB-2004.
PA (BURN-) BURNHAM INST.
PA (BGHM) BRIGHAM & WOMENS HOSPITAL INC.
Query Match 4.8%; Score 47.2; DB 12; Length 3097;
Best Local Similarity 43.7%; Pred. No. 45;
RESULT 1141
ID ABD11900 standard; DNA; 3111 BP.
DE Pseudomonas aeruginosa polynucleotide #10504.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 4.8%; Score 47.2; DB 11; Length 3111;

Best Local Similarity 43.1%; Pred. No. 45;
RESULT 1142
ID AAS06335 standard; cDNA; 3132 BP.
DE DNA encoding human glutamate receptor-like protein, MEM4.
PN WO20014473-A2.
PD 21-JUN-2001.
PA (CURA-) CURAGEN CORP.
Query Match 4.8%; Score 47.2; DB 4; Length 3132;
Best Local Similarity 43.7%; Pred. No. 45;
RESULT 1143
ID AB233750 standard; cDNA; 3132 BP.
DE Human TRICH encoding cDNA SEQ ID NO 56.
PN WO200246415-A2.
PD 13-JUN-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 4.8%; Score 47.2; DB 6; Length 3132;
Best Local Similarity 43.7%; Pred. No. 45;
RESULT 1144
ID ADN49411 standard; DNA; 3132 BP.
DE Human glutamate receptor (MEM4) DNA.
PN US2004086931-A1.
PD 06-MAY-2004.
PA (SPAD/) SPADERNA S K.
PA (QUIN/) QUINN K E.
PA (SHIM/) SHIMKETS R A.
PA (PAD/) PADIGARU M.
PA (SPYT/) SPYTEK K A.
Query Match 4.8%; Score 47.2; DB 12; Length 3132;
Best Local Similarity 43.7%; Pred. No. 45;
RESULT 1145
ID ABD07318 standard; DNA; 3135 BP.
DE Pseudomonas aeruginosa polynucleotide #5922.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 4.8%; Score 47.2; DB 11; Length 3135;
Best Local Similarity 44.1%; Pred. No. 45;
RESULT 1146
ID AAC76703 standard; cDNA; 3207 BP.
DE Human ORFX ORF2258 polynucleotide sequence SEQ ID NO:4515.
PN WO200058473-A2.
PD 05-OCT-2000.
PA (CURA-) CURAGEN CORP.
Query Match 4.8%; Score 47.2; DB 3; Length 3207;
Best Local Similarity 43.7%; Pred. No. 45;
RESULT 1147
ID ACA03544 standard; DNA; 3639 BP.
DE Synthetic DNA encoding immunogenic HIV peptide #27.
PN WO2003004657-A1.
PD 16-JAN-2003.
PA (CHIR-) CHIRON CORP.
Query Match 4.8%; Score 47.2; DB 8; Length 3639;
Best Local Similarity 47.6%; Pred. No. 45;
RESULT 1148
ID ACC78508 standard; DNA; 3639 BP.
DE HIV p24PolratRevNeg.Opt.native_B nucleotide sequence.
PN WO2003020876-A2.
PD 13-MAR-2003.
PA (CHIR-) CHIRON CORP.
Query Match 4.8%; Score 47.2; DB 8; Length 3639;
Best Local Similarity 47.6%; Pred. No. 45;
RESULT 1149
ID ADM02119 standard; cDNA; 3955 BP.
DE Human cDNA of the invention SEQ ID NO:804.
PN EPI347046-A1.
PD 24-SEP-2003.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 4.8%; Score 47.2; DB 11; Length 3955;
Best Local Similarity 49.2%; Pred. No. 45;
RESULT 1150
ID AAA70414 standard; DNA; 4319 BP.
DE HIV Gag-polymerase expression cassette coding sequence GagPol.ModSP.
PN WO200039302-A2.

PD 06-JUL-2000.
PA (CHIR-) CHIRON CORP.
Query Match 4.8%; Score 47.2; DB 3; Length 4319;
Best Local Similarity 47.6%; Pred. No. 45;
RESULT 1151
ID ADI60576 standard; DNA; 4532 BP.
DE Secreted polypeptide encoding gene #115.
PN WO2003025142-A2.
PD 27-MAR-2003.
PA (HYSE-) HYSEQ INC.
Query Match 4.8%; Score 47.2; DB 10; Length 4532;
Best Local Similarity 49.2%; Pred. No. 45;
RESULT 1152
ID ADO24366 standard; cDNA; 4973 BP.
DE Human PRO87327 encoding cDNA SEQ ID NO:5.
PN WO2004043397-A2.
PD 27-MAY-2004.
PA (GETH-) GENENTECH INC.
Query Match 4.8%; Score 47.2; DB 12; Length 4973;
Best Local Similarity 49.2%; Pred. No. 45;
RESULT 1153
ID AAV21186 standard; DNA; 5676 BP.
DE Amycolatopsis mediterranei strain wt3136 5.7 kb KpnI DNA fragment.
PN WO9807868-A1.
PD 26-FEB-1998.
PA (NOVS-) NOVARTIS AG.
Query Match 4.8%; Score 47.2; DB 2; Length 5676;
Best Local Similarity 44.9%; Pred. No. 44;
RESULT 1154
ID AD853354 standard; DNA; 6402 BP.
DE Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:3896.
PN WO2003065993-A2.
PD 14-AUG-2003.
PA (GENE-) GENE LOGIC INC.
Query Match 4.8%; Score 47.2; DB 10; Length 6402;
Best Local Similarity 43.0%; Pred. No. 44;
RESULT 1155
ID AA252055 standard; DNA; 8908 BP.
DE Packaging construct PHDMHgm2 DNA.
PN WO200015819-A1.
PD 23-MAR-2000.
PA (CHIL-) CHILDRENS MEDICAL CENT.
Query Match 4.8%; Score 47.2; DB 3; Length 8908;
Best Local Similarity 47.6%; Pred. No. 44;
RESULT 1156
ID AA287298 standard; DNA; 11220 BP.
DE S. venezuelae macrolide biosynthetic gene pikAII, SEQ ID NO:32.
PN WO20000620-A2.
PD 06-JAN-2000.
PA (MINU-) UNIV MINNESOTA.
Query Match 4.8%; Score 47.2; DB 3; Length 11220;
Best Local Similarity 47.3%; Pred. No. 44;
RESULT 1157
ID ADJ91917 standard; DNA; 11220 BP.
DE Streptomyces macrolide biosynthetic protein (PikAII) coding sequence.
PN US2003194784-A1.
PD 16-OCT-2003.
PA (SHER/) SHERMAN D H.
PA (LIUH/) LIU H.
PA (XUEY/) XUE Y.
PA (ZHAO/) ZHAO L.
Query Match 4.8%; Score 47.2; DB 12; Length 11220;
Best Local Similarity 47.3%; Pred. No. 44;
RESULT 1158
ID ADJ72366 standard; DNA; 23949 BP.
DE Streptomyces roseosporus daptomycin biosynthesis gene fragment.
PN WO2003014297-A2.
PD 20-FEB-2003.
PA (CUBI-) CUBIST PHARM INC.
Query Match 4.8%; Score 47.2; DB 10; Length 23949;
Best Local Similarity 44.7%; Pred. No. 43;
RESULT 1159
ID ADC26979 standard; DNA; 27705 BP.

DE Sorangium cellulosum tmba gene cluster tmbA DNA.
PN US2003054547-A1.
PD 20-MAR-2003.
PA (JULI/) JULIEN B.
Query Match 4.8%; Score 47.2; DB 10; Length 27705;
Best Local Similarity 46.1%; Pred. No. 43;
RESULT 1160
ID AAV21187 standard; DNA; 53789 BP.
DE Amycolatopsis mediterranei rifamycin synthesis gene cluster fragment.
PN WO9807868-A1.
PD 26-FEB-1998.
PA (NOVS) NOVARTIS AG.
Query Match 4.8%; Score 47.2; DB 2; Length 53789;
Best Local Similarity 44.9%; Pred. No. 42;
RESULT 1161
ID ABD16054 standard; DNA; 441 BP.
DE Pseudomonas aeruginosa polynucleotide #14658.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 4.8%; Score 47; DB 11; Length 441;
Best Local Similarity 46.1%; Pred. No. 52;
RESULT 1162
ID ADB68842 standard; DNA; 536 BP.
DE Minority luxI consensus sequence DNA 14.
PN WO2003057902-A2.
PD 17-JUL-2003.
PA (FRAU) FRAUNHOFER USA INC.
Query Match 4.8%; Score 47; DB 10; Length 536;
Best Local Similarity 12.9%; Pred. No. 51;
RESULT 1163
ID ADC08861 standard; DNA; 597 BP.
DE Corn DNA sequence seq ID1166 related to grain filling.
PN WO2003000905-A2.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 4.8%; Score 47; DB 10; Length 597;
Best Local Similarity 49.8%; Pred. No. 51;
RESULT 1164
ID ACA26778 standard; DNA; 675 BP.
DE Prokaryotic essential gene #8435.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 4.8%; Score 47; DB 8; Length 675;
Best Local Similarity 47.0%; Pred. No. 51;
RESULT 1165
ID ADO63457 standard; DNA; 715 BP.
DE Transcription factor G3083 orthologous sequence, SEQ ID 1924.
PN WO2004031349-A2.
PD 15-APR-2004.
PA (MEND-) MENDEL BIOTECHNOLOGY INC.
Query Match 4.8%; Score 47; DB 12; Length 715;
Best Local Similarity 48.1%; Pred. No. 51;
RESULT 1166
ID ABO78042 standard; cDNA; 758 BP.
DE Maize SCIP-1 orthologue encoding cDNA SEQ ID NO 5.
PN US2002069428-A1.
PD 06-JUN-2002.
PA (PION-) PIONEER HI-BRED INT INC.
Query Match 4.8%; Score 47; DB 6; Length 758;
Best Local Similarity 46.9%; Pred. No. 51;
RESULT 1167
ID ABX12766 standard; DNA; 930 BP.
DE DNA encoding murine ischaemia activated protein (IAP).
PN US2002160495-A1.
PD 31-OCT-2002.
PA (UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.
Query Match 4.8%; Score 47; DB 8; Length 930;
Best Local Similarity 50.7%; Pred. No. 50;
RESULT 1168
ID ADL17042 standard; cDNA; 1120 BP.
DE Streptomyces coelicolor Bcl-2 domain cDNA #1.

PN US2004023866-A1.
PD 05-FEB-2004.
PA (GODZ/) GODZIK A.
PA (REED/) REED J C.
Query Match 4.8%; Score 47; DB 12; Length 1120;
Best Local Similarity 48.7%; Pred. No. 50;
RESULT 1169
ID ABD15922 standard; DNA; 1260 BP.
DE Pseudomonas aeruginosa polynucleotide #14526.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 4.8%; Score 47; DB 11; Length 1260;
Best Local Similarity 46.1%; Pred. No. 50;
RESULT 1170
ID ABD16234 standard; DNA; 1260 BP.
DE Pseudomonas aeruginosa polynucleotide #14838.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 4.8%; Score 47; DB 11; Length 1260;
Best Local Similarity 46.1%; Pred. No. 50;
RESULT 1171
ID ABZ66692 standard; DNA; 1293 BP.
DE Orthosomycin biosynthetic polynucleotide SEQ ID NO 46.
PN WO200279505-A2.
PD 10-OCT-2002.
PA (ECOP-) ECOPIA BIOSCIENCES INC.
Query Match 4.8%; Score 47; DB 10; Length 1293;
Best Local Similarity 44.1%; Pred. No. 50;
RESULT 1172
ID AAO22481 standard; DNA; 1320 BP.
DE groEL-1 gene partial sequence.
PN WO9204452-A.
PD 19-MAR-1992.
PA (INSP) INST PASTEUR.
Query Match 4.8%; Score 47; DB 2; Length 1320;
Best Local Similarity 44.2%; Pred. No. 50;
RESULT 1173
ID ABQ54643 standard; cDNA; 1354 BP.
DE Human ovarian antigen HE2KN09 cDNA, SEQ ID NO:523.
PN WO200200677-A1.
PD 03-JAN-2002.
PA (HUNA-) HUMAN GENOME SCI INC.
Query Match 4.8%; Score 47; DB 6; Length 1354;
Best Local Similarity 44.6%; Pred. No. 50;
RESULT 1174
ID AAV20099 standard; DNA; 1416 BP.
DE Pseudomonas LipR kinase coding sequence.
PN WO9806836-A2.
PD 19-FEB-1998.
PA (GENV) GENENCOR INT INC.
Query Match 4.8%; Score 47; DB 2; Length 1416;
Best Local Similarity 45.7%; Pred. No. 50;
RESULT 1175
ID AAAL3891 standard; DNA; 1416 BP.
DE Pseudomonas alcaligenes LipR nucleotide sequence SEQ ID NO:3.
PN US6048710-A.
PD 11-APR-2000.
PA (GENV) GENENCOR INT INC.
Query Match 4.8%; Score 47; DB 3; Length 1416;
Best Local Similarity 45.7%; Pred. No. 50;
RESULT 1176
ID AAD22868 standard; DNA; 1416 BP.
DE Pseudomonas alcaligenes LipR DNA.
PN US6313283-B1.
PD 06-NOV-2001.
PA (GENV) GENENCOR INT INC.
Query Match 4.8%; Score 47; DB 6; Length 1416;
Best Local Similarity 45.7%; Pred. No. 50;
RESULT 1177
ID ACA27226 standard; DNA; 1536 BP.
DE Prokaryotic essential gene #8883.

PN WO200277183-A2.
 PD 03-OCT-2002.
 PA (ELIT-) ELITRA PHARM INC.
 Query Match 4.8%; Score 47; DB 8; Length 1536;
 Best Local Similarity 51.1%; Pred. No. 50;
 RESULT 1178
 ID AAQ22482 standard; DNA; 1620 BP.
 DE groEL-1 gene coding region.
 PN WO9204452-A.
 PD 19-MAR-1992.
 PA (INSP) INST PASTEUR.
 Query Match 4.8%; Score 47; DB 2; Length 1620;
 Best Local Similarity 44.2%; Pred. No. 50;
 RESULT 1179
 ID ABX56033 standard; DNA; 1707 BP.
 DE M. echinospora calicheamicin biosynthesis gene call.
 PN WO200279465-A2.
 PD 10-OCT-2002.
 PA (SLOK) SLOAN KETTERING INST CANCER RES.
 Query Match 4.8%; Score 47; DB 8; Length 1707;
 Best Local Similarity 48.0%; Pred. No. 50;
 RESULT 1180
 ID AAAG4515 standard; cDNA; 1722 BP.
 DE Nucleotide sequence of truncated FEZ1 transcript G3612.
 PN WO200050585-A2.
 PD 31-AUG-2000.
 PA (UYJE-) UNIV JEFFERSON THOMAS.
 Query Match 4.8%; Score 47; DB 3; Length 1722;
 Best Local Similarity 45.9%; Pred. No. 50;
 RESULT 1181
 ID ADA71120 standard; DNA; 1790 BP.
 DE Rice gene, SEQ ID 4443.
 PN WO2003000898-A1.
 PD 03-JAN-2003.
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 Query Match 4.8%; Score 47; DB 8; Length 1790;
 Best Local Similarity 50.2%; Pred. No. 50;
 RESULT 1182
 ID ACA23626 standard; DNA; 1968 BP.
 DE Prokaryotic essential gene #5283.
 PN WO200277183-A2.
 PD 03-OCT-2002.
 PA (ELIT-) ELITRA PHARM INC.
 Query Match 4.8%; Score 47; DB 8; Length 1968;
 Best Local Similarity 45.2%; Pred. No. 49;
 RESULT 1183
 ID AAN92408 standard; DNA; 2061 BP.
 DE Sequence encoding pseudorabies virus (PRV) glycoprotein gH.
 PN WO8910965-A.
 PD 16-NOV-1989.
 PA (UFJO) UPJOHN CO.
 Query Match 4.8%; Score 47; DB 1; Length 2061;
 Best Local Similarity 44.7%; Pred. No. 49;
 RESULT 1184
 ID AAQ22484 standard; DNA; 2167 BP.
 DE gro es el operon with promoter sequence.
 PN WO9204452-A.
 PD 19-MAR-1992.
 PA (INSP) INST PASTEUR.
 Query Match 4.8%; Score 47; DB 2; Length 2167;
 Best Local Similarity 44.2%; Pred. No. 49;
 RESULT 1185
 ID ADD22490 standard; DNA; 2335 BP.
 DE HLA-B*6 T cell recognised tumour antigenic polypeptide, SEQ No 140.
 PN JP2003111595-A.
 PD 15-APR-2003.
 PA (ITOY/) ITO Y.
 Query Match 4.8%; Score 47; DB 10; Length 2335;
 Best Local Similarity 46.9%; Pred. No. 49;
 RESULT 1186
 ID AD115967 standard; cDNA; 2335 BP.
 DE Human PP 100 cDNA.
 PN WO2003008450-A1.

PD 30-JAN-2003.
 PA (ITOY/) ITOH K.
 Query Match 4.8%; Score 47; DB 10; Length 2335;
 Best Local Similarity 46.9%; Pred. No. 49;
 RESULT 1187
 ID AAQ22485 standard; DNA; 2668 BP.
 DE groEL-1 gene.
 PN WO9204452-A.
 PD 19-MAR-1992.
 PA (INSP) INST PASTEUR.
 Query Match 4.8%; Score 47; DB 2; Length 2668;
 Best Local Similarity 44.2%; Pred. No. 49;
 RESULT 1188
 ID AAV23493 standard; DNA; 4377 BP.
 DE Pseudomonas LipQ, LipR, OrfV operon.
 PN WO9806836-A2.
 PD 19-FEB-1998.
 PA (GENV) GENENCOR INT INC.
 Query Match 4.8%; Score 47; DB 2; Length 4377;
 Best Local Similarity 45.7%; Pred. No. 48;
 RESULT 1189
 ID AAAL3904 standard; DNA; 4377 BP.
 DE Pseudomonas alcaligenes nucleotide sequence SEQ ID NO:28.
 PN US6048710-A.
 PD 11-APR-2000.
 PA (GENV) GENENCOR INT INC.
 Query Match 4.8%; Score 47; DB 3; Length 4377;
 Best Local Similarity 45.7%; Pred. No. 48;
 RESULT 1190
 ID AAF30869 standard; DNA; 4377 BP.
 DE Pseudomonas alcaligenes LipQ, LipR and OrfZ gene region.
 PN US6225106-B1.
 PD 01-MAY-2001.
 PA (GENV) GENENCOR INT INC.
 Query Match 4.8%; Score 47; DB 4; Length 4377;
 Best Local Similarity 45.7%; Pred. No. 48;
 RESULT 1191
 ID AAD22881 standard; DNA; 4377 BP.
 DE P. alcaligenes DNA comprising cosmids #71, #201, #505 and #726.
 PN US6133283-B1.
 PD 06-NOV-2001.
 PA (GENV) GENENCOR INT INC.
 Query Match 4.8%; Score 47; DB 6; Length 4377;
 Best Local Similarity 45.7%; Pred. No. 48;
 RESULT 1192
 ID AAF88336 standard; DNA; 6459 BP.
 DE S. spinosa DNA fragment encoding ORF19, SEQ ID 43.
 PN DE19957268-A1.
 PD 08-MAR-2001.
 PA (FARB) BAYER AG.
 Query Match 4.8%; Score 47; DB 4; Length 6459;
 Best Local Similarity 46.9%; Pred. No. 48;
 RESULT 1193
 ID ABK52418 standard; DNA; 6868 BP.
 DE DNA encoding propionibacterium associated proteins.
 PN JP2002112790-A.
 PD 16-APR-2002.
 PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
 Query Match 4.8%; Score 47; DB 6; Length 6868;
 Best Local Similarity 51.7%; Pred. No. 48;
 RESULT 1194
 ID AAF88313 standard; DNA; 50000 BP.
 DE S. spinosa DNA fragment SEQ ID 2.
 PN DE19957268-A1.
 PD 08-MAR-2001.
 PA (FARB) BAYER AG.
 Query Match 4.8%; Score 47; DB 4; Length 50000;
 Best Local Similarity 46.9%; Pred. No. 45;
 RESULT 1195
 ID AAF88316 standard; DNA; 50000 BP.
 DE S. spinosa DNA fragment SEQ ID 5.
 PN DE19957268-A1.
 PD 08-MAR-2001.

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PA (FARB) BAYER AG.
 Query Match 4.8%; Score 47; DB 4; Length 50000;
 Best Local Similarity 46.9%; Pred. No. 45;
 RESULT 1196
 ID AA221501 standard; DNA; 80161 BP.
 DE DNA fragment of Saccharopolyspora spinosa containing bioynthetic genes.
 Query Match 4.8%; Score 47; DB 2; Length 80161;
 Best Local Similarity 46.9%; Pred. No. 45;
 RESULT 1197
 ID AD139159 standard; DNA; 85692 BP.
 DE Streptomyces hygroscopicus geldanamycin gene cluster, SEQ ID NO:1.
 PN WO2003106653-A2.
 PD 24-DEC-2003.
 PA (KOSA-) KOSAN BIOSCIENCES INC.
 PA (REID/) REID R C.
 Query Match 4.8%; Score 47; DB 12; Length 85692;
 Best Local Similarity 43.9%; Pred. No. 45;
 RESULT 1198
 Query Match 4.8%; Score 47; DB 4; Length 110000;
 Best Local Similarity 45.1%; Pred. No. 44;
 RESULT 1199
 Query Match 4.8%; Score 47; DB 4; Length 110000;
 Best Local Similarity 45.1%; Pred. No. 44;
 RESULT 1200
 ID AAA68102 standard; DNA; 296 BP.
 DE E. grandis caffeoyl CoA methyl transferase DNA sequence SEQ ID NO:195.
 PN WO200022099-A1.
 PD 20-APR-2000.
 PA (GENE-) GENESIS RES & DEV CORP LTD.
 PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.
 Query Match 4.7%; Score 46.8; DB 3; Length 296;
 Best Local Similarity 54.7%; Pred. No. 56;
 RESULT 1201
 ID ADD41852 standard; DNA; 296 BP.
 DE Caffeoyl CoA methyl transferase DNA #3.
 PN US2003131373-A1.
 PD 10-JUL-2003.
 PA (BLOK/) BLOKSBERG L N.
 PA (HAVU/) HAVUKALA I.
 Query Match 4.7%; Score 46.8; DB 10; Length 296;
 Best Local Similarity 54.7%; Pred. No. 56;
 RESULT 1202
 ID ABZ13007 standard; DNA; 768 BP.
 DE Arabidopsis thaliana stress regulated gene SEQ ID NO 812.
 PN WO200216655-A2.
 PD 28-FEB-2002.
 PA (SCRI) SCRIPPS RES INST.
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 Query Match 4.7%; Score 46.8; DB 6; Length 768;
 Best Local Similarity 46.0%; Pred. No. 55;
 RESULT 1203
 Query Match 4.7%; Score 46.8; DB 11; Length 792;
 Best Local Similarity 50.4%; Pred. No. 55;
 RESULT 1204
 ID AAV73801 standard; DNA; 801 BP.
 DE KSHV LUR terminal repeat unit DNA.
 PN US5849564-A.
 PD 15-DEC-1998.
 PA (UYCO) UNIV COLUMBIA NEW YORK.
 Query Match 4.7%; Score 46.8; DB 2; Length 801;
 Best Local Similarity 45.3%; Pred. No. 55;
 RESULT 1205
 ID AAA30291 standard; DNA; 801 BP.
 DE Rhadino virus cis-acting element, RVCAE.
 PN WO200029626-A1.
 PD 25-MAY-2000.
 PA (KIEFF) KIEFF E D.
 PA (BALL/) BALLESTAS M E.

PA (KAYE/) KAYE K M.
 Query Match 4.7%; Score 46.8; DB 3; Length 801;
 Best Local Similarity 45.3%; Pred. No. 55;
 RESULT 1206
 ID ABA93488 standard; DNA; 801 BP.
 DE Kaposi's sarcoma-associated herpesvirus terminal repeat unit.
 PN US6322792-B1.
 PD 27-NOV-2001.
 PA (KIEFF) KIEFF E D.
 Query Match 4.7%; Score 46.8; DB 6; Length 801;
 Best Local Similarity 45.3%; Pred. No. 55;
 RESULT 1207
 ID ADJ65097 standard; DNA; 801 BP.
 DE HHV8 terminal repeat region, TR.
 PN US2004037847-A1.
 PD 26-FEB-2004.
 PA (KIEFF) KIEFF E D.
 PA (BALL/) BALLESTAS M E.
 PA (KAYE/) KAYE K M.
 Query Match 4.7%; Score 46.8; DB 12; Length 801;
 Best Local Similarity 45.3%; Pred. No. 55;
 RESULT 1208
 ID ADI17814 standard; DNA; 872 BP.
 DE DNA (SeqID 1882) that confers an altered visual phenotype in plants.
 PN WO2003020741-A1.
 PD 13-MAR-2003.
 PA (DOWC) DOW CHEM CO.
 PA (DOWC) DOW AGROSCIENCES LLC.
 Query Match 4.7%; Score 46.8; DB 10; Length 872;
 Best Local Similarity 48.8%; Pred. No. 55;
 RESULT 1209
 ID ACA37750 standard; DNA; 984 BP.
 DE Prokaryotic essential gene #19407.
 PN WO200277183-A2.
 PD 03-OCT-2002.
 PA (ELIT-) ELITRA PHARM INC.
 Query Match 4.7%; Score 46.8; DB 8; Length 984;
 Best Local Similarity 50.4%; Pred. No. 54;
 RESULT 1210
 ID ABD06351 standard; DNA; 1071 BP.
 DE Pseudomonas aeruginosa polynucleotide #4955.
 PN US6551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Query Match 4.7%; Score 46.8; DB 11; Length 1071;
 Best Local Similarity 50.4%; Pred. No. 54;
 RESULT 1211
 ID ABD06390 standard; DNA; 1131 BP.
 DE Pseudomonas aeruginosa polynucleotide #4994.
 PN US6551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Query Match 4.7%; Score 46.8; DB 11; Length 1131;
 Best Local Similarity 50.4%; Pred. No. 54;
 RESULT 1212
 ID ABD06380 standard; DNA; 1215 BP.
 DE Pseudomonas aeruginosa polynucleotide #4984.
 PN US6551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Query Match 4.7%; Score 46.8; DB 11; Length 1215;
 Best Local Similarity 50.4%; Pred. No. 54;
 RESULT 1213
 ID ADA45210 standard; cDNA; 1358 BP.
 DE Recombinant Max & JLP N-terminal region protein, M2L21I coding sequence.
 PN WO2003066652-A2.
 PD 14-AUG-2003.
 PA (UTEM) UNIV TEMPLE.
 Query Match 4.7%; Score 46.8; DB 9; Length 1358;
 Best Local Similarity 54.1%; Pred. No. 54;
 RESULT 1214
 ID ADA45206 standard; cDNA; 1358 BP.
 DE Recombinant Max and JLP N-terminal region protein, M2, coding sequence.

PN WO2003066652-A2.
PD 14-AUG-2003.
PA (UTEM) UNIV TEMPLE.
Query Match 4.7%; Score 46.8; DB 9; Length 1358;
Best Local Similarity 54.1%; Pred. No. 54;
RESULT 1215
ID ADA45208 standard; cDNA; 1358 BP.
DE Recombinant Max and JLP N-terminal region protein, M2LZI coding sequence.
PN WO2003066652-A2.
PD 14-AUG-2003.
PA (UTEM) UNIV TEMPLE.
Query Match 4.7%; Score 46.8; DB 9; Length 1358;
Best Local Similarity 54.1%; Pred. No. 54;
RESULT 1216
ID ACA40293 standard; DNA; 1464 BP.
DE Prokaryotic essential gene #21950.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 4.7%; Score 46.8; DB 8; Length 1464;
Best Local Similarity 42.2%; Pred. No. 54;
RESULT 1217
ID ACA37666 standard; DNA; 2739 BP.
DE Prokaryotic essential gene #19123.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 4.7%; Score 46.8; DB 8; Length 2739;
Best Local Similarity 45.1%; Pred. No. 53;
RESULT 1218
ID ABD08987 standard; DNA; 3171 BP.
DE Pseudomonas aeruginosa polynucleotide #7591.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 4.7%; Score 46.8; DB 11; Length 3171;
Best Local Similarity 43.4%; Pred. No. 53;
RESULT 1219
ID ABD09358 standard; DNA; 3210 BP.
DE Pseudomonas aeruginosa polynucleotide #7962.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 4.7%; Score 46.8; DB 11; Length 3210;
Best Local Similarity 43.4%; Pred. No. 53;
RESULT 1220
ID AAH47802 standard; DNA; 3535 BP.
DE Chimeric CBD-fused FR901379 acylase DNA.
PN WO200131038-A1.
PD 03-MAY-2001.
PA (FUJI) FUJISAWA PHARM CO LTD.
Query Match 4.7%; Score 46.8; DB 4; Length 3535;
Best Local Similarity 49.3%; Pred. No. 53;
RESULT 1221
ID AA15781 standard; cDNA; 4176 BP.
DE Human polynucleotide SEQ ID NO 34.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 4.7%; Score 46.8; DB 4; Length 4176;
Best Local Similarity 49.4%; Pred. No. 52;
RESULT 1222
ID AAQ95540 standard; DNA; 4356 BP.
DE Cardiac adenylyl cyclase gene.
PN TW243453-A.
PD 21-MAR-1995.
PA (AMCY) AMERICAN CYANAMID CO.
Query Match 4.7%; Score 46.8; DB 2; Length 4356;
Best Local Similarity 45.9%; Pred. No. 52;
RESULT 1223
ID ADA45191 standard; cDNA; 4667 BP.
DE Murine JLP coding sequence.
PN WO2003066652-A2.

PD 14-AUG-2003.
PA (UTEM) UNIV TEMPLE.
Query Match 4.7%; Score 46.8; DB 9; Length 4667;
Best Local Similarity 54.1%; Pred. No. 52;
RESULT 1224
ID ADC10001 standard; DNA; 5220 BP.
DE Human NOVX polypeptide coding sequence SEQ ID NO: 21.
PN WO2003000842-A2.
PD 03-JAN-2003.
PA (CURA-) CURAGEN CORP.
Query Match 4.7%; Score 46.8; DB 10; Length 5220;
Best Local Similarity 42.6%; Pred. No. 52;
RESULT 1225
ID AAF32248 standard; DNA; 5692 BP.
DE Streptomyces sp. cyclic lipopeptide acylase encoding DNA SEQ ID NO:1.
PN WO200102585-A1.
PD 11-JAN-2001.
PA (FUJI) FUJISAWA PHARM CO LTD.
Query Match 4.7%; Score 46.8; DB 4; Length 5692;
Best Local Similarity 49.3%; Pred. No. 52;
RESULT 1226
ID AAD54224 standard; DNA; 5862 BP.
DE Streptomyces platensis subspecies rosaceus dorrigocin ORF7 DNA.
PN WO200288176-A2.
PD 07-NOV-2002.
PA (ECOP-) ECOPIA BIOSCIENCES INC.
Query Match 4.7%; Score 46.8; DB 10; Length 5862;
Best Local Similarity 46.8%; Pred. No. 52;
RESULT 1227
ID ACA37617 standard; DNA; 10232 BP.
DE Prokaryotic essential gene #19274.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 4.7%; Score 46.8; DB 8; Length 10232;
Best Local Similarity 44.0%; Pred. No. 51;
RESULT 1228
ID AA458472 standard; DNA; 18660 BP.
DE Nucleotide sequence of the bleomycin (BLM) gene cluster ORFs 31-40.
PN WO200040704-A1.
PD 13-JUL-2000.
PA (REGC) UNIV CALIFORNIA.
Query Match 4.7%; Score 46.8; DB 3; Length 18660;
Best Local Similarity 47.5%; Pred. No. 50;
RESULT 1229
ID AB168348 standard; DNA; 25000 BP.
DE Kidney cancer related gene sequence SEQ ID NO:6685.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Query Match 4.7%; Score 46.8; DB 6; Length 25000;
Best Local Similarity 47.3%; Pred. No. 50;
RESULT 1230
ID AA11992 standard; DNA; 37856 BP.
DE S. Celluloseum DNA encoding polyketide and hereropolyketide enzymes.
PN DE19846493-A1.
PD 13-APR-2000.
PA (GBFB) GES BIOTECHNOLOGISCHE FORSCHUNG MBH.
Query Match 4.7%; Score 46.8; DB 3; Length 37856;
Best Local Similarity 48.2%; Pred. No. 49;
RESULT 1231
Query Match 4.7%; Score 46.8; DB 4; Length 110000;
Best Local Similarity 42.2%; Pred. No. 48;
RESULT 1232
ID ABD15774 standard; DNA; 270 BP.
DE Pseudomonas aeruginosa polynucleotide #14378.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 4.7%; Score 46.6; DB 11; Length 270;
Best Local Similarity 50.2%; Pred. No. 61;
RESULT 1233
ID ABD01848 standard; DNA; 489 BP.

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DE Pseudomonas aeruginosa polynucleotide #452.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 4.7%; Score 46.6; DB 11; Length 489;
Best Local Similarity 47.9%; Pred. No. 60;
RESULT 1234
ID ACA38033 standard; DNA; 723 BP.
DE Prokaryotic essential gene #19690.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 4.7%; Score 46.6; DB 8; Length 723;
Best Local Similarity 45.3%; Pred. No. 59;
RESULT 1235
ID ABD13964 standard; DNA; 777 BP.
DE Pseudomonas aeruginosa polynucleotide #12569.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 4.7%; Score 46.6; DB 11; Length 777;
Best Local Similarity 53.6%; Pred. No. 59;
RESULT 1236
ID ABD14635 standard; DNA; 786 BP.
DE Pseudomonas aeruginosa polynucleotide #13239.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 4.7%; Score 46.6; DB 11; Length 786;
Best Local Similarity 53.6%; Pred. No. 59;
RESULT 1237
ID ACC59353 standard; DNA; 948 BP.
DE R ruber esterase estA coding sequence #1.
PN WO2003031625-A1.
PD 17-APR-2003.
PA (DEGS ) DEGUSSA AG.
PA (SCHW/) SCHWAB H.
Query Match 4.7%; Score 46.6; DB 10; Length 948;
Best Local Similarity 46.0%; Pred. No. 59;
RESULT 1238
ID ACC59354 standard; DNA; 948 BP.
DE R ruber esterase estA coding sequence #2.
PN WO2003031625-A1.
PD 17-APR-2003.
PA (DEGS ) DEGUSSA AG.
PA (SCHW/) SCHWAB H.
Query Match 4.7%; Score 46.6; DB 10; Length 948;
Best Local Similarity 46.0%; Pred. No. 59;
RESULT 1239
ID ABD01827 standard; DNA; 981 BP.
DE Pseudomonas aeruginosa polynucleotide #431.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 4.7%; Score 46.6; DB 11; Length 981;
Best Local Similarity 47.9%; Pred. No. 59;
RESULT 1240
ID ABD11883 standard; DNA; 981 BP.
DE Pseudomonas aeruginosa polynucleotide #10487.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 4.7%; Score 46.6; DB 11; Length 981;
Best Local Similarity 47.7%; Pred. No. 59;
RESULT 1241
ID ABD08147 standard; DNA; 1062 BP.
DE Pseudomonas aeruginosa polynucleotide #6751.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 4.7%; Score 46.6; DB 11; Length 1062;
Best Local Similarity 47.2%; Pred. No. 59;
RESULT 1242
ID ACA38086 standard; DNA; 1224 BP.
DE Prokaryotic essential gene #19743.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 4.7%; Score 46.6; DB 8; Length 1224;
Best Local Similarity 52.3%; Pred. No. 58;
RESULT 1243
ID AAD53021 standard; DNA; 1299 BP.
DE Streptomyces species emas gene.
PN WO200292801-A2.
PD 21-NOV-2002.
PA (SYGN ) SYNGENTA PARTICIPATIONS AG.
Query Match 4.7%; Score 46.6; DB 10; Length 1299;
Best Local Similarity 48.0%; Pred. No. 58;
RESULT 1244
ID ABD04946 standard; DNA; 1380 BP.
DE Pseudomonas aeruginosa polynucleotide #3550.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 4.7%; Score 46.6; DB 11; Length 1380;
Best Local Similarity 45.1%; Pred. No. 58;
RESULT 1245
ID ABZ71149 standard; DNA; 1473 BP.
DE S. murayamaensis ATCC 21414 kinamycin encoding DNA SEQ ID NO:36.
PN WO200302066-A2.
PD 09-JAN-2003.
PA (DIVE-) DIVERSA CORP.
Query Match 4.7%; Score 46.6; DB 8; Length 1473;
Best Local Similarity 46.4%; Pred. No. 58;
RESULT 1246
ID ACC59357 standard; DNA; 1494 BP.
DE R ruber vector pMSS12 coding sequence insert #4.
PN WO2003031625-A1.
PD 17-APR-2003.
PA (DEGS ) DEGUSSA AG.
PA (SCHW/) SCHWAB H.
Query Match 4.7%; Score 46.6; DB 10; Length 1494;
Best Local Similarity 46.0%; Pred. No. 58;
RESULT 1247
ID ACC59352 standard; DNA; 1494 BP.
DE R ruber vector pMSS12 coding sequence insert #2.
PN WO2003031625-A1.
PD 17-APR-2003.
PA (DEGS ) DEGUSSA AG.
PA (SCHW/) SCHWAB H.
Query Match 4.7%; Score 46.6; DB 10; Length 1494;
Best Local Similarity 46.0%; Pred. No. 58;
RESULT 1248
ID ABD08270 standard; DNA; 1530 BP.
DE Pseudomonas aeruginosa polynucleotide #6874.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 4.7%; Score 46.6; DB 11; Length 1530;
Best Local Similarity 47.2%; Pred. No. 58;
RESULT 1249
ID AAL61148 standard; DNA; 1710 BP.
DE Human mutant ARX gene #1.
PN WO2003045989-A1.
PD 05-JUN-2003.
PA (WOME-) WOMEN'S & CHILDREN'S HOSPITAL.
Query Match 4.7%; Score 46.6; DB 9; Length 1710;
Best Local Similarity 46.3%; Pred. No. 58;
RESULT 1250
ID ABD04953 standard; DNA; 1947 BP.
DE Pseudomonas aeruginosa polynucleotide #3557.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 4.7%; Score 46.6; DB 11; Length 1947;
Best Local Similarity 45.1%; Pred. No. 58;

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RESULT 1251
ID ABD4312 standard; DNA; 2325 BP.
DE Pseudomonas aeruginosa polynucleotide #12916.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 4.7%; Score 46.6; DB 11; Length 2325;
Best Local Similarity 53.6%; Pred. No. 57;
RESULT 1252
ID ADB87421 standard; DNA; 2500 BP.
DE Transgene expression regulatory element, STAR66F.
PN WO2003004704-A2.
PD 16-JAN-2003.
PA (CHRO-) CHROMAGENICS BV.
Query Match 4.7%; Score 46.6; DB 10; Length 2500;
Best Local Similarity 46.1%; Pred. No. 57;
RESULT 1253
ID ADJ35230 standard; DNA; 2500 BP.
DE Human stabilising anti-repression, STAR, element #66.
PN WO2003106674-A2.
PD 24-DEC-2003.
PA (CHRO-) CHROMAGENICS BV.
Query Match 4.7%; Score 46.6; DB 12; Length 2500;
Best Local Similarity 46.1%; Pred. No. 57;
RESULT 1254
ID ADL96848 standard; DNA; 2500 BP.
DE Stabilizing Anti-Repressor DNA sequence, T2F STAR 66F.
PN WO2003106684-A2.
PD 24-DEC-2003.
PA (CHRO-) CHROMAGENICS BV.
Query Match 4.7%; Score 46.6; DB 12; Length 2500;
Best Local Similarity 46.1%; Pred. No. 57;
RESULT 1255
ID AC44572 standard; cDNA; 3285 BP.
DE Alpha-amylase/glucosylase fusion nucleotide sequence SEQ ID NO:46.
PN WO2003018766-A2.
PD 06-MAR-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 4.7%; Score 46.6; DB 8; Length 3285;
Best Local Similarity 48.7%; Pred. No. 57;
RESULT 1256
ID ABL15824 standard; cDNA; 3790 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 41954.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NV.
Query Match 4.7%; Score 46.6; DB 4; Length 3790;
Best Local Similarity 47.2%; Pred. No. 57;
RESULT 1257
ID ACA26449 standard; DNA; 3963 BP.
DE Prokaryotic essential gene #8106.
PN WO20027183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 4.7%; Score 46.6; DB 8; Length 3963;
Best Local Similarity 43.1%; Pred. No. 57;
RESULT 1258
ID AAL61172 standard; DNA; 4770 BP.
DE Actinosynnema pretiosum polyketide synthase (PKS) gene #3.
PN WO2003045312-A2.
PD 05-JUN-2003.
PA (UNIW) UNIV WASHINGTON.
Query Match 4.7%; Score 46.6; DB 8; Length 4770;
Best Local Similarity 44.8%; Pred. No. 56;
RESULT 1259
ID ADC10001 standard; DNA; 5220 BP.
DE Human NOVX polypeptide coding sequence SEQ ID NO: 21.
PN WO200300842-A2.
PD 03-JAN-2003.
PA (CURA-) CURAGEN CORP.
Query Match 4.7%; Score 46.6; DB 10; Length 5220;
Best Local Similarity 44.2%; Pred. No. 56;
RESULT 1260

ID ABS78655 standard; DNA; 5811 BP.
DE S. macromyceticus DNA encoding PKSE protein macromomycin.
PN CA2387401-A1.
PD 04-SEP-2002.
PA (ECOP-) ECOPIA BIOSCIENCES INC.
Query Match 4.7%; Score 46.6; DB 6; Length 5811;
Best Local Similarity 47.6%; Pred. No. 56;
RESULT 1261
ID ABD01877 standard; DNA; 7419 BP.
DE Pseudomonas aeruginosa polynucleotide #481.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 4.7%; Score 46.6; DB 11; Length 7419;
Best Local Similarity 47.9%; Pred. No. 56;
RESULT 1262
ID ABD01792 standard; DNA; 7449 BP.
DE Pseudomonas aeruginosa polynucleotide #396.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 4.7%; Score 46.6; DB 11; Length 7449;
Best Local Similarity 47.9%; Pred. No. 56;
RESULT 1263
ID ABL66291 standard; DNA; 14800 BP.
DE Lung cancer related gene sequence SEQ ID NO:4628.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Query Match 4.7%; Score 46.6; DB 6; Length 14800;
Best Local Similarity 44.8%; Pred. No. 54;
RESULT 1264
ID ADP13447 standard; DNA; 14800 BP.
DE Renal cell carcinoma differentially expressed gene #183.
PN WO2004048933-A2.
PD 10-JUN-2004.
PA (AMHP) WYETH.
PA (TWIN) TWINE N C.
PA (BURC) BURCZYNSKI M E.
PA (TREP) TREPICCHIO W L.
PA (DORN) DORNER A.
PA (STOV) STOVER J A.
PA (SLON) SLONI D K.
Query Match 4.7%; Score 46.6; DB 12; Length 14800;
Best Local Similarity 44.8%; Pred. No. 54;
RESULT 1265
ID AAS94858 standard; DNA; 14835 BP.
DE Human DNA sequence #113 expressed during foam cell differentiation.
PN WO200177389-A2.
PD 18-OCT-2001.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 4.7%; Score 46.6; DB 6; Length 14835;
Best Local Similarity 44.8%; Pred. No. 54;
RESULT 1266
ID AAD54223 standard; DNA; 24081 BP.
DE Streptomyces platensis subspecies roseaceus dorrigocin ORF6 DNA.
PN WO200288176-A2.
PD 07-NOV-2002.
PA (ECOP-) ECOPIA BIOSCIENCES INC.
Query Match 4.7%; Score 46.6; DB 10; Length 24081;
Best Local Similarity 46.7%; Pred. No. 54;
RESULT 1267
ID ADQ07566 standard; DNA; 25467 BP.
DE Streptomyces kanamyceticus kanamycin biosynthesis genes SEQ ID NO:1.
PN JP2004173537-A.
PD 24-JUN-2004.
PA (MEIJ) MEIJI SEIKA KAISHA LTD.
Query Match 4.7%; Score 46.6; DB 12; Length 25467;
Best Local Similarity 46.9%; Pred. No. 54;
RESULT 1268
ID ABZ71131 standard; DNA; 36321 BP.
DE Streptomyces murayamaensis ATCC 21414 kinamycin related DNA SEQ ID NO:1.
PN WO2003002066-A2.

PD 09-JAN-2003.
PA (DIVE-) DIVERSA CORP. 4.7%; Score 46.6; DB 8; Length 36321;
Query Match 46.4%; Pred. No. 53;
Best Local Similarity 46.4%; Pred. No. 53;
RESULT 1269
ID ACF30939 standard; DNA; 53905 BP.
DE Rice cultivar Asominori fertility restorer gene Rf-1, SEQ ID NO:28.
PN WO2003027290-A1.
PD 03-APR-2003.
PA (NLSB) JAPAN TOBACCO INC.
PA (SYGN) SYNGENTA LTD.
Query Match 4.7%; Score 46.6; DB 8; Length 53905;
Best Local Similarity 46.2%; Pred. No. 53;
RESULT 1270
ID ADI09998 standard; DNA; 53905 BP.
DE Rice cultivar Asominori fertility restorer gene Rf-1, SEQ ID NO:28.
PN WO2004005515-A1.
PD 15-JAN-2004.
PA (NLSB) JAPAN TOBACCO INC.
PA (SYGN) SYNGENTA LTD.
Query Match 4.7%; Score 46.6; DB 12; Length 53905;
Best Local Similarity 46.2%; Pred. No. 53;
RESULT 1271
ID ABL59157 standard; cDNA; 1072 BP.
DE Nucleotide sequence of human glutathione peroxidase-6 (GPx6).
PN US2002031506-A1.
PD 14-MAR-2002.
PA (INCY-) INCYTE PHARM INC.
Query Match 4.7%; Score 46.4; DB 4; Length 1072;
Best Local Similarity 50.0%; Pred. No. 63;
RESULT 1280
ID ABL59157 standard; cDNA; 1072 BP.
DE Nucleotide sequence of human glutathione peroxidase-6 (GPx6).
PN US2002031506-A1.
PD 14-MAR-2002.
PA (INCY-) INCYTE PHARM INC.
Query Match 4.7%; Score 46.4; DB 4; Length 1072;
Best Local Similarity 50.0%; Pred. No. 63;
RESULT 1281
ID AAI58027 standard; cDNA; 1100 BP.
DE Human polynucleotide SEQ ID NO 230.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 4.7%; Score 46.4; DB 4; Length 1100;
Best Local Similarity 50.0%; Pred. No. 63;
RESULT 1282
ID AAI59813 standard; cDNA; 1205 BP.
DE Human polynucleotide SEQ ID NO 3802.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 4.7%; Score 46.4; DB 4; Length 1205;
Best Local Similarity 50.0%; Pred. No. 63;
RESULT 1283
ID ADI42681 standard; DNA; 1219 BP.
DE Plant transcription factor polynucleotide #735.
PN US2004019927-A1.
PD 29-JAN-2004.
PA (SHER-) SHERMAN B K.
PA (RIEC-) RIECHMANN J L.
PA (JIAN-) JIANG C.
PA (HEAR-) HEARD J E.
PA (HAKE-) HAAKE V.
PA (CREE-) CREELMAN R A.
PA (RATC-) RATCLIFFE O.
PA (ADAM-) ADAM L J.
PA (REUB-) REUBER T L.
PA (KEDD-) KEDDIE J.
PA (BROU-) BROUN P E.
PA (PILG-) PILGRIM M L.
PA (DUBE-) DUBELL A N.
PA (PINE-) PINEDA O.
PA (YUGG-) YU G.
Query Match 4.7%; Score 46.4; DB 12; Length 1219;
Best Local Similarity 44.2%; Pred. No. 63;
RESULT 1284
ID ADO02930 standard; cDNA; 1219 BP.
DE Corn orthologue of Thalea transcription factor, cDNA #98.
PN US2004045049-A1.
PD 04-MAR-2004.
PA (ZHAN-) ZHANG J.
PA (FROM-) FROMM M E.

PD 09-JAN-2003.
PA (DIVE-) DIVERSA CORP. 4.7%; Score 46.6; DB 8; Length 36321;
Query Match 46.4%; Pred. No. 53;
Best Local Similarity 46.4%; Pred. No. 53;
RESULT 1269
ID ACF30939 standard; DNA; 53905 BP.
DE Rice cultivar Asominori fertility restorer gene Rf-1, SEQ ID NO:28.
PN WO2003027290-A1.
PD 03-APR-2003.
PA (NLSB) JAPAN TOBACCO INC.
PA (SYGN) SYNGENTA LTD.
Query Match 4.7%; Score 46.6; DB 8; Length 53905;
Best Local Similarity 46.2%; Pred. No. 53;
RESULT 1270
ID ADI09998 standard; DNA; 53905 BP.
DE Rice cultivar Asominori fertility restorer gene Rf-1, SEQ ID NO:28.
PN WO2004005515-A1.
PD 15-JAN-2004.
PA (NLSB) JAPAN TOBACCO INC.
PA (SYGN) SYNGENTA LTD.
Query Match 4.7%; Score 46.6; DB 12; Length 53905;
Best Local Similarity 46.2%; Pred. No. 53;
RESULT 1271
ID ABL59157 standard; cDNA; 1072 BP.
DE Nucleotide sequence of human glutathione peroxidase-6 (GPx6).
PN US2002031506-A1.
PD 14-MAR-2002.
PA (INCY-) INCYTE PHARM INC.
Query Match 4.7%; Score 46.4; DB 4; Length 1072;
Best Local Similarity 50.0%; Pred. No. 63;
RESULT 1280
ID ABL59157 standard; cDNA; 1072 BP.
DE Nucleotide sequence of human glutathione peroxidase-6 (GPx6).
PN US2002031506-A1.
PD 14-MAR-2002.
PA (INCY-) INCYTE PHARM INC.
Query Match 4.7%; Score 46.4; DB 4; Length 1072;
Best Local Similarity 50.0%; Pred. No. 63;
RESULT 1281
ID AAI58027 standard; cDNA; 1100 BP.
DE Human polynucleotide SEQ ID NO 230.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 4.7%; Score 46.4; DB 4; Length 1100;
Best Local Similarity 50.0%; Pred. No. 63;
RESULT 1282
ID AAI59813 standard; cDNA; 1205 BP.
DE Human polynucleotide SEQ ID NO 3802.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 4.7%; Score 46.4; DB 4; Length 1205;
Best Local Similarity 50.0%; Pred. No. 63;
RESULT 1283
ID ADI42681 standard; DNA; 1219 BP.
DE Plant transcription factor polynucleotide #735.
PN US2004019927-A1.
PD 29-JAN-2004.
PA (SHER-) SHERMAN B K.
PA (RIEC-) RIECHMANN J L.
PA (JIAN-) JIANG C.
PA (HEAR-) HEARD J E.
PA (HAKE-) HAAKE V.
PA (CREE-) CREELMAN R A.
PA (RATC-) RATCLIFFE O.
PA (ADAM-) ADAM L J.
PA (REUB-) REUBER T L.
PA (KEDD-) KEDDIE J.
PA (BROU-) BROUN P E.
PA (PILG-) PILGRIM M L.
PA (DUBE-) DUBELL A N.
PA (PINE-) PINEDA O.
PA (YUGG-) YU G.
Query Match 4.7%; Score 46.4; DB 12; Length 1219;
Best Local Similarity 44.2%; Pred. No. 63;
RESULT 1284
ID ADO02930 standard; cDNA; 1219 BP.
DE Corn orthologue of Thalea transcription factor, cDNA #98.
PN US2004045049-A1.
PD 04-MAR-2004.
PA (ZHAN-) ZHANG J.
PA (FROM-) FROMM M E.

PA (HEAR/) HEARD J E.
PA (RIEG/) RIECHMANN J L.
PA (ADAM/) ADAM L J.
PA (BROU/) BROUN P E.
PA (PINE/) PINEDA O.
PA (REUB/) REUBER T L.
PA (KEDD/) KEDDIE J S.
PA (YUGG/) YU G.
PA (JIAN/) JIANG C.
PA (SAMA/) SAMAHA R S.
PA (PILG/) PILGRIM M L.
PA (CREE/) CREELMAN R A.
PA (DUBE/) DUBELL A N.
PA (RATC/) RATCLIFFE O.
PA (KUMI/) KUMIMOTO R.
PA (SHER/) SHERMAN B K.
Query Match 4.7%; Score 46.4; DB 12; Length 1219;
Best Local Similarity 44.2%; Pred. No. 63;
RESULT 1285
ID AA265013 standard; cDNA; 1227 BP.
DE Membrane-bound protein PRO828 encoding cDNA.
PN WO9963088-A2.
PD 09-DEC-1999.
PA (GETH) GENENTECH INC.
Query Match 4.7%; Score 46.4; DB 3; Length 1227;
Best Local Similarity 50.0%; Pred. No. 63;
RESULT 1286
ID AA846137 standard; cDNA; 1227 BP.
DE Human DNA encoding PRO polypeptide sequence #213.
PN WO200168848-A2.
PD 20-SEP-2001.
PA (GETH) GENENTECH INC.
Query Match 4.7%; Score 46.4; DB 4; Length 1227;
Best Local Similarity 50.0%; Pred. No. 63;
RESULT 1287
ID AAF44159 standard; cDNA; 1227 BP.
DE Human PRO828 (UNQ469) nucleotide sequence SEQ ID NO:188.
PN WO200073454-A1.
PD 07-DEC-2000.
PA (GETH) GENENTECH INC.
Query Match 4.7%; Score 46.4; DB 5; Length 1227;
Best Local Similarity 50.0%; Pred. No. 63;
RESULT 1288
ID ABJ88133 standard; cDNA; 1227 BP.
DE Human PRO828 cDNA sequence SEQ ID NO:123.
PN WO200200690-A2.
PD 03-JAN-2002.
PA (GETH) GENENTECH INC.
Query Match 4.7%; Score 46.4; DB 6; Length 1227;
Best Local Similarity 50.0%; Pred. No. 63;
RESULT 1289
ID ABK28599 standard; cDNA; 1227 BP.
DE Human DNAS7037-1444 encoding PRO828.
PN WO200109327-A2.
PD 08-FEB-2001.
PA (GETH) GENENTECH INC.
Query Match 4.7%; Score 46.4; DB 6; Length 1227;
Best Local Similarity 50.0%; Pred. No. 63;
RESULT 1290
ID ABJ95622 standard; cDNA; 1227 BP.
DE Human angiogenesis related cDNA PRO828 SEQ ID NO: 123.
PN WO200208284-A2.
PD 31-JAN-2002.
PA (GETH) GENENTECH INC.
PA (BAKE/) BAKER K P.
PA (FERR/) FERRARA N.
PA (GERR/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (MARS/) MARSTERS S A.

PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (STEP/) STEPHAN J F.
PA (WATA/) WATANABE C K.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 4.7%; Score 46.4; DB 6; Length 1227;
Best Local Similarity 50.0%; Pred. No. 63;
RESULT 1291
ID ACA89587 standard; cDNA; 1227 BP.
DE cDNA encoding human PRO polypeptide #213.
PN US2003036141-A1.
PD 20-FEB-2003.
Query Match 4.7%; Score 46.4; DB 8; Length 1227;
Best Local Similarity 50.0%; Pred. No. 63;
RESULT 1292
ID ACA73597 standard; cDNA; 1227 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #213.
PN US2003036146-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 4.7%; Score 46.4; DB 8; Length 1227;
Best Local Similarity 50.0%; Pred. No. 63;
RESULT 1293
ID ACA05912 standard; cDNA; 1227 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #213.
PN US2003036162-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 4.7%; Score 46.4; DB 8; Length 1227;
Best Local Similarity 50.0%; Pred. No. 63;
RESULT 1294
ID ACA66746 standard; cDNA; 1227 BP.
DE cDNA encoding human PRO protein #213.
PN US2003036137-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 4.7%; Score 46.4; DB 8; Length 1227;
Best Local Similarity 50.0%; Pred. No. 63;
RESULT 1295
ID ACA64292 standard; cDNA; 1227 BP.
DE Novel human secreted and transmembrane protein PRO828 cDNA.
PN US2003003531-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 4.7%; Score 46.4; DB 8; Length 1227;
Best Local Similarity 50.0%; Pred. No. 63;
RESULT 1296
ID ACF20321 standard; cDNA; 1227 BP.
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.
PN US2003040063-A1.
PD 27-FEB-2003.
Query Match 4.7%; Score 46.4; DB 8; Length 1227;
Best Local Similarity 50.0%; Pred. No. 63;
RESULT 1297
ID ACF19707 standard; cDNA; 1227 BP.
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.
PN US2003040064-A1.
PD 27-FEB-2003.
Query Match 4.7%; Score 46.4; DB 8; Length 1227;
Best Local Similarity 50.0%; Pred. No. 63;
RESULT 1298
ID ACD21995 standard; cDNA; 1227 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #213.
PN US2003027267-A1.
PD 06-FEB-2003.
Query Match 4.7%; Score 46.4; DB 8; Length 1227;
Best Local Similarity 50.0%; Pred. No. 63;
RESULT 1299
ID ACF13160 standard; cDNA; 1227 BP.
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.
PN US2003036160-A1.
PD 20-FEB-2003.

Query Match 4.7%; Score 46.4; DB 8; Length 1227;
Best Local Similarity 50.0%; Pred. No. 63;
RESULT 1300
ID ACD25263 standard; cDNA; 1227 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #213.
PN US2003044925-A1.
PD 06-MAR-2003.
Query Match 4.7%; Score 46.4; DB 8; Length 1227;
Best Local Similarity 50.0%; Pred. No. 63;
RESULT 1301
ID ACF00312 standard; cDNA; 1227 BP.
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.
PN US2003054474-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.7%; Score 46.4; DB 8; Length 1227;
Best Local Similarity 50.0%; Pred. No. 63;
RESULT 1302
ID ACA72369 standard; cDNA; 1227 BP.
DE Novel human secreted and transmembrane protein PRO828 cDNA.
PN US2003032114-A1.
PD 13-FEB-2003.
Query Match 4.7%; Score 46.4; DB 8; Length 1227;
Best Local Similarity 50.0%; Pred. No. 63;
RESULT 1303
ID ACD04893 standard; cDNA; 1227 BP.
DE Novel human secreted and transmembrane protein PRO828 cDNA.
PN US2003032101-A1.
PD 13-FEB-2003.
Query Match 4.7%; Score 46.4; DB 8; Length 1227;
Best Local Similarity 50.0%; Pred. No. 63;
RESULT 1304
ID ACD18354 standard; cDNA; 1227 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #213.
PN US2003036124-A1.
PD 20-FEB-2003.
Query Match 4.7%; Score 46.4; DB 8; Length 1227;
Best Local Similarity 50.0%; Pred. No. 63;
RESULT 1305
ID ACD08361 standard; cDNA; 1227 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #213.
PN US2003040054-A1.
PD 27-FEB-2003.
Query Match 4.7%; Score 46.4; DB 8; Length 1227;
Best Local Similarity 50.0%; Pred. No. 63;
RESULT 1306
ID ACA88795 standard; cDNA; 1227 BP.
DE Novel human secreted and transmembrane protein PRO828 cDNA.
PN US2003036133-A1.
PD 20-FEB-2003.
Query Match 4.7%; Score 46.4; DB 8; Length 1227;
Best Local Similarity 50.0%; Pred. No. 63;
RESULT 1307
ID ACA70237 standard; cDNA; 1227 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #213.
PN US2003036134-A1.
PD 20-FEB-2003.
Query Match 4.7%; Score 46.4; DB 8; Length 1227;
Best Local Similarity 50.0%; Pred. No. 63;
RESULT 1308
ID ACD12459 standard; cDNA; 1227 BP.
DE Novel human secreted and transmembrane protein PRO828 cDNA.
PN US2003022294-A1.
PD 30-JAN-2003.
Query Match 4.7%; Score 46.4; DB 8; Length 1227;
Best Local Similarity 50.0%; Pred. No. 63;
RESULT 1309
ID ACC74374 standard; cDNA; 1227 BP.
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.
PN US2003027275-A1.
PD 06-FEB-2003.
Query Match 4.7%; Score 46.4; DB 8; Length 1227;
Best Local Similarity 50.0%; Pred. No. 63;

RESULT 1310
ID ACD16002 standard; cDNA; 1227 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #213.
PN US2003027324-A1.
PD 06-FEB-2003.
Query Match 4.7%; Score 46.4; DB 8; Length 1227;
Best Local Similarity 50.0%; Pred. No. 63;
RESULT 1311
ID ACD25570 standard; cDNA; 1227 BP.
DE Novel human secreted and transmembrane protein PRO828 cDNA.
PN US2003036118-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 4.7%; Score 46.4; DB 8; Length 1227;
Best Local Similarity 50.0%; Pred. No. 63;
RESULT 1312
ID ACD18047 standard; cDNA; 1227 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #213.
PN US2003036123-A1.
PD 20-FEB-2003.
Query Match 4.7%; Score 46.4; DB 8; Length 1227;
Best Local Similarity 50.0%; Pred. No. 63;
RESULT 1313
ID ACC88334 standard; cDNA; 1227 BP.
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.
PN US2003036148-A1.
PD 20-FEB-2003.
Query Match 4.7%; Score 46.4; DB 8; Length 1227;
Best Local Similarity 50.0%; Pred. No. 63;
RESULT 1314
ID ACD21688 standard; cDNA; 1227 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #213.
PN US2003040060-A1.
PD 27-FEB-2003.
Query Match 4.7%; Score 46.4; DB 8; Length 1227;
Best Local Similarity 50.0%; Pred. No. 63;
RESULT 1315
ID ACD18755 standard; cDNA; 1227 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #213.
PN US2003044916-A1.
PD 06-MAR-2003.
Query Match 4.7%; Score 46.4; DB 8; Length 1227;
Best Local Similarity 50.0%; Pred. No. 63;
RESULT 1316
ID ABX98365 standard; cDNA; 1227 BP.
DE Human cDNA encoding a secreted/transmembrane protein, SEQ ID 425.
PN US2003036156-A1.
PD 20-FEB-2003.
Query Match 4.7%; Score 46.4; DB 8; Length 1227;
Best Local Similarity 50.0%; Pred. No. 63;
RESULT 1317
ID ACD14116 standard; cDNA; 1227 BP.
DE Human PRO polynucleotide #213.
PN US2003032117-A1.
PD 13-FEB-2003.
Query Match 4.7%; Score 46.4; DB 8; Length 1227;
Best Local Similarity 50.0%; Pred. No. 63;
RESULT 1318
ID ACD09896 standard; cDNA; 1227 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #213.
PN US2003036128-A1.
PD 20-FEB-2003.
Query Match 4.7%; Score 46.4; DB 8; Length 1227;
Best Local Similarity 50.0%; Pred. No. 63;
RESULT 1319
ID ACC88641 standard; cDNA; 1227 BP.
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.
PN US2003027286-A1.
PD 06-FEB-2003.
Query Match 4.7%; Score 46.4; DB 8; Length 1227;
Best Local Similarity 50.0%; Pred. No. 63;
RESULT 1320
ID ACD21381 standard; cDNA; 1227 BP.

DE Human secreted/transmembrane protein (PRO) cDNA #213.
PN US2003054483-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.7%; Score 46.4; DB 8; Length 1227;
Best Local Similarity 50.0%; Pred. No. 63;
RESULT 1321
ID ABX75753 standard; cDNA; 1227 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO828.
PN US2003022298-A1.
PD 30-JAN-2003.
Query Match 4.7%; Score 46.4; DB 8; Length 1227;
Best Local Similarity 50.0%; Pred. No. 63;
RESULT 1322
ID ABX797956 standard; cDNA; 1227 BP.
DE Human PRO polynucleotide #213.
PN US2003032102-A1.
PD 13-FEB-2003.
Query Match 4.7%; Score 46.4; DB 8; Length 1227;
Best Local Similarity 50.0%; Pred. No. 63;
RESULT 1323
ID ACA97432 standard; cDNA; 1227 BP.
DE Novel human secreted and transmembrane protein PRO828 cDNA.
PN US2003036117-A1.
PD 20-FEB-2003.
Query Match 4.7%; Score 46.4; DB 8; Length 1227;
Best Local Similarity 50.0%; Pred. No. 63;
RESULT 1324
ID ACA57895 standard; cDNA; 1227 BP.
DE Human PRO828 cDNA.
PN US2003036143-A1.
PD 20-FEB-2003.
Query Match 4.7%; Score 46.4; DB 8; Length 1227;
Best Local Similarity 50.0%; Pred. No. 63;
RESULT 1325
ID ACD14423 standard; cDNA; 1227 BP.
DE Human PRO polynucleotide #213.
PN US2003032130-A1.
PD 13-FEB-2003.
Query Match 4.7%; Score 46.4; DB 8; Length 1227;
Best Local Similarity 50.0%; Pred. No. 63;
RESULT 1326
ID ACC91206 standard; cDNA; 1227 BP.
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.
PN US2003032138-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 4.7%; Score 46.4; DB 8; Length 1227;
Best Local Similarity 50.0%; Pred. No. 63;
RESULT 1327
ID ACC88948 standard; cDNA; 1227 BP.
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.
PN US2003036132-A1.
PD 20-FEB-2003.
Query Match 4.7%; Score 46.4; DB 8; Length 1227;
Best Local Similarity 50.0%; Pred. No. 63;
RESULT 1328
ID ACD07145 standard; cDNA; 1227 BP.
DE Human PRO polynucleotide #213.
PN US2003008353-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 4.7%; Score 46.4; DB 8; Length 1227;
Best Local Similarity 50.0%; Pred. No. 63;
RESULT 1329
ID ACA67596 standard; cDNA; 1227 BP.
DE Human PRO polynucleotide #213.
PN US2003017542-A1.
PD 23-JAN-2003.
Query Match 4.7%; Score 46.4; DB 8; Length 1227;
Best Local Similarity 50.0%; Pred. No. 63;
RESULT 1330
ID ACC81651 standard; cDNA; 1227 BP.

DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.
PN US2003032137-A1.
PD 13-FEB-2003.
Query Match 4.7%; Score 46.4; DB 8; Length 1227;
Best Local Similarity 50.0%; Pred. No. 63;
RESULT 1331
ID ACC89255 standard; cDNA; 1227 BP.
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.
PN US2003027269-A1.
PD 06-FEB-2003.
Query Match 4.7%; Score 46.4; DB 8; Length 1227;
Best Local Similarity 50.0%; Pred. No. 63;
RESULT 1332
ID ACC86611 standard; cDNA; 1227 BP.
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.
PN US2003027268-A1.
PD 06-FEB-2003.
Query Match 4.7%; Score 46.4; DB 8; Length 1227;
Best Local Similarity 50.0%; Pred. No. 63;
RESULT 1333
ID ACC89869 standard; cDNA; 1227 BP.
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.
PN US2003027274-A1.
PD 06-FEB-2003.
Query Match 4.7%; Score 46.4; DB 8; Length 1227;
Best Local Similarity 50.0%; Pred. No. 63;
RESULT 1334
ID ACC93048 standard; cDNA; 1227 BP.
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.
PN US2003032135-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 4.7%; Score 46.4; DB 8; Length 1227;
Best Local Similarity 50.0%; Pred. No. 63;
RESULT 1335
ID ABX80751 standard; cDNA; 1227 BP.
DE Human secreted/transmembrane protein cDNA, #73.
PN US2003027162-A1.
PD 06-FEB-2003.
Query Match 4.7%; Score 46.4; DB 8; Length 1227;
Best Local Similarity 50.0%; Pred. No. 63;
RESULT 1336
ID ACA72676 standard; cDNA; 1227 BP.
DE Human PRO polynucleotide #213.
PN US2003022295-A1.
PD 30-JAN-2003.
Query Match 4.7%; Score 46.4; DB 8; Length 1227;
Best Local Similarity 50.0%; Pred. No. 63;
RESULT 1337
ID ACA89194 standard; cDNA; 1227 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #213.
PN US2003022297-A1.
PD 30-JAN-2003.
Query Match 4.7%; Score 46.4; DB 8; Length 1227;
Best Local Similarity 50.0%; Pred. No. 63;
RESULT 1338
ID ACA69930 standard; cDNA; 1227 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #213.
PN US2003032105-A1.
PD 13-FEB-2003.
Query Match 4.7%; Score 46.4; DB 8; Length 1227;
Best Local Similarity 50.0%; Pred. No. 63;
RESULT 1339
ID ACA97073 standard; cDNA; 1227 BP.
DE Novel human secreted and transmembrane protein PRO828 cDNA.
PN US2003032123-A1.
PD 13-FEB-2003.
Query Match 4.7%; Score 46.4; DB 8; Length 1227;
Best Local Similarity 50.0%; Pred. No. 63;
RESULT 1340
ID ACA91069 standard; cDNA; 1227 BP.
DE Novel human secreted and transmembrane protein PRO828 cDNA.
PN US2003032108-A1.

PD 13-FEB-2003.
Query Match
Best Local Similarity 4.7%; Score 46.4; DB 8; Length 1227;
RESULT 1351
ID ACA74677 standard; cDNA; 1227 BP.
DE cDNA encoding human PRO polypeptide #213.
FN US2003036138-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 4.7%; Score 46.4; DB 8; Length 1227;
RESULT 1352
ID ACA70544 standard; cDNA; 1227 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #213.
FN US2003032109-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 4.7%; Score 46.4; DB 8; Length 1227;
RESULT 1353
ID ACD14730 standard; cDNA; 1227 BP.
DE Human PRO polynucleotide #213.
FN US2003040066-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 4.7%; Score 46.4; DB 8; Length 1227;
RESULT 1354
ID ACA68402 standard; cDNA; 1227 BP.
DE Novel human secreted and transmembrane protein PRO828 cDNA.
FN US2003032104-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 4.7%; Score 46.4; DB 8; Length 1227;
RESULT 1355
ID ABX98867 standard; cDNA; 1227 BP.
DE Novel human secreted and transmembrane protein PRO828 cDNA.
FN US2003036157-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 4.7%; Score 46.4; DB 8; Length 1227;
RESULT 1356
ID ACC81344 standard; cDNA; 1227 BP.
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.
FN US2003032120-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 4.7%; Score 46.4; DB 8; Length 1227;
RESULT 1357
ID ACA95668 standard; cDNA; 1227 BP.
DE Novel human secreted and transmembrane protein PRO828 cDNA.
FN US2003036155-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 4.7%; Score 46.4; DB 8; Length 1227;
RESULT 1358
ID ACD04586 standard; cDNA; 1227 BP.
DE Novel human secreted and transmembrane protein PRO828 cDNA.
FN US2003022296-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 4.7%; Score 46.4; DB 8; Length 1227;
RESULT 1359
ID ACC88027 standard; cDNA; 1227 BP.
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.
FN US2003027281-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 4.7%; Score 46.4; DB 8; Length 1227;
RESULT 1360
ID ACF12689 standard; cDNA; 1227 BP.
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.
FN US2003040058-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 4.7%; Score 46.4; DB 8; Length 1227;
PD 20-FEB-2003.

PD 13-FEB-2003.
Query Match
Best Local Similarity 4.7%; Score 46.4; DB 8; Length 1227;
RESULT 1341
ID ACA70851 standard; cDNA; 1227 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #213.
FN US2003032111-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 4.7%; Score 46.4; DB 8; Length 1227;
RESULT 1342
ID ACA95361 standard; cDNA; 1227 BP.
DE Novel human secreted and transmembrane protein PRO828 cDNA.
FN US2003032119-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 4.7%; Score 46.4; DB 8; Length 1227;
RESULT 1343
ID ACD44260 standard; cDNA; 1227 BP.
DE cDNA encoding human PRO828 polypeptide.
FN US2002127576-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 4.7%; Score 46.4; DB 8; Length 1227;
RESULT 1344
ID ACC86304 standard; cDNA; 1227 BP.
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.
FN US2003027263-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 4.7%; Score 46.4; DB 8; Length 1227;
RESULT 1345
ID ACC90176 standard; cDNA; 1227 BP.
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.
FN US2003027271-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 4.7%; Score 46.4; DB 8; Length 1227;
RESULT 1346
ID ACD12784 standard; cDNA; 1227 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #213.
FN US2003036125-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 4.7%; Score 46.4; DB 8; Length 1227;
RESULT 1347
ID ACF20014 standard; cDNA; 1227 BP.
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.
FN US2003040068-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 4.7%; Score 46.4; DB 8; Length 1227;
RESULT 1348
ID ABX76958 standard; cDNA; 1227 BP.
DE Human PRO polynucleotide #213.
FN US2003027280-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 4.7%; Score 46.4; DB 8; Length 1227;
RESULT 1349
ID ACA71290 standard; cDNA; 1227 BP.
DE Novel human secreted and transmembrane protein PRO828 cDNA.
FN US2003022300-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 4.7%; Score 46.4; DB 8; Length 1227;
RESULT 1350
ID ACA68933 standard; cDNA; 1227 BP.
DE Novel human secreted and transmembrane protein PRO828 cDNA.
FN US2003036136-A1.
PD 20-FEB-2003.

RESULT 1361
ID ABX79431 standard; cDNA; 1227 BP.
DE Human secreted/transmembrane protein cDNA, #73.
PN US2002142961-A1.
PD 03-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 4.7%; Score 46.4; DB 8; Length 1227;
Best Local Similarity 50.0%; Pred. No. 63;
RESULT 1362
ID ACA96404 standard; cDNA; 1227 BP.
DE Human PRO polynucleotide #213.
PN US2003017540-A1.
PD 23-JAN-2003.
Query Match 4.7%; Score 46.4; DB 8; Length 1227;
Best Local Similarity 50.0%; Pred. No. 63;
RESULT 1363
ID ACA65178 standard; cDNA; 1227 BP.
DE Human PRO polynucleotide #213.
PN US2003032106-A1.
PD 13-FEB-2003.
Query Match 4.7%; Score 46.4; DB 8; Length 1227;
Best Local Similarity 50.0%; Pred. No. 63;
RESULT 1364
ID ACA73904 standard; cDNA; 1227 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #213.
PN US2003032129-A1.
PD 13-FEB-2003.
Query Match 4.7%; Score 46.4; DB 8; Length 1227;
Best Local Similarity 50.0%; Pred. No. 63;
RESULT 1365
ID ACA74316 standard; cDNA; 1227 BP.
DE Novel human secreted and transmembrane protein PRO828 cDNA.
PN US2003032131-A1.
PD 13-FEB-2003.
Query Match 4.7%; Score 46.4; DB 8; Length 1227;
Best Local Similarity 50.0%; Pred. No. 63;
RESULT 1366
ID ACA96711 standard; cDNA; 1227 BP.
DE Human PRO polynucleotide #213.
PN US2003032103-A1.
PD 13-FEB-2003.
Query Match 4.7%; Score 46.4; DB 8; Length 1227;
Best Local Similarity 50.0%; Pred. No. 63;
RESULT 1367
ID ACD10817 standard; cDNA; 1227 BP.
DE cDNA encoding human PRO polypeptide #213.
PN US2003032107-A1.
PD 13-FEB-2003.
Query Match 4.7%; Score 46.4; DB 8; Length 1227;
Best Local Similarity 50.0%; Pred. No. 63;
RESULT 1368
ID ACC91513 standard; cDNA; 1227 BP.
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.
PN US2003032139-A1.
PD 13-FEB-2003.
Query Match 4.7%; Score 46.4; DB 8; Length 1227;
Best Local Similarity 50.0%; Pred. No. 63;
RESULT 1369
ID ACA93452 standard; cDNA; 1227 BP.
DE Novel human secreted and transmembrane protein PRO828 cDNA.
PN US2003032187-A1.
PD 30-JAN-2003.
Query Match 4.7%; Score 46.4; DB 8; Length 1227;
Best Local Similarity 50.0%; Pred. No. 63;
RESULT 1370
ID ACD02848 standard; cDNA; 1227 BP.
DE cDNA encoding human PRO polypeptide #213.
PN US2003032301-A1.
PD 30-JAN-2003.
Query Match 4.7%; Score 46.4; DB 8; Length 1227;
Best Local Similarity 50.0%; Pred. No. 63;
RESULT 1371
ID ACC87413 standard; cDNA; 1227 BP.

DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.
PN US2003036165-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 4.7%; Score 46.4; DB 8; Length 1227;
Best Local Similarity 50.0%; Pred. No. 63;
RESULT 1372
ID ACC85997 standard; cDNA; 1227 BP.
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.
PN US2003027262-A1.
PD 06-FEB-2003.
Query Match 4.7%; Score 46.4; DB 8; Length 1227;
Best Local Similarity 50.0%; Pred. No. 63;
RESULT 1373
ID ABX81134 standard; DNA; 1227 BP.
DE Human secreted or transmembrane protein related PCR primer #48.
PN US2003027985-A1.
PD 06-FEB-2003.
Query Match 4.7%; Score 46.4; DB 8; Length 1227;
Best Local Similarity 50.0%; Pred. No. 63;
RESULT 1374
ID ACA65485 standard; cDNA; 1227 BP.
DE Human PRO polynucleotide #213.
PN US2003032110-A1.
PD 13-FEB-2003.
Query Match 4.7%; Score 46.4; DB 8; Length 1227;
Best Local Similarity 50.0%; Pred. No. 63;
RESULT 1375
ID ACA94302 standard; cDNA; 1227 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #213.
PN US2003036142-A1.
PD 20-FEB-2003.
Query Match 4.7%; Score 46.4; DB 8; Length 1227;
Best Local Similarity 50.0%; Pred. No. 63;
RESULT 1376
ID ACA98046 standard; cDNA; 1227 BP.
DE Human PRO polynucleotide #213.
PN US2003036145-A1.
PD 20-FEB-2003.
Query Match 4.7%; Score 46.4; DB 8; Length 1227;
Best Local Similarity 50.0%; Pred. No. 63;
RESULT 1377
ID ACA91548 standard; cDNA; 1227 BP.
DE Novel human secreted and transmembrane protein PRO828 cDNA.
PN US2003036154-A1.
PD 20-FEB-2003.
Query Match 4.7%; Score 46.4; DB 8; Length 1227;
Best Local Similarity 50.0%; Pred. No. 63;
RESULT 1378
ID ACA90762 standard; cDNA; 1227 BP.
DE Novel human secreted and transmembrane protein PRO828 cDNA.
PN US2003036153-A1.
PD 20-FEB-2003.
Query Match 4.7%; Score 46.4; DB 8; Length 1227;
Best Local Similarity 50.0%; Pred. No. 63;
RESULT 1379
ID ACD16309 standard; cDNA; 1227 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #213.
PN US2003044931-A1.
PD 06-MAR-2003.
Query Match 4.7%; Score 46.4; DB 8; Length 1227;
Best Local Similarity 50.0%; Pred. No. 63;
RESULT 1380
ID ACD17470 standard; cDNA; 1227 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #213.
PN US2003036150-A1.
PD 20-FEB-2003.
Query Match 4.7%; Score 46.4; DB 8; Length 1227;
Best Local Similarity 50.0%; Pred. No. 63;
RESULT 1381
ID ACC92127 standard; cDNA; 1227 BP.
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.
PN US2003040069-A1.

PD 27-FEB-2003.
Query Match
Best Local Similarity 4.7%; Score 46.4; DB 8; Length 1227;
RESULT 1382
ID AC74984 standard; cDNA; 1227 BP.
DE cDNA encoding human PRO polypeptide #213.
PN US200302293-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 4.7%; Score 46.4; DB 8; Length 1227;
RESULT 1383
ID AC91855 standard; cDNA; 1227 BP.
DE Human PRO polynucleotide #213.
PN US2003032128-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 4.7%; Score 46.4; DB 8; Length 1227;
RESULT 1384
ID AC71499 standard; cDNA; 1227 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #213.
PN US2003032116-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 4.7%; Score 46.4; DB 8; Length 1227;
RESULT 1385
ID ACC90899 standard; cDNA; 1227 BP.
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.
PN US2003032122-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 4.7%; Score 46.4; DB 8; Length 1227;
RESULT 1386
ID AC365909 standard; cDNA; 1227 BP.
DE cDNA encoding human PRO protein #213.
PN US2003036139-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 4.7%; Score 46.4; DB 8; Length 1227;
RESULT 1387
ID AC92950 standard; cDNA; 1227 BP.
DE Novel human secreted and transmembrane protein PRO828 cDNA.
PN US2003017476-A1.
PD 23-JAN-2003.
Query Match
Best Local Similarity 4.7%; Score 46.4; DB 8; Length 1227;
RESULT 1388
ID AC95054 standard; cDNA; 1227 BP.
DE cDNA encoding human PRO polypeptide #213.
PN US2003017541-A1.
PD 23-JAN-2003.
Query Match
Best Local Similarity 4.7%; Score 46.4; DB 8; Length 1227;
RESULT 1389
ID AC16616 standard; cDNA; 1227 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #213.
PN US2003017543-A1.
PD 23-JAN-2003.
Query Match
Best Local Similarity 4.7%; Score 46.4; DB 8; Length 1227;
RESULT 1390
ID AC15695 standard; cDNA; 1227 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #213.
PN US2003036152-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 4.7%; Score 46.4; DB 8; Length 1227;
RESULT 1391
ID ABX17034 standard; cDNA; 1227 BP.
DE Human PRO polynucleotide #47.
PN US2002123463-A1.
PD 05-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match

Best Local Similarity 50.0%; Pred. No. 63;
RESULT 1392
ID ABX16798 standard; cDNA; 1227 BP.
DE Human cDNA encoding secreted/transmembrane protein #213.
PN US2002127584-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 4.7%; Score 46.4; DB 8; Length 1227;
RESULT 1393
ID AC67889 standard; cDNA; 1227 BP.
DE Novel human secreted and transmembrane protein PRO828 cDNA.
PN US2002177164-A1.
PD 28-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 4.7%; Score 46.4; DB 9; Length 1227;
RESULT 1394
ID AC97739 standard; cDNA; 1227 BP.
DE Human PRO polynucleotide #213.
PN US2003032115-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 4.7%; Score 46.4; DB 9; Length 1227;
RESULT 1395
ID AC99188 standard; cDNA; 1227 BP.
DE Novel human secreted and transmembrane protein PRO828 cDNA.
PN US2003032140-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 4.7%; Score 46.4; DB 9; Length 1227;
RESULT 1396
ID ACC91820 standard; cDNA; 1227 BP.
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.
PN US2003040076-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 4.7%; Score 46.4; DB 9; Length 1227;
RESULT 1397
ID AC11231 standard; cDNA; 1227 BP.
DE Novel human secreted and transmembrane protein PRO828 cDNA.
PN US2003008352-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 4.7%; Score 46.4; DB 9; Length 1227;
RESULT 1398
ID AC15081 standard; cDNA; 1227 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #213.
PN US2003044922-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 4.7%; Score 46.4; DB 9; Length 1227;
RESULT 1399
ID AC88338 standard; cDNA; 1227 BP.
DE Human secreted and transmembrane polypeptide PRO828 cDNA.
PN US2002197615-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 4.7%; Score 46.4; DB 9; Length 1227;
RESULT 1400
ID AC81845 standard; cDNA; 1227 BP.
DE cDNA encoding human PRO828 polypeptide.
PN US2003017981-A1.
PD 23-JAN-2003.
Query Match
Best Local Similarity 4.7%; Score 46.4; DB 9; Length 1227;
RESULT 1401
ID AC11845 standard; cDNA; 1227 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #213.
PN US2003032118-A1.

PD 13-FEB-2003.
Query Match
Best Local Similarity 4.7%; Score 46.4; DB 9; Length 1227;
RESULT 1402
ID ACF28361 standard; cDNA; 1227 BP.
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.
PN US2003068752-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 4.7%; Score 46.4; DB 9; Length 1227;
RESULT 1403
ID ACF16537 standard; cDNA; 1227 BP.
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.
PN US2003054455-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 4.7%; Score 46.4; DB 9; Length 1227;
RESULT 1404
ID ACF02655 standard; cDNA; 1227 BP.
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.
PN US2003049741-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 4.7%; Score 46.4; DB 9; Length 1227;
RESULT 1405
ID ACF02962 standard; cDNA; 1227 BP.
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.
PN US2003049743-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 4.7%; Score 46.4; DB 9; Length 1227;
RESULT 1406
ID ACF21549 standard; cDNA; 1227 BP.
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.
PN US2003049769-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 4.7%; Score 46.4; DB 9; Length 1227;
RESULT 1407
ID ACF10233 standard; cDNA; 1227 BP.
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.
PN US2003068743-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 4.7%; Score 46.4; DB 9; Length 1227;
RESULT 1408
ID ACF78126 standard; cDNA; 1227 BP.
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.
PN US2003054479-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 4.7%; Score 46.4; DB 9; Length 1227;
RESULT 1409
ID ACD46831 standard; cDNA; 1227 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #213.
PN US2003068685-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 4.7%; Score 46.4; DB 9; Length 1227;
RESULT 1410
ID ACD49594 standard; cDNA; 1227 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #213.
PN US2003068725-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 4.7%; Score 46.4; DB 9; Length 1227;
RESULT 1411
ID ACF28361 standard; cDNA; 1227 BP.
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.
PN US2003068752-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 4.7%; Score 46.4; DB 9; Length 1227;
RESULT 1412
ID ACD89051 standard; cDNA; 1227 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #213.
PN US2003068682-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 4.7%; Score 46.4; DB 9; Length 1227;
RESULT 1413
ID ACD84446 standard; cDNA; 1227 BP.
DE Human PRO polynucleotide #213.
PN US2003068701-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 4.7%; Score 46.4; DB 9; Length 1227;
RESULT 1414
ID ACD99220 standard; cDNA; 1227 BP.
DE cDNA encoding human PRO polypeptide #213.
PN US2003068755-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 4.7%; Score 46.4; DB 9; Length 1227;
RESULT 1415
ID ADA78177 standard; cDNA; 1227 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #213.
PN US2003073180-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 4.7%; Score 46.4; DB 9; Length 1227;
RESULT 1416
ID ACF48962 standard; cDNA; 1227 BP.
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.
PN US2003104539-A1.
PD 05-JUN-2003.
Query Match
Best Local Similarity 4.7%; Score 46.4; DB 9; Length 1227;
RESULT 1417
ID ACD09282 standard; cDNA; 1227 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #213.
PN US2003036131-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 4.7%; Score 46.4; DB 9; Length 1227;
RESULT 1418
ID ACF12075 standard; cDNA; 1227 BP.
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.
PN US2003040075-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 4.7%; Score 46.4; DB 9; Length 1227;
RESULT 1419
ID ACF41309 standard; cDNA; 1227 BP.
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.
PN US2003054459-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 4.7%; Score 46.4; DB 9; Length 1227;
RESULT 1420
ID ACF15923 standard; cDNA; 1227 BP.
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.

PN US200304930-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 4.7%; Score 46.4; DB 9; Length 1227;
RESULT 1430
ID ACF50497 standard; cDNA; 1227 BP.
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.
PN US200304549-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 4.7%; Score 46.4; DB 9; Length 1227;
RESULT 1431
ID ACH07968 standard; cDNA; 1227 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #213.
PN US2003049749-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 50.0%; Pred. No. 63;
RESULT 1432
ID ACF13774 standard; cDNA; 1227 BP.
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.
PN US2003064462-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 4.7%; Score 46.4; DB 9; Length 1227;
RESULT 1433
ID ACD41700 standard; cDNA; 1227 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #213.
PN US2003065159-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 50.0%; Pred. No. 63;
RESULT 1434
ID ADA37699 standard; cDNA; 1227 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO828.
PN US2003008297-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 4.7%; Score 46.4; DB 9; Length 1227;
RESULT 1435
ID ACF32113 standard; cDNA; 1227 BP.
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.
PN US2003064447-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 4.7%; Score 46.4; DB 9; Length 1227;
RESULT 1436
ID ACF23391 standard; cDNA; 1227 BP.
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.
PN US2003073184-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 50.0%; Pred. No. 63;
RESULT 1437
ID ACF40081 standard; cDNA; 1227 BP.
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.
PN US2003064463-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 4.7%; Score 46.4; DB 9; Length 1227;
RESULT 1438
ID ACD45603 standard; cDNA; 1227 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #213.
PN US2003064451-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 4.7%; Score 46.4; DB 9; Length 1227;
PN US200304930-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 4.7%; Score 46.4; DB 9; Length 1227;
RESULT 1421
ID ACF16230 standard; cDNA; 1227 BP.
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.
PN US2003040071-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 4.7%; Score 46.4; DB 9; Length 1227;
RESULT 1422
ID ACF32057 standard; cDNA; 1227 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #213.
PN US2003054471-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 4.7%; Score 46.4; DB 9; Length 1227;
RESULT 1423
ID ACF18865 standard; cDNA; 1227 BP.
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.
PN US2003064452-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 4.7%; Score 46.4; DB 9; Length 1227;
RESULT 1424
ID ACF09312 standard; cDNA; 1227 BP.
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.
PN US2003068705-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 4.7%; Score 46.4; DB 9; Length 1227;
RESULT 1425
ID ACF78433 standard; cDNA; 1227 BP.
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.
PN US2003054473-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 4.7%; Score 46.4; DB 9; Length 1227;
RESULT 1426
ID ACF52032 standard; cDNA; 1227 BP.
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.
PN US2003064440-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 4.7%; Score 46.4; DB 9; Length 1227;
RESULT 1427
ID ACF26519 standard; cDNA; 1227 BP.
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.
PN US2003068704-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 4.7%; Score 46.4; DB 9; Length 1227;
RESULT 1428
ID ACF24312 standard; cDNA; 1227 BP.
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.
PN US2003068722-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 4.7%; Score 46.4; DB 9; Length 1227;
RESULT 1429
ID ACF63623 standard; cDNA; 1227 BP.
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.
PN US2003073183-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.

Best Local Similarity 50.0%; Pred. No. 63;
RESULT 1439
ID ACF53260 standard; cDNA; 1227 BP.
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.
PN US2003068721-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.7%; Score 46.4; DB 9; Length 1227;
Best Local Similarity 50.0%; Pred. No. 63;
RESULT 1440
ID ACF727440 standard; cDNA; 1227 BP.
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.
PN US2003068699-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.7%; Score 46.4; DB 9; Length 1227;
Best Local Similarity 50.0%; Pred. No. 63;
RESULT 1441
ID ACF45278 standard; cDNA; 1227 BP.
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.
PN US2003068707-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.7%; Score 46.4; DB 9; Length 1227;
Best Local Similarity 50.0%; Pred. No. 63;
RESULT 1442
ID ACF29896 standard; cDNA; 1227 BP.
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.
PN US2003073175-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.7%; Score 46.4; DB 9; Length 1227;
Best Local Similarity 50.0%; Pred. No. 63;
RESULT 1443
ID ACD89972 standard; cDNA; 1227 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #213.
PN US2003068695-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.7%; Score 46.4; DB 9; Length 1227;
Best Local Similarity 50.0%; Pred. No. 63;
RESULT 1444
ID ACD84753 standard; cDNA; 1227 BP.
DE Human PRO polynucleotide #213.
PN US2003068703-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.7%; Score 46.4; DB 9; Length 1227;
Best Local Similarity 50.0%; Pred. No. 63;
RESULT 1445
ID ACD98913 standard; cDNA; 1227 BP.
DE cDNA encoding human PRO polypeptide #213.
PN US2003068732-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.7%; Score 46.4; DB 9; Length 1227;
Best Local Similarity 50.0%; Pred. No. 63;
RESULT 1446
ID ACF77205 standard; cDNA; 1227 BP.
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.
PN US2003082717-A1.
PD 01-MAY-2003.
Query Match 4.7%; Score 46.4; DB 9; Length 1227;
Best Local Similarity 50.0%; Pred. No. 63;
RESULT 1447
ID ACF76898 standard; cDNA; 1227 BP.
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.
PN US2003104548-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 4.7%; Score 46.4; DB 9; Length 1227;
Best Local Similarity 50.0%; Pred. No. 63;
RESULT 1448

ID ACF49883 standard; cDNA; 1227 BP.
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.
PN US2003104542-A1.
PD 05-JUN-2003.
Query Match 4.7%; Score 46.4; DB 9; Length 1227;
Best Local Similarity 50.0%; Pred. No. 63;
RESULT 1449
ID ACF50190 standard; cDNA; 1227 BP.
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.
PN US2003104543-A1.
PD 05-JUN-2003.
Query Match 4.7%; Score 46.4; DB 9; Length 1227;
Best Local Similarity 50.0%; Pred. No. 63;
RESULT 1450
ID ADA21385 standard; cDNA; 1227 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO828.
PN US2003054404-A1.
PD 20-MAR-2003.
Query Match 4.7%; Score 46.4; DB 9; Length 1227;
Best Local Similarity 50.0%; Pred. No. 63;
RESULT 1451
ID ACD09589 standard; cDNA; 1227 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #213.
PN US2003036127-A1.
PD 20-FEB-2003.
Query Match 4.7%; Score 46.4; DB 9; Length 1227;
Best Local Similarity 50.0%; Pred. No. 63;
RESULT 1452
ID ACD08668 standard; cDNA; 1227 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #213.
PN US2003040061-A1.
PD 27-FEB-2003.
Query Match 4.7%; Score 46.4; DB 9; Length 1227;
Best Local Similarity 50.0%; Pred. No. 63;
RESULT 1453
ID ACF12382 standard; cDNA; 1227 BP.
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.
PN US2003036130-A1.
PD 20-FEB-2003.
Query Match 4.7%; Score 46.4; DB 9; Length 1227;
Best Local Similarity 50.0%; Pred. No. 63;
RESULT 1454
ID ACC94890 standard; cDNA; 1227 BP.
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.
PN US2003054468-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.7%; Score 46.4; DB 9; Length 1227;
Best Local Similarity 50.0%; Pred. No. 63;
RESULT 1455
ID ACD22609 standard; cDNA; 1227 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #213.
PN US2003054470-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.7%; Score 46.4; DB 9; Length 1227;
Best Local Similarity 50.0%; Pred. No. 63;
RESULT 1456
ID ACF15309 standard; cDNA; 1227 BP.
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.
PN US2003044917-A1.
PD 06-MAR-2003.
Query Match 4.7%; Score 46.4; DB 9; Length 1227;
Best Local Similarity 50.0%; Pred. No. 63;
RESULT 1457
ID ACC97404 standard; cDNA; 1227 BP.
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.
PN US2003044929-A1.
PD 06-MAR-2003.
Query Match 4.7%; Score 46.4; DB 9; Length 1227;
Best Local Similarity 50.0%; Pred. No. 63;
RESULT 1458
ID ACC92434 standard; cDNA; 1227 BP.

DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.
 PN US2003059880-A1.
 PA (GETH) GENENTECH INC. 4.7%; Score 46.4; DB 9; Length 1227;
 Query Match
 Best Local Similarity 50.0%; Pred. No. 63;
 RESULT 1459
 ID ACF14081 standard; cDNA; 1227 BP.
 DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.
 PN US2003064465-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC. 4.7%; Score 46.4; DB 9; Length 1227;
 Query Match
 Best Local Similarity 50.0%; Pred. No. 63;
 RESULT 1460
 ID ACF14388 standard; cDNA; 1227 BP.
 DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.
 PN US2003054478-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC. 4.7%; Score 46.4; DB 9; Length 1227;
 Query Match
 Best Local Similarity 50.0%; Pred. No. 63;
 RESULT 1461
 ID ADA10172 standard; cDNA; 1227 BP.
 DE Human cDNA encoding secreted/transmembrane protein, PRO828.
 PN US2003059831-A1.
 PD 27-MAR-2003.
 PA (GETH) GENENTECH INC. 4.7%; Score 46.4; DB 9; Length 1227;
 Query Match
 Best Local Similarity 50.0%; Pred. No. 63;
 RESULT 1462
 ID ACF09619 standard; cDNA; 1227 BP.
 DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.
 PN US2003068718-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC. 4.7%; Score 46.4; DB 9; Length 1227;
 Query Match
 Best Local Similarity 50.0%; Pred. No. 63;
 RESULT 1463
 ID ACD45910 standard; cDNA; 1227 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #213.
 PN US2003064454-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC. 4.7%; Score 46.4; DB 9; Length 1227;
 Query Match
 Best Local Similarity 50.0%; Pred. No. 63;
 RESULT 1464
 ID ACD48059 standard; cDNA; 1227 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #213.
 PN US2003064461-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC. 4.7%; Score 46.4; DB 9; Length 1227;
 Query Match
 Best Local Similarity 50.0%; Pred. No. 63;
 RESULT 1465
 ID ACD67790 standard; cDNA; 1227 BP.
 DE cDNA encoding human PRO polypeptide #213.
 PN US2003068724-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC. 4.7%; Score 46.4; DB 9; Length 1227;
 Query Match
 Best Local Similarity 50.0%; Pred. No. 63;
 RESULT 1466
 ID ACF25598 standard; cDNA; 1227 BP.
 DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.
 PN US2003068727-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC. 4.7%; Score 46.4; DB 9; Length 1227;
 Query Match
 Best Local Similarity 50.0%; Pred. No. 63;
 RESULT 1467
 ID ACF29282 standard; cDNA; 1227 BP.
 DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.
 PN US2003068772-A1.

PD 10-APR-2003.
 PA (GETH) GENENTECH INC. 4.7%; Score 46.4; DB 9; Length 1227;
 Query Match
 Best Local Similarity 50.0%; Pred. No. 63;
 RESULT 1468
 ID ACD85060 standard; cDNA; 1227 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #213.
 PN US2003068714-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC. 4.7%; Score 46.4; DB 9; Length 1227;
 Query Match
 Best Local Similarity 50.0%; Pred. No. 63;
 RESULT 1469
 ID ACD84139 standard; cDNA; 1227 BP.
 DE Human PRO polynucleotide #213.
 PN US2003068758-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC. 4.7%; Score 46.4; DB 9; Length 1227;
 Query Match
 Best Local Similarity 50.0%; Pred. No. 63;
 RESULT 1470
 ID ACD88130 standard; cDNA; 1227 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #213.
 PN US2003068776-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC. 4.7%; Score 46.4; DB 9; Length 1227;
 Query Match
 Best Local Similarity 50.0%; Pred. No. 63;
 RESULT 1471
 ID ACF30817 standard; cDNA; 1227 BP.
 DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.
 PN US2003069407-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC. 4.7%; Score 46.4; DB 9; Length 1227;
 Query Match
 Best Local Similarity 50.0%; Pred. No. 63;
 RESULT 1472
 ID ACF32420 standard; cDNA; 1227 BP.
 DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.
 PN US2003104555-A1.
 PD 05-JUN-2003.
 PA (GETH) GENENTECH INC. 4.7%; Score 46.4; DB 9; Length 1227;
 Query Match
 Best Local Similarity 50.0%; Pred. No. 63;
 RESULT 1473
 ID ACH12080 standard; cDNA; 1227 BP.
 DE cDNA encoding human PRO polypeptide #213.
 PN US2003049768-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC. 4.7%; Score 46.4; DB 9; Length 1227;
 Query Match
 Best Local Similarity 50.0%; Pred. No. 63;
 RESULT 1474
 ID ACH12387 standard; cDNA; 1227 BP.
 DE cDNA encoding human PRO polypeptide #213.
 PN US2003049771-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC. 4.7%; Score 46.4; DB 9; Length 1227;
 Query Match
 Best Local Similarity 50.0%; Pred. No. 63;
 RESULT 1475
 ID ACD40779 standard; cDNA; 1227 BP.
 DE Human secreted/transmembrane protein (PRO) cDNA #213.
 PN US2003032134-A1.
 PD 13-FEB-2003.
 PA (GETH) GENENTECH INC. 4.7%; Score 46.4; DB 9; Length 1227;
 Query Match
 Best Local Similarity 50.0%; Pred. No. 63;
 RESULT 1476
 ID ADA17716 standard; cDNA; 1227 BP.
 DE cDNA encoding human PRO828 polypeptide.
 PN US2003054987-A1.
 PD 20-MAR-2003.
 Query Match
 Best Local Similarity 50.0%; Pred. No. 63;
 RESULT 1477
 ID ACF29282 standard; cDNA; 1227 BP.
 DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.
 PN US2003068772-A1.

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Best Local Similarity 50.0%; Pred. No. 63;
RESULT 1477
ID ACF18251 standard; cDNA; 1227 BP.
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.
PN US2003054481-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 4.7%; Score 46.4; DB 9; Length 1227;
Best Local Similarity 50.0%; Pred. No. 63;
RESULT 1478
ID ACF08698 standard; cDNA; 1227 BP.
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.
PN US2003049778-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 4.7%; Score 46.4; DB 9; Length 1227;
Best Local Similarity 50.0%; Pred. No. 63;
RESULT 1479
ID ACF31499 standard; cDNA; 1227 BP.
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.
PN US2003049782-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 4.7%; Score 46.4; DB 9; Length 1227;
Best Local Similarity 50.0%; Pred. No. 63;
RESULT 1480
ID ACF52339 standard; cDNA; 1227 BP.
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.
PN US2003054476-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 4.7%; Score 46.4; DB 9; Length 1227;
Best Local Similarity 50.0%; Pred. No. 63;
RESULT 1481
ID ACD50208 standard; cDNA; 1227 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #213.
PN US2003068733-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 4.7%; Score 46.4; DB 9; Length 1227;
Best Local Similarity 50.0%; Pred. No. 63;
RESULT 1482
ID ACF38911 standard; cDNA; 1227 BP.
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.
PN US2003068692-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 4.7%; Score 46.4; DB 9; Length 1227;
Best Local Similarity 50.0%; Pred. No. 63;
RESULT 1483
ID ACF26826 standard; cDNA; 1227 BP.
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.
PN US2003068709-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 4.7%; Score 46.4; DB 9; Length 1227;
Best Local Similarity 50.0%; Pred. No. 63;
RESULT 1484
ID ACF24926 standard; cDNA; 1227 BP.
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.
PN US2003068716-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 4.7%; Score 46.4; DB 9; Length 1227;
Best Local Similarity 50.0%; Pred. No. 63;
RESULT 1485
ID ACF46506 standard; cDNA; 1227 BP.
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.
PN US2003068740-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 4.7%; Score 46.4; DB 9; Length 1227;
Best Local Similarity 50.0%; Pred. No. 63;
RESULT 1486
ID ACF28054 standard; cDNA; 1227 BP.
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.
PN US2003068751-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 4.7%; Score 46.4; DB 9; Length 1227;
Best Local Similarity 50.0%; Pred. No. 63;
RESULT 1487
ID ACD89358 standard; cDNA; 1227 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #213.
PN US2003068684-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 4.7%; Score 46.4; DB 9; Length 1227;
Best Local Similarity 50.0%; Pred. No. 63;
RESULT 1488
ID ACF63930 standard; cDNA; 1227 BP.
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.
PN US2003073179-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 4.7%; Score 46.4; DB 9; Length 1227;
Best Local Similarity 50.0%; Pred. No. 63;
RESULT 1489
ID ACF60570 standard; cDNA; 1227 BP.
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.
PN US2003087374-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 4.7%; Score 46.4; DB 9; Length 1227;
Best Local Similarity 50.0%; Pred. No. 63;
RESULT 1490
ID ACH12694 standard; cDNA; 1227 BP.
DE cDNA encoding human PRO polypeptide #213.
PN US2003049773-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 4.7%; Score 46.4; DB 9; Length 1227;
Best Local Similarity 50.0%; Pred. No. 63;
RESULT 1491
ID ACH10117 standard; cDNA; 1227 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #213.
PN US2003049777-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 4.7%; Score 46.4; DB 9; Length 1227;
Best Local Similarity 50.0%; Pred. No. 63;
RESULT 1492
ID ACD03972 standard; cDNA; 1227 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #213.
PN US2003040055-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 4.7%; Score 46.4; DB 9; Length 1227;
Best Local Similarity 50.0%; Pred. No. 63;
RESULT 1493
ID ACD10510 standard; cDNA; 1227 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #213.
PN US2003036164-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 4.7%; Score 46.4; DB 9; Length 1227;
Best Local Similarity 50.0%; Pred. No. 63;
RESULT 1494
ID ACD12152 standard; cDNA; 1227 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #213.
PN US2003040074-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 4.7%; Score 46.4; DB 9; Length 1227;
Best Local Similarity 50.0%; Pred. No. 63;
RESULT 1495
ID ACF42537 standard; cDNA; 1227 BP.
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.
PN US2003054480-A1.
PD 20-MAR-2003.
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PA (GETH) GENENTECH INC.
Query Match 4.7%; Score 46.4; DB 9; Length 1227;
Best Local Similarity 50.0%; Pred. No. 63;
RESULT 1496
ID ADA27824 standard; cDNA; 1227 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO828.
PN US2003054359-A1.
PD 20-MAR-2003.
Query Match 4.7%; Score 46.4; DB 9; Length 1227;
Best Local Similarity 50.0%; Pred. No. 63;
RESULT 1497
ID ACF18558 standard; cDNA; 1227 BP.
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.
PN US2003059885-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.7%; Score 46.4; DB 9; Length 1227;
Best Local Similarity 50.0%; Pred. No. 63;
RESULT 1498
ID ACF02348 standard; cDNA; 1227 BP.
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.
PN US2003049740-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.7%; Score 46.4; DB 9; Length 1227;
Best Local Similarity 50.0%; Pred. No. 63;
RESULT 1499
ID ACF21856 standard; cDNA; 1227 BP.
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.
PN US2003049770-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 4.7%; Score 46.4; DB 9; Length 1227;
Best Local Similarity 50.0%; Pred. No. 63;
RESULT 1500
ID ACF10540 standard; cDNA; 1227 BP.
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.
PN US2003073169-A1.
PD 17-APR-2003.
Query Match 4.7%; Score 46.4; DB 9; Length 1227;
Best Local Similarity 50.0%; Pred. No. 63;